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    protein search, using sw model

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Plasmodium falcipa Plasmodium falcipa Plasmodium falcipa Human polypeptide Plasmodium falcipa

Plasmodium falcipa Plasmodium falcipa Staphylococcus epi

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Nucleolar/endosoma

Human polypeptide
Plasmodium falcipa
Drosophila melanog
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Plasmodium falcipa
Novel human diagno

Drosophila melanog Drosophila melanog Plasmodium falcipa Bacillus subtilis

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Plasmodium falcipa	Plasmodium falcipa	Malarial PfEMP3 ep	Novel human secret	Drosophila melanog	Plasmodium falcipa	Plasmodium falcipa	Human kinesin moto	Human kinesin supe	CD4-EBA175 fusion	Staphylococcus epi	Novel human protei	Carbamoy1-phosphat	Novel human diagno	Heliothis armigera	Staphylococcus aur	Novel human secret	Amino acid sequenc	Staphylococcus aur	Prostate cancer-as	Mouse ischaemic co	Human protein SEO	Staphylococcus aur
AAB18223 ABR77620	AAR46608	AAR46605	AAU31618	ABB57815	AAB18306	AAB18250	AAU79590	AAE14400	AAR41043	ABP40333	ABB97247	AAR55694	ABG17495	AAY58277	AAU34207	AAU31620	AAB84702	AAU37017	ABG61923	ABB57163	AAM78854	AAU34338
21	15	15	22	22	21	21	23	23	14	23	23	15	22	21	22	22	22	22	23	23	22	22
3135	1663	1588	2637	4097	1193	1844	1388	1388	1786	1010	1084	2391	3444	1123	2025	2986	1341	5795	1014	1327	1960	2437
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ALIGNMENTS

AC AAW54145; XX XX DT 23-SEP-1998 (first

23-SEP-1998 (first entry)
P. falciparum synthetic gp190 protein.

XX KW gp190; malaria; MSP-1; merozoite surface protein; stability; vaccine; KW monoclonal antibody; passive immunisation; parasite.

OS Plasmodium falciparum.
OS Synthetic.

XX 09-APR-1998.

02-OCT-1997; 97WO-EP05441.

PR 02-OCT-1996; 96DE-4040817. XX PA (BUJA/) BUJARD H.

A (BUJA/) BUJAKD H. X T Bujard H, Pan W, Tolle R; WPI; 1998-240088/21. N-PSDB; AAV21451, AAV35363. Recombinant production of complete gp190/MSP-1 Plasmodium surface protein - useful in anti-malaria vaccines, also stabilising genes by reducing their AT content

Example 1; Fig 3c; 48pp; German.

This sequence represents a modified Plasmodium falciparum gpl90/MSP-1 (merozoite surface) protein. The gene encoding this protein has been stabilised by reducing the AT content of the nucleotide sequence. Such a protein is useful in vaccines against malaria or for producing monoclonal antibodies (for passive immunisation). The complete gpl90 protein can now be produced outside the parasite and has, at least over extended regions, the native pattern of folding. Larger amounts of the protein can be

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TFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFD
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21-FEB-1985;
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                                                                                                                   The sequence encoding the P195 protein of Plasmodium falciparum (AAN50530) and a peptide comprising at least one of its epitopes (see AAP50777) are claimed. Also claimed is a vaccine for inducing immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new DNA sequence, together with a carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVTTSTPGSKGSVASGGSGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS
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use in vaccines against
                   Riveros-Moreno
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                                                               sequence encoding plasmodium expressing the protein for us
                  Odink K, Lockyer
LTD
                                                                                                  Claim 6; Fig 1; 51pp; English.
(WELL ) WELLCOME FOUNDATION
                 Sandhu J,
                                  WPI; 1985-224845/37
N-PSDB; AAN50530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYK
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1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 has been modified (see AAX25586) compared to the native sequence (see AAX25587) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell culture and in transgenic mice. The invention provides modified recombinant nucleic acid sequences and methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified recombinant nucleic acid sequences useful for producing malarial DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provides mountain the containing that are defined and increasing the mRNA levels and protein expression of proteins that are difficult to express in cell culture systems, mammalian cell culture systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower corganisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 protein in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
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301 DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 355
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                                                                                                                                                                                                                                                                             MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usage;
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                                                                                                        Ā
                                                                                                                                                                                                                                     Merozoite surface protein MSP-1-42.
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100.08; Pre-
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                                                                                                      AAY05832 standard; Protein; 355
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                                                                                                                                                                                                                                                                                                                   transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen LH, Meade H;
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                                                                                                                                                AAY05832;
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                                                              RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against target for the development of a vaccine against the plant and interpret of a vaccine sequence encoding MSP-1-42 has been modified (see AAX56008) compared to the native sequence (see AAX56009) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in sequence. These alterations allow MSP-1-42 to be expressed in sequence. Instability motifically to express in cell culture systems. The invention allows expression of MSP-1 protein in the milk of invention allows expression of MSP-1 protein in the milk of transgenic animals. and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1324 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1444 LNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified malarial protein for use in anti-malarial vaccines
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                    Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                   (GENZ ) GENZYME TRANSGENICS CORP.
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                                                                                                                                                                                                                                                                           98WO-US22226.
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97US-0062592
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Matches 355; Conservative
                                                                                                                                              Plasmodium falciparum.
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                                                                                                        transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                              Meade H;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Chen LH,
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This present sequence comprises a 42 kDa C-terminal portion of malaria merczoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. Nucleic acids (see AAX25586 and AAX25593) encoding MSP-1-42 have been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals. The invention provides modified recombinant nucleic acid sequences and methods for increasing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified recombinant nucleic acid sequences useful for producing
                                                                                                                                                                           NEKNYLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
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   Mismatches
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   355; Conservative
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   Matches
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Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. A nucleic acid (see AAX56008) encoding MSP-1-42 has been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals by reducing the AT content and removing mRNA instability motifs. The invention allows expression of MSP-1-42 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic
                                                                                                                  GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV
                                                                                                                                                                                                                                                                                                                     VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein for use in anti-malarial vaccines
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protein engineering; protein expression; codon usage;
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Pred. No. 4.5e-75;
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100.0%;
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Seguence Query Match

AAY09373;

AAY0937 RESULT

1564 301

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241 1504

181

98WO-US22226

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20-OCT-1998;
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                                                                                                                                                                   Gaps
         to express in cell culture systems, especially mammalian cell culture systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower corganisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk vector containing the altered MSP-1-42 nucleic acid.
mRNA levels and protein expression of proteins that are difficult
                                                                                                                                                                                                                                                                                                                                                                                                               DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Asn in native MSP-1-42 (N181Q mutation)"
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/note= "Asn in native MSP-1-42 (N2620 mutation)"
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                                                                                                                                              Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineering; protein expression; codon usage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "beta-casein signal peptide"
                                                                                                                                           22.3%; Score 1881; DB 20;
100.0%; Pred. No. 4.5e-75;
ive 0; Mismatches 0;
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                                                                                                                                                                 355; Conservative
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1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 75
                                                                                                                                                                                                                                                                                                                   The present sequence represents a 42 kDa C-terminal portion of manalaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The sequence has been modified to include an N-terminal beta-casein signal peptide and an N-terminal faxHistary. In addition, NIBIQ and N262Q mutations have been introduced eliminate 2 N-01ycosylation sites. These modifications allow the MSP-1-42 protein to be expressed in the milk of transgenic mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 VFENLAKTVLSNLLDGNLQGMLQISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG
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                                                                                                                                                                                                                               protein for use in anti-malarial vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1869; DB 20;
Pred. No. 1.6e-74;
0; Mismatches 2;
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                                                                     (GENZ ) GENZYME TRANSGENICS CORP.
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98US-0085649.
97US-0062592.
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Matches 353; Conservative
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                                                                                                                                                             WPI; 1999-288313/24.
P-PSDB; AAX56008.
                                                                                                                                                                                                                                  Modified malarial
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                                                                                                                  Chen LH, Meade H;
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15-MAY-1998;
                       20-0CT-1997;
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256 VFENLAKTVLSNLLDGNLQGMLQISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 315
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                                                                                                                                                                                                                      Merozoite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The sequence has been modified to include plasmodium falciparum. The sequence has been modified to include on N-terminal beta-casein signal peptide and an N-terminal 6xHis tag. In addition, N1810 and N2620 mutations have been introduced to eliminate 2 N-glycosylation sites. These modifications allow the MSP-1-42 protein to be expressed in the milk of transgenic mice. The invention generally relates to modified recombinant nucleic acid sequences and methods for increasing the mRNA levels and coll culture systems, mammalian cell culture systems or in cell culture systems. The preferred difficult protein candidates for transgenic animals. The preferred difficult protein candidates for transgenic animals. The preferred difficult protein candidates for expression are those derived from lower organisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGM 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEG 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 75
                                                                                                                                                                                                                                                                                                                                      New modified recombinant nucleic acid sequences useful for producing malarial DNA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (N181Q mutation)"
                                                                                                   (N262Q mutation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                         signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1869; DB 20;
Pred. No. 1.6e-74;
                                                                        /note= "Asn in native MSP-1-42
                                                                                                   /note= "Asn in native MSP-1-42
                      'note= "beta-casein
Location/Qualifiers
                                   371..376
/note= "6xHis tag"
                                                                                                                                                                                                                                             (GENZ ) GENZYME TRANSGENICS CORP.
                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 11; 43pp; English.
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                                                                                                                                                                                                       98US-0085649
97US-0062592
                                                                                                                                                                                98WO-US22225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                               WPI; 1999-302742/25.
                                                                                      Misc-difference 278
                                                                                                                                                                                                                                                                       Chen LH, Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAX25593
                                                              Misc-difference
                                                                                                                             WO9920766-A2
                                                                                                                                                                               20-OCT-1998;
                                                                                                                                                                                                       15-MAY-1998;
                                                                                                                                                                                                                      20-OCT-1997;
                                                                                                                                                       29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
 Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%; Score 1333; DB 22; Length 262; 99.6%; Pred. No. 3.2e-51; Live 0; Mismatches 1; Indels 0
surface protein; protazoacide; vaccine; malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ś
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                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                            AAB37610 standard; Protein; 262
                                                                                                                                                                                                                                                                                                                                                                                                                        Merozoite surface protein-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99GB-0009072.
99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-GB01558
                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-015762/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AA;
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us-09-269-874a-3.rag

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chromatography.
                                                                                                                                                                                                                                                                                                                                                               08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1987;
                                                                                                                                                                                                         11-NOV-1990
                                                                                                                                                                                                                                                                                                                                             28-SEP-1988
                                                                                                                                                                                                                                                                                                                           EP283829-A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                        AAP80547
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                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                           Region
                                                                                                          1610
 1430
                                   1490
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                                                                                                                                                                                                                                                                                                                                                                                Producing malaria vaccine, useful for treatment or prevention of all forms of malaria in humans, by expressing immunogenic merozoite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKIL 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKYKSDLDSIKKYI-----------NDKQGENEKYLPFLNNIETLYKTVN 1429
         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                            Major merozoite surface protein-1; MSP1-42; melittin signal peptide; malaria vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a major merozoite surface protein-1 C-terminal fragment of 42kDa (MSP1-42). This fragment is linked to amelittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a malaria vaccine, which is used to treat or prevent malaria, caused hany of the four species of Plasmodium that infect humans.
13.8%; Score 1165.5; DB 22; Length 375; 59.2%; Pred. No. 1.1e-43; ive 54; Mismatches 76; Indels 21;
                                                                                                                                            A major merozoite surface protein-1 fragment of 42kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 87-88; 95pp; English.
                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                 fragment in a baculovirus system
                                                                                       AAB83926 standard; Protein; 375
                                  VFENLAKTVLSNLLDGNLQGML 262
                                                                                                                                                                                                                                                                                                 HAWAII.
CHINESE HONG KONG
                                                                                                                                                                                                                                                                                                                                    HO WKK;
                         VFENLAKTVLSNLLDGNLQGML
                                                                                                                                                                                                                                                                      01-DEC-1999; 99US-0168327.
22-AUG-2000; 2000US-0226861.
                                                                                                                                                                                                                                                              99US-0165178.
                                                                                                                                                                                                                                            2000WO-US31064
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                (UYHA-) UNIV HAWAII.
(UYCH-) UNIV CHINESE HONG
(QUEE-) QUEEN EMMA FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                        Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                    Lap-Yin P,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-335879/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 AA;
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF89840.
                                                                                                                                                                                                        WO200134188-A1
                                                                                                                                                                                                                                           09-NOV-2000;
                                                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                          23-JUL-2001
                                                                                                                                                                                                                           17-MAY-2001
                                                                                                         AAB83926;
                                                                                                                                                                                                                                                                                                                                    Hui GSN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                           1504
                                           241
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                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The polypeptide contains at least one epitope of the 190 kD precursor of the major merozoite surface antigen of P.falciparum. The polypeptide is immunogenic and can be used in vaccines to protect against malaria. Presence of the affinity peptide allows the polypeptide to be purified by affinity chromatography resins. Antibodies raised against the polypeptide are useful for diagnosis and for purificn. by affinity
REECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSY 1609
                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNSRRTNPSDNSSDSAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHML----TLCD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                          247 TKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHLDE
                                                                                                                                                                                                   NHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide p190-3; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 913; DB 9;
Pred. No. 1.2e-32;
); Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l..7
/label=affinity peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                AAP80547 standard; protein; 355 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 28; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF ) F. HOFFMANN-LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
80.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takacs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
                                                                                                                                                                                                                                                                 PLFDGIFCSS 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gentz H,
                                                                                                                                                                                                                                                                                          PLFDGIFCSS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-272339/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide p190-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN81151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
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The polypeptide contains at least one epitope of the 190 kD precursor of the major merozoite surface antigen of P.falciparum. The polypeptide is immunogenic and can be used in vaccines to protect against malaria. Presence of the affinity peptide allows the polypeptide to be purified by affinity chromatography resins. Antibodies raised against the polypeptide are useful for diagnosis and for purificn. by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides - derived from Plasmodium falciparum 190 kD precursor useful in vaccines, and encoding DNA sequences
                                                  81 ELFDLTHHHHHLTLCDNIHGFKYLIDGYEEINELLYKLNFYYDLLRAKLNDRCANSYCQIPF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 VLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTIENINELIEESKTIDKNKNATKEEEK 128
                                                                                                                               NLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTID 264
--- TNPSDNSSDSDAKSYADLKHRVQNYLFTIKELKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 TLCDNIHGFRYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNNVCANDYCQIPFNLKIRANELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 VLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK
                                     146 QLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 KKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 905; DB 9; Lengtn Lengtn Lengtn Lengtn No. 1.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide p190-1; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..8
/label=affinity peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                              AAP80544 standard; protein; 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polypeptides -
surface antigen precursor usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF ) F. HOFFMANN-LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 26; 45pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Β,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88EP-0103564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87GB-0006599
                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.9
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gentz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-272339/39.
                                                                                                                                                                                                                                                                                                                                                            Polypeptide p190-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAN81148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromatography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1987;
                                                                                                                                                                                                                                                                                                                       11-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP283829-A.
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                                                                                                                                                                                                                                                                                    AAP80544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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46
                                                                                                             902
                                                                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 GSVASGGSVASGGSCASRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 QELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence encodes a polypeptide which contains the unique sequence of the surface antigen of P. falciparum, but lacks the immunodomlnant repeat sequences which may allow the parasite to evade and decoy the immune system. The DNA for the stage-specific late schizoint-merozoite antigen 31-1 in p31-1 (W08503725) was modified to delete the entire sequence coding for the repitope. The expression plasmid, 31-1 Repeated Delete, was introduced into E.coli K12 to produce the modified peptide. The transformant has been deposited in the Deutsche Sammlung von Microorganismen as been deposited in the Deutsche Sammlung von Microorganismen as E.coli K12 (95636cl) (p31-1 Repeat Delete). The peptide was used in compens. to treat and prevent protozoan parasitic infections.
                                     100 LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLY
                                                                                            LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLY
                   NIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKK
                                                                                                                                                                  antigen 31-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 910.5; DB 9;
Pred. No. 8.6e-33;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizont-merozoite repitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) for prodn. of antiprotozoal vaccines surface antigen sequence with deleted repitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 QELWKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTS-
                                                                                                                                                                                                                                                                                                     AAP82523 standard; protein; 219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      stage-specific late protozoan parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%;
76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87EP-0108867
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; ; p; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                               31-1 Repeated Delete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1988-030152/05.
N-PSDB; AAN82176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humbert Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1986;
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Matches 182;
                                                                                                                                                                                                                                                                                                                                         AAP82523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                 160
                                                                                            220
                                                                                                                                                                                                                                                                RESULT 12
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Plasmodium falciparum.
                                                                                           08-MAR-1988;
                                                                                                         19-MAR-1987;
                                                                            28-SEP-1988
                                                                                                                                                                                                                                                                                                          Matches 136;
                                                            EP283829-A.
                                                                                                                                      Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW36103;
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Region
                        Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSCNSRRTNPSDNSSDS 120
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                            1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFOKEKMVLNEGTSGT 60
                                                                                                                                                                                                                                                                                                The sequence encodes a Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae and Plasmodium ovale antigen which may be used in the diagnosis of malaria and as a vaccine against malaria.
                                                                                                                                                                                                                                                      - by
DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEI 174
                                                                                                                                                                                                                                                                                                                                                               ;
6
                                                                                                                                                                                                                                                      falciparum
protecting
                                                                                                                                                                                                                                                                                                                                              Length 244;
                                                                                         Storage-specific, late schizont merozoite malaria antigen.
                                                                                                                                                                                                                                                                                                                                             Score 794; DB 6; Length 24
Pred. No. 1.2e-27;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide p190-2b; P.falciparum; merozoite; vaccine.
                                                                                                                                                                                                                 Shaw A;
                                                                                                                                                                                                                                                   Prodn. of antigens of Plasmodium species, esp. of recombinant DNA methods giving polypeptide(s) for against malaria or for diagnosis.
                                                                                                                                                                                                                Cheung A,
                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP80546 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 49pp; English.
                                             AAP50304 standard; Protein; 244
                                                                                                                                                                                                                 McGarvey M,
                                                                                                                                                                                                                                                                                                                                             9.4%;
                                                                                                                                                                    85WO-GB00072.
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                              160; Conservative
                                                                                                                                                                                                                              WPI; 1985-223371/36.
N-PSDB; AAN50355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptide p190-2b
                                                                                                                                                                                                               Mach B, Perrin L,
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                               244 AA;
                                                                                                                                                                                                 (BIOJ ) BIOGEN NV
                                                                                                        Malaria; vaccine,
                                                                                                                       Plasmodium spp
                                                                                                                                                                    20-FEB-1985;
                                                                                                                                                                                  20-FEB-1984;
                                                                          22-OCT-1991
                                                                                                                                     WO8503725-A.
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                                                                                                                                                    29-AUG-1985
                                                           AAP50304;
                                                                                                                                                                                                                                                                                                                                Sequence
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                               RESULT 14
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                                      AAP50304
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polypeptides - derived from Plasmodium falciparum 190 kD precursor, useful in vaccines, and encoding DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKL
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Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 677; DB 9; Length 13.
Pred. No. 9.5e-23;
Tref. No. 9.5e-23;
Tref. No. 9.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                 /label=affinity peptide
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36103 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 27; 45pp; German
                                                                                                                                                                                                                                                                                                                                                                                             B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                      (HOFF ) F. HOFFMANN-LA ROCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic polypeptides
surface antigen precursor, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88EP-0103564
                                                                                                                                                                                                                                                                                       87GB-0006599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 95.8
ses 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                             Gentz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-272339/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN81150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromatography
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/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                  Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merozoite surface antigen 1; MSP-1; pl15MSP-1; antigen; immunogen; malaria; vaccine; Venezuela equine encephalitis virus; DVEE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                   Į,
                                                                                                                                                                                                                   Nato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 637; DB 18;
Pred. No. 3.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum MSP-1 peptide p115MSP-1.
                                                                                                                                                                                                                   Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50527 standard; Protein; 115
                                                                                                                                                                                                                   Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%;
ilarity 99.1%;
Conservative
                                                                                                   97WO-FR00291
                                                                                                                                  96FR-0001821
                                                                                                                                                                   PASTEUR.
NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2001; 2001WO-US14716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2000; 2000US-202430P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector; immunisation.
                                                                                                                                                                                                                                                                  WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA;
                                                                                                                                                                                                                                                                                     P-PSDB; AAW22592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200185927-A1
                                                                                                                                                                 (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                                                   Barnwell JW,
                                    WO9730159-A2
                                                                                                  14-FEB-1997;
                                                                                                                                  14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2001.
                                                                   21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM50527;
                                                                                                                                                                                                                                     Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50527
   Q
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                                                 /note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 KD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..95
/note= "amino acids derived from P. falciparum MSP1 p19
   p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDK¢VENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P. falciparum MSP1
                                                                                                                                                                                                                                                                                                                                                                 Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium vivax; merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immuņity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                    Nato F;
 /note= "amino acids derived from
fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 637; DB 18;
Pred. No. 3.9e-21;
1; Mismatches 0;
                                                                                                                                                                                                                                                                    Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tragment"
                                                                                                                                                                                                                                                                    Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW22592 standard; Protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PfMSP1(p19)A protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.68;
                                                                                                                                                                                 96FR-0001822
                                                                                                                                                                                                                  PASTEUR.
NEW YORK STATE.
                                                                                                                                                  97WO-FR00290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.1
Matches 113; Conservative
                                  96..116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96..116
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                                                                                                                                                                                                                                                                                                                  WPI; 1997-425033/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AA;
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT94550
                                                                                                                                                                                                                  (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                                                                                                  Barnwell JW,
                                                                                  WO9730158-A2
                                                                                                                                                  14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                purification
                                                                                                                                                                                   14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1998
                                                                                                                 21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                     Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
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                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1526
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Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VENT/) VENTER J C
                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                            108 AA;
   N-PSDB; AAC68977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18171;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                    67
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                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                             δλ
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                                                                                                                                                                                                                                                                                                                                                                                                            1002 QLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSV 1061
                                                                   Novel vaccine for immunizing mammals against Plasmodium falciparum infection, comprises a viral vector system expressing protein corresponding to specific domain of major merozoite surface protein 1 of Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSV 60
                                                                                                                                                                                          invention relates to a malaria vaccine comprising an expression vector, preferably a defective Venezuela equine encephalitis (DVEE) viral vector system, which expresses pl15MSP-1 or its immunogenic fragment after administration to a patient. The pl15MSP-1 protein or fragment raises a humoral and/or cell-mediated response to the erythrocytic merozoite malaria antigen, protecting the patient from a subsequent malaria infection. The DVEE viral vector system continues to express antigen in the patient for a period of days, amonths or even years. The pl15MSP-1 antigen may also include a signal peptide and/or an anchor peptide sequence, which enhances the immunogenic response of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1062 FFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNY 1116
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0
                                                                                                                                                   present sequence is that of immunogenic protein pl15MSP-1,
                                                                                                                                                         specific domain (amino acids 1002-1116) of the major merozoite surface protein 1 (MSP-1) of the erythrocyte stage of the West African Wellcome strain of Plasmodium falciparum. The
                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 115;
8.1e-19;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Syed S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morgan W,
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 584;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB37609 standard; Protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holder A, Birdsall B, Feeney J,
                                                                                                                             Disclosure; Page 4; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merozoite surface protein-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0311817.
99CA-2271451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Matches 115; Conservative
(GEOU ) UNIV GEORGETOWN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                         Nikodem
                                             WPI; 2002-049444/06.
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                      115 AA;
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                                                                                                                                                                                                                                                                                                                                         Sequence
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                         Davidson
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                              The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1520 NLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNG 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum chromosome 2 related protein SEQ ID NO:28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1580 GCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 560; DB 22;
Pred. No. 8.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gardner M, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 70-75; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18171 standard; Protein; 1979 AA.
Example 5; Fig 15; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.68;
94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US26796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365347/31
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consideration are useful for the development of vaccines against P. falciparum infection comprising (I) or (II).

Consideration (II) are useful for the development of vaccines against antibody raised to immunogens comprising the vaccines against antibody raised to immunogens comprising the sequences of (I), are antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of fargs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum Sequencing of the Plasmodium chromosome 2 and the campeaut identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite infectode, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18152 represent nucleotide and protein sequences given in the present inventor, but which are not specifically mentioned within the specification.
                 888888888888888888888888888888888
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1979 AA; Sequence

82; 333 321 427 492 551 535 595 648 702 759 RTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDL'TNHMLTLCDNIHGFKYLID 169 KDNELENQLKDTLKSISSLSNKIVNYESKIEELE-KELKEVKDKNI---DN------N 173 322 KNKQIDLLNKQEKEKEKEKEKEKEKEKEKEKEKEYDTLIKELKDEKISILEKVHSIKVRE 381 Gaps GYEEINELLYKLNFY---FDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRK BINNLNEKLEETINKEYTNLQNNYTNEINMLNNDIHMLNGNIĶTMNTQISTLKNDVHLLNE PLDNIKDNVGKME-----DYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKL 279 YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKN-----PPPPANS GNTPNTLLDKNKKIEEHEKE - - - IKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDI - S AKVETKESTEPNEYPNGVTYPLSYNDINNALNEL-NSFGDLINPFDYTKEPSKNIYTDNE 382 MDIEKREH-------NFLHMEDOLKDLKNSFVKNNNOLKVYKCEIKNLKTELE NEIYDSKFNNNIDLINFE-KMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME 483 TKIETQELQEMVDIKQKELDQLQEKYNAQIESI-----SIELSKKEKEYNQYKNTYIE DYSLRNIVVEKELKYYKNL-----ISKIENEIETLVENIK------KDEEQLFEK KITKDENKP---DEKILEVS-DIVKVQVQKVLLMNKIDEL-KKTQLILKNVELKHN--IH QIDKLNNEKGTLNSKISELNVQIMDLKEEKDFLNNQIVDLSNQIDLLTRKMEEKENKMLE 649 VPNSYKQE-----NKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSE PSTEGEITGQATTKPGQQAGSALE - - - GDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPP 174 DYE--NKLKEKEDFVKQKIDMLNEKEN-----EK -----KFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLL QENKYKQEMELLRGNIKSSENILNNDEEVCDLK----RKLSLKESEMKMMKEEHDKKLAE Indels 373; Length 1979; DB (21; 6.6%; Score 559.5; DB 21; 1larity 22.2%; Pred. No. 2.9e-16; Conservative 314; Mismatches 609; LKDDCDVRIREMNEKNEDKINMLKEEYEDKINTLKEQNED-Similarity RK----Matches 370; Query Match 712 110 126 334 536 296 969 703 170 227 269 390 449 493 552 g g õ g ò 셤 ò q õ g ò g ò g ò a ò g ò ద ô à ò

¥. 96

AAB37608 standard; protein;

(first entry)

27-FEB-2001 AAB37608;

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1287 INNLKKKNEDMCIKYNEMNIKYGDICVKYEEMSLTYKETSLKYEQIKVKYDEKCSOY--- 1343 1019 FDKKKTVGKYKMQIKKLTLL-----KEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAE 1073 1029 VYKKQSNAQQVDHKKKSWILLKDKSKEKIKDKENQINVEKNEEKDL----KKKDDEI-- 1081 EHILDYDEEINKSRSNLFQLKNEICSLTTEVMELNNKKN---ELIEENNKLNLVDQGKKK 1187 VEVKIKELNYLKTIQDKLADFKKNNN-----FVGIADLSTDYNHNNLLTKFLSTGMV 1504 998 961 811 MKEEYEDKMNTLN-----EQNEDKMNSLKEEYENKINQINSNNEIKIKDVV-NEY-I EEVDKLKVTLDEKKKQFDKEINYAHIKAHEKEQILLITEME--ELKCQRDNKYSDLYEKYI 962 FYNESFTNFVKSKADDINSLNDE---SKRKKLEEDINKLKKTLQLSFDLYNKYKLKERL 1074 TENTLENTKILLKHYKGLVKY----YNGESSPLKTLSEESIQTEDNYASLENFKVLSKLE VNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEV LKKDVEKQKKEIEKLNKQLTKCNKQIDELNEEVEKLNNENIELITYSNDL----NNKFDMK DDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIEN-EYEVLY----LKPLAGV DEIRFOYDEKCFOYDEINKKYGALLNINITNKMVDSKVDRNNN-----EIISVDNK--VE SIKKYINDKQGENEKYLPF - - - LNNIETLYKT - VNDK - - IDLFVIHLEAKVLNYTYEKSN FENLAKTVLSNLLDGNLQCMLNISQHQCVKKQCPQNSGCFRHLDEREECKC-----LLN KDNDKIKNLLEEAKK - - - VSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSL -----LGKNKNIYQELIGQKSSENFYEKILKDSDT 919 KLIKSICMIINIECCDDIENEDIIRRIEEYINNNKGLKKEVEEKEHKRHSSFNILKSKEK 1293 YRSLKKQLENNVMTFN-VNVK--DILNSRFNKRENFKNV-LESDLIPYK-DLTSSNYVVK DPYKFLNKEKRDKF------LSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLD TKEE-ESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFM--EIYEKEMVCNLYKL YKQ----EGDKC-----VENPNPTCNENNGGCDA-DAKCT 1588 1130 GKLKD---NLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENN-760 APVNN-KTENVSKLDYLEKLYEF-LNT--SYICHKYILVSH-KLFENILS---979 1082 1131 1178 1188 1348 1399 1505 1238 1344 1559 RESULT 21 AAB37608 1245 861 752 810 867 924 a QΥ q qq g a οχ q δ g δ qq δy g ŏ q ò g δy g Db g ò ò g Qγ οy δ QΥ δλ

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p19

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This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 KD C-terminal fragment (pl9) of MSP-1 from Plasmodium falciparum. ppl is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
                                                                                                encoded by restriction enzyme sequence used create the chimeric sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                        /note= "derived from P. falciparum C-terminal fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                      "derived from P. vivax MSP1"
                                                                                                                                                                                                                                                                                                                                      Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.4%; Score 539; DB 18;
98.9%; Pred. No. 8.6e-17;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendis K,
                 note= "signal peptide"
                                           /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                                                                                                      Barnwell JW, Longacre-Andre S,
                                                                                              /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36102 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PfMSP1(p19)S protein sequence.
                                                                                                                                                                                                                                                                  96FR-0001821.
                                                                                                                                                                                                                                       97WO-FR00291
                                                                                                                                                                                                                                                                                                          STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 98.9°
Matches 92; Conservative
                           20..127
                                                                                                                          35..127
                                                                      /note=
                                                                                                                                                                                                                                                                                            PASTEUR.
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AA;
                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW22592
                                                                                                                                                                                                                                                                                           (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                W09730159-A2
                                                                                                                                                                                                                                                                 14-FEB-1996;
                                                                                                                                                                                                           21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Peptide
                              Protein
                                                                                                                                                                                                                                                                                                                                                    Roth C;
                                                                                                                           Region
                                                         Region
                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                 fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, compared to natural MSP-1_4_9. The present sequence is the wild type MSP-1 protein. This sequence was used to generate the variants of the present invention. The non-natural variants of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
                                                                                                                                                                                                                                                                 Syed S, Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NISOHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNFTCNENNGGCDADA 60
                                                                                                                                                                                                                                                                                                                   Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing malaria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96;
                                         surface protein; protazoacide; vaccine; malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 556; DB 22;
Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN 1621
                                                                                                                                                                                                                                                              Holder A, Birdsall B, Feeney J, Morgan W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 48; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW22593 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Plasmodium vivax.
- Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PfMSP1(p19)S protein sequence
              Merozoite surface protein-1.
                                                                                                                                                                                          99US-0311817.
99CA-2271451.
                                                                                                                                                  20-APR-2000; 2000WO-GB01558.
                                                                                                                                                                            99GB-0009072
                                                                                                                                                                                                                                    (MEDI-) MEDICAL RES COUNCIL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to treat malaria.
                                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 96; Conservat
                                                                                                                                                                                                                                                                                         WPI; 2001-015762/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA;
                                                                                             WO200063245-A2.
                                                                                                                                                                             20-APR-1999;
                                                                                                                                                                                            13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1998
                                         Merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW22593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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157 LC-DNIHGFKYLIDGYE----EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 NKNATKE-----EEKKKLYQAQYDLSIYNKQ----LEEAHNLISVLEKRIDTLKKNENIK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | | : | : | : | : | 316 RNSEQYLKDIEDAEKQASTKVELFHKHETTISNIFKESEILGVETKSQKKINKAEDIMKE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|| :: | | | : | 435 EITNIKQGGEKIYSKAKDIQITTERNLIV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IERHNSEIQTQVKGFQENLNKLNE-PHNYDNAEDELNNDKSTNAKVLIETNLESVKHNLS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                  A MAEP compound having a binding affinity for a Duffy blood group antigen of primate red blood cells, is antigenic for the complete protein, and may be used in diagnosis, treatment and vaccination against invasion by p.vivax and P.knowlesi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 DISFDEKKKSIEKAYEKMGN---TLKELEKMDDEKNIEKEVEEAQIQYKRIF--IDHDVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 NELDVLKKLVFGYRKPLDNIKDNVGKMEDYI-----KKNKKTIENINELIEESKKTIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : :: : |:|| | |::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 KDKCTTEISNSKRGKD-----KIEFLEKFKPNEESNS------NKVN--INEINE--NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLORVAAMIEEAKAHKNNIDIALEDAQIDTEVSKIEQINREIMNKKDEIKSYLSEIKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 TDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLTNFEKMMGKRYSYKVE----KLTHHNT------FASYEN-----
                                                                                                                                                                                                                                                                                      Malarial apical end merozoite proteins and peptide(s) - used for developing cpds. for treating, preventing and diagnosing malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 IMNDEVEKSKIVMEKIELYKKEIDEIKQKTNEY-----KQGDT-SNFY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4%; Score 455.5; DB 11; Best Local Similarity 20.5%; Pred. No. 6.1e-12; Matches 319; Conservative 221; Mismatches 469;
                                                                                                                                                                                                                     Wertheimer SP;
               Duffy blood group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 DNSSDSDAKSYADLKHRVRNYLLTIKEL-
                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 1a; 66pp; English.
                                                                                                                         90WO-US01849
                                                                                                                                                  89US-0334270,
89US-0334041,
                                                                                                                                                                                                                     MR,
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                                                                                                                                                                                                                     Galinski
                                                                                                                                                                                          (UYNY-) NEW YORK UNIV.
                                                                                                                                                                                                                                              WPI; 1990-334616/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1254 AA;
                Malaria; vaccine;
                                          Plasmodium vivax.
                                                                                                                                                                                                                                                           N-PSDB; AAQ06328
                                                                                                                         03-APR-1990;
                                                                                                                                                                                                                     Barnwell JW,
                                                                                                                                                    06-APR-1989;
                                                                                                                                                               05-APR-1989;
                                                                   WO9011772-A
                                                                                              18-OCT-1990
                                                                                                                                                                                                                                                                                                                  infection
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 kD c-terminal fragment (P19) of MSP-1 from Plasmodium falciparum. P19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1526 NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 NISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADA 94
                                                                                                                                                 merozoite surface protein-1 p19 vaccines, diagnosis and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                        /note= "derived from P. falciparum C-terminal fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 127;
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                                                                                                                         MSP1"
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                                                                                                                                                                                                                                                                                                                                                                                   Nato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 539; DB 18;
Pred. No. 8.6e-17;
; Mismatches 0;
                                                                                                                      'note= "derived from P. vivax
                                                                                                                                                                                                                                                                                                                                                                                 Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1586 KCTEEDSGSNGKKITCECTKPDSYPLFDGIFCS 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "signal peptide"
                                                                                           'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 1254 AA.
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant protein containing the fragment - useful in anti-malarial

    Plasmodium vivax.
    Plasmodium falciparum.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                 Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                          35..127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA;
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                                                                                                                                                                                                                                                                                                                                                                                Barnwell JW,
                                                                                                                                                                                                                                 WO9730158-A2
                                                                                                                                                                                                                                                                                    14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purification
                                                                                                                                                                                                                                                                                                               14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-1991
                                                                                                                                                                                                                                                           21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
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            Chimeric
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                                                     Peptide
                                                                               Protein
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Merozoite apical-end protein; MAEP; Plasmodium vivax; antigen; malaria; human; erythrocyte; antimalarial vaccine; antibody; blood stage parasite; Duffy blood group antigen; red blood cell; therapy.

Plasmodium vivax.

US5646247-A. 08-JUL-1997

Merozoite apical-end protein clone 5.3.

(first entry)

10-NOV-1997

AAW24575;

è	536	OVE	
. q	495	TEKNRINGIDSTITNIEGALKESKONYEIGFLEKLEEIGKNEKLKVDITKKSINSTVGNE	
ογ	549	YMEDYSLRNIVVEKELKYYKNLISKIENEIFTLVENIKKDEEQLFEKKITKDEN 6	
Dp	555	SSLFNNFDLNQYDFNKNINDYENKMGEIYNEFEGSLNKISENLKNASENTSDYN 608	
ογ	603	KPDEKILEVSDIVKVQVQKVLLANKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPY	
Q C	609	SAKTLKLESFR	
Oy Dp	663	YLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNS 701 :: : : : : : : : : FIFNMKESLDKINEMIKKEQLTVNEGHGNVKQLVENIKELVDENNLSDILKQATGRNEEI 705	
οy	702		
qq	706	OKITHSTLKNKAKTILGHVDTSAKYVGIKITPBLALTELLGDAKLKTAQELKF 758	
λ P	747	PVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKI 803 :	
, è	804	THE PRESENT SCHOOL DITTENDED TO A SECOND STATE OF THE PROPERTY	
7 음	785	82	
Qy	864	YKLKDNDKIKNLLEERAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSL 923	
QQ	828	YKNKISSIKSKEEAVSVKIGNVSKKHSELSKITCSDKS	
ζ	924	KLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINS	
QQ O	866	YDNIIALEKQTELQNLRNSFTQEKTNTNSDSKLEKIKTDFESLKNALKTLEGEVNA 921	
oy Db	981	LNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIK 1033	
ò	1034	KLTLLKEOLESKLNSINNPKHVI ONFSVFFNKKKEAFTAFTFNTF NTKTIJKHYKGIV 1092	
· 6			
Qy	1093	KYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHH 1152	
Dp	1009	KNYEDTVQDVLTLNEHFNTKQVSNHEPTNFDKSNKSSEELTKAVTDSKT 1057	
οy	1153	TGNSPS	
QQ	1058	IISKLKGVIIEVNENTEM-NTIESSAKEIEALYNELKN 1094	
Qy	1213	KKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSV 1269	
qq	1095	KKTSLNEIYQTSNEVKLQEMKSNADKYID1123	
Οy	1270	NKRE	
QQ	1124	VSKIFNTVLDTQKSNIVTNQHSIN-NVKDKLKGKLQELI 1161	
οy	1330	ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKD	
Db	1162	::	
οy	1390	SEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLXKTV-NDKIDLFVIHLEAKVLN 1445	
QQ	1193	GOTNKSEHDNVAKHKEKIVHLINRVESLKGDVKNHDDDQYMKKLNASLLN 1242	

AAW24575 standard; Protein; 1254 AA.

RESULT 25 AAW24575 ID AAW2

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AAV24575 and AAV24576 represent the merozoite apical end proteins (MAEP) isolated from two different Plasmodium vivax strains. These proteins are the antigens of the invention, and immunoreact with antibodies against a native MAEP sequence. P. vivax is one of the four malarial species that infects humans, and is difficult to target for a vaccine, as it cannot be cultured in vitro. The preinvasion orientation of malarial merozoites indicates that the apical end plays an important role in the invasion process. The MAEP protein binds to the surface of susceptible crythrocytes from P. vivax susceptible humans and primates, and also binds to rabbit erythrocytes. The antigen can be used for the production of antimalarial vaccines. The antigen can be used for the production of antimalarial particularly P. vivax) blood stage parasites. Synthetic process, and are immunochemically reactive with antibodies raised antigens can be used similarly. As the antigens specifically bind to a cusceptible mammallan red blood cells), and are necessary in the process of invasion of red blood cells), and are necessary in the process of invasion of red blood cells), and are necessary in the process of invasion of red blood cells by a malarial organism. The antigens can ammalian blood cells by malarial organism in susceptible red containing the propagation of a malarial organism in susceptible red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LC-DNIHGFKYLIDGYE----EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium merozoite apical end protein – useful as antigen for production of anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18; Length 1254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%; Score 455.5; DB 18; ilarity 20.5%; Pred. No. 6.1e-12; Conservative 221; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 DNSSDSDAKSYADLKHRVRNYLLTIKEL------
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                                                                                                                                                                                                                                                                                                              91US-0792865.
89US-0334041.
89US-0334270.
90WO-US01849.
                                                                                                                                                                                                                                                                                                                                                                                 900S-0608639
                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                89US-0334041
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galinski MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-362995/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1254 AA;
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Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT80072
                                                                                                                                                                                                                                                                                                              04-OCT-1991;
05-APR-1989;
06-APR-1989;
03-APR-1990;
02-NOV-1990;
                                                                                                                                                                                                                                                                                05-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnwell JW,
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THE STATEMENTEL TREATED THE STATEMENT STATEMENTEL SESTEE STATEMENT	Qy 1093 KYYNGESSPLKTLSEE Db 1009 KNYEDTVQDVLTLNEE QY 1153 LIABLKEVIKNYYT Db 1058 IISKLKGVIIEVN QY 1213 KKPASTHVGAESNTIT Db 1095 KKTSLNEIYQTSNEVY QY 1270 IDNILSKIENEYEVIX QY 1330 ESDLIPYKDLTSSNY QY 1330 ESDLIPYKDLTSSNY QY 1340 SENKKSDLDSIKKYIF Db 1162 DADSEFF QY 1390 SENKKSDLDSIKKYIF DD 1193 QQTNKSEHDNVAKH	318	PA (VENT/) CARDNER M. XX PI HOffman S, Carucci I XX DR WPI; 2000-365347/31. XX Proteins encoded by c PT Plasmodium falciparun PT diagnosis of P.falciparu PT diagnosis of P.falciparu PT CC Disclosure; Page 75-8 XX CC The present invention CC Dy chromosome 2 of th CC Also described are: CC Also described are: CC C(1) and (II) are use: CC useful in the detecti CC useful in the detecti

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the human malarial parasite, Plasmodium falciparum.

(1) nucleotide sequences (II) encoding (I); and (2)
falciparum infection comprising (I) or (II).

seful for the development of vaccines against
tion. (I) and polyclonal antisera or a monoclonal
immunogens comprising the sequences of (I), are
tinn of infection with P. falciparum. Furthermore,
an they are rifins or secreted or membrane proteins)
                                                                                                                                                                                                     ITTSQ----NVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSV 1269
                                                                                                                                                                                                                                  : : | | :|
VKLQEMKSNADKYID-----1123
                                                                                                                                                                                                                                                                                                                                                                                                           YVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKIL 1389
SESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHH 1152
                               rgnspsenntdvnnalesykkflpegtdvatvvsesgsdtleqsQP 1212
                                                                                                                                                                                                                                                                                                       SYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVL 1329
                                                                                                                                                                                                                                                                                                                                    -----ENTEM-NTIESSAK-----EIEALYNE-----LKN 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              um; chromosome 2; human malaria parasite; vaccine; ia; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDKQGENEKYLPFLNNIETLYKTV-NDKIDLFVIHLEAKVLN 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 2 of the human malarial parasite, um, useful as antimalarial vaccines and in the iparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            um chromosome 2 related protein SEQ ID NO:29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 2485 AA.
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g g q Op 셤 g q q g q οy ò Вb δ g ŏ 셤 ò ò ογ Οý οy δ g ò g δ ŏ ŏ δý can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in subsequent identification of the Plasmodium chromsome 2 and the complexity of the parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70078 and AAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. 84; 1172 1086 721-INN----CKDDYNNILKEY 1187 919 835 | | : |:| :| | | : | ---HIKCVSSFNNTSDDISSHSSVNKKEPFFALKNNSIRHIPKENNIIYTSGKSFNHVQD 704 504 661 781 SGGSGNSRRTNPSDNSSDSAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNI 161 -----NI 604 HGFKYLIDGYEEINELLYKLNFYF---DLLRAKLNDVCANDYCQIPFN----LKIRANE 213 H-YKERKDSFKE-----NFLFFKEKILPSK-KDTCV-----FNEROKDLFEKSNE 647 LDVLKKLVFGYRKPLDNIK--DNVGKMEDYIKKNKKTIENI---NELIEESKKTI----D 264 KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINE 324 IKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN- 383 807 ----KNIDISAKVETKESTEPN--------EYPN-----GVTYPLSYNDIN 417 SNNIKSMDIFNYVKRKSNLYNNLSSNRDSTVDMHNKYNSEEYINIQRTNKIYELSNKRIR 867 Gaps NALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINE-IKEKIKIEKKKIESDKKSYE-N--YKLYSMDEIFKVSLKEKKYIDNISNNMERVTYKNEMINEKIS-----KMDDILYPC DRSKSL------NDITK-EYEKLLNEIYDSKFNNNI---------VEKELKYYKNLISKIENE--IET---LVENI------KKDEEQLFEKKITKDENK EMEKVMEKEMEKVMEKEVEKE-LKNEMNNRMNRM---NNEMKNEI---NIYKN----YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQA GSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEF LNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPV----DLTNFEKMMGKRYSYKVEKLTHHNTFAS-YENSKHNLEKLTKALKYMEDYSLRNIV----PDEKIL--EVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEP Length 2485; 543; -----NEIYVDNDKELEIVNEEKKLIYPFNYESDVHKNMNMSIN----Indels DB 21; 579; 5.4%; Score 453.5; DB 2: ilarity 20.7%; Pred. No. 1.7e-11; Conservative 257; Mismatches 579 SNSNNNNNNNISSSSSSSKKNHVIINKKISSY---Similarity 2485 AA; Query Match Best Local Simi Matches 361; Sequence 920 102 569 162 605 214 265 705 325 764 808 898 505 980 260 604 1087 662 1134 782 648 384 418 722 g 요 Q g Pp g g 임 g g g ó ð ò δ õ ò õ ŏ ò δλ g ò ò ò

1907 1992 SKLNSLNNP------KHVLQN------FSVFFNKKKEAEIAETEN 1076 ILLKIEGRSKKYSDITLYNEDKSNLEND-----NETINEYENVCSNIDVNEWEDKV 1618 KFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCL 1556 -FNIKNNIKTIIHNEE 1231 MKRIYQTINKNVFPIYNFNRYENFLINHLTYNFPKNDLFKLSYKVSMNNIRNLYIANKHI 1291 1341 KNRKDKTYLNKIFHYKKKKDARFFIN------DEIGSNDYMYDIKKKYSNDENNY 1389 FNKRENFKNVLESDLIPYKDLTSSNYVVKDPYK-FLNKEKRDKFLSSYNYIKDSIDTDIN 1377 :| :| : :::: :| SLKLESVKNSNNNCSNNKGDDNIGNÆNMTTNVTIASDEHISTKGDIHDESFSRDDNDC GNNEENNEENNEENNEENNDI EKNDIKDNNSCOVKENI IVMNNTNNMDVDNDDNNNNYNN **VVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSR** FANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVI LENKKKGYIDETNVNEN---YESDNEYDSDEDDTESDNDDEQNKENERGDEKDGYEEMNG ---KIKNLLEEAKKV IGQKS----SENFYEKILKDSDTFYNESFTNFVKSKADDINS---LNDESKRKKLEEDIN KLKKTLQLSF----DLY----NKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLE TL----ENTKILLKHYKG---LVKYYNGESSPLKTLSEESIQT-----EDNYASLENFK VLSKLEGKLK-----DNLNLEKKKLSYLSSGLHHLIAELKEVIKN--------KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHV G----AESNTITTSQNVDDEVDD------VIIVPIFGESEEDYDD----LGQ HLEAKVLNYTYEKSNV-EVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLT KG-AHGVVF-----SAWRSENVDFF------NHSFFENLN-----LNYKQEG--DKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDG STSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL KLNEKMNISMSNDEDMIPTLNSEHGNNFPSCQPNLLEKKSTY -- IDLNLYDSNSMDDFTE NQKNEPFLNYTNEKDIHMK--SNSSYNVNDKMNLFNNNEKTEKNNTS-----epidermidis open reading frame protein sequence SEQ ID NO: 2964 MYSMFDSLNNSLSQLF-MEIYEKEMVCNL-YKLKDND-VDNSCLAQKEENIFRPLFN - - LNKKDKVWKR -Ź standard; Protein; 5024 (first entry) 03-SEP-2001 AAG82935 AAG82935 1188 1568 1619 1732 1319 RESULT 27 AAG82935 ID AAG82 1292 1390 1044 1448 1077 1508 1221 1672 1259 1773 1378 1438 1868 1497 1908 1557 1936 943 1124 1164

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3853 LEYIKSLEKINNAQKSALEDKVTQSHDLLELEHLVNEGTNLNDIMGELANAIVNNYAPTK 3912
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  3322 IEDIEHAINEVNQAKKQLRGKQKLYQTIDLADKELSKLDDLTSQQSSSISNQIYTAKTRT
                                                                                                                                             EKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE
                                                                                                                                                                                    EVAQAIEKAKSLNHAMKALNKIYKNADKVLD---SSRFINE---DOPEKEAYQQAINHVD
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                                                             ---GDLINPFDYT-KEPSK-NIYTDNERKKFINEI-KEKIKI
                                                                                                                                                                                                                          ---FASYENSKHNLEKLTKALKYMEDYSLRNI-----V
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(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used to produce hosts calls which express the polypeptides. (II) wis the production of vectors containing them whitch are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the present invention. AAH55091 to AAH55098 represent invention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 779-781; 2188pp; English.
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                                                                                                                                                                                                                              99US-0164258
                                                               Staphylococcus epidermidis
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                     NKALKEAKGVLNKNSGTNVN----INDIQHLLTQIDNAKDQLNGERRLKEHQQKSEVFII 4365
                                                                                                                                   ---DVTN-----KVNSANTLTE----L 4264
                        KDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSI---DTDINFANDVLGYYKILSEKY 1393
                                                                      ----KIDLFVI 1437
                                                                                                                     1438 HLEAKVLNYTYE-----KSNVEVKI-----KELN-YLKTIQDKLADF----KKNN 1477
                                                                                                                                                                  1478 NFVGI-ADLSTDYNH----NNLLTKFLSTGMVFENLAKTVLSNLLDGN--LQGMLNISQ 1529
                                                                                                                                                                                                                 1530 HQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCV-ENPNPTCNENNGGCDADAKCT 1588
                                                                                                                                                                                                                                      4484 AQ-TKAHNDIKDTLKRQLDEIEHANATSNSKAQAKQMVNEBARKAFSNINHATSNDLVNQ 4542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3159
                                                                     1394 KSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND-
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                                                                                                                                                                                                                                                                                                                                                ABP38314 standard; Protein; 10182 AA
LATE-KSKDLKLIKGLKDLNKAQLE--
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gene therapy.
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                                                                                                  Indels 498;
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                                              Length 10182;
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                                           Ouery Match 5.3%; Score 448; DB 23; Best Local Similarity 20.6%; Pred. No. 1.6e-10; Matches 364; Conservative 250; Mismatches 651;
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                                                                                                                8861 INYI-----NADNLRKDNFTQAINNARDALNKTQGQNLDFNAIDTFKDDIFKTKDALN-G
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                                                                     ENFYEKILKDSDTFYNESFTNFVKSKADDINSLN----DESKRKKLEEDINKLKKTLQLS
                                                                                                                                                                                                     IERLTAAKSKAEKLIDSLKFINKAQFTHANDEIMNTNSIAQLSRIVNQAFDLNDAMKSLR
                                                                                                                                                                                                                                                                                                                                                                          -----LKRQFNKALKEAKGVLNKNSGTNVN----INDIQHLLTQIDNAKDQLNGERRL
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The invention relates to isolated polynucleotide (I) and probes; polypeptide (II) sequences. (I) is useful as hybridisation probes; colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags controlly the control of (II) is useful for generating antibodies against it, detecting or controlly an polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical calsorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABG00010-ABG30377 represent novel human of diagnostic mainto acid sequence data for this patient did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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	ELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMD	YNY:	FEQKYKMVLEENBRMNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE	INEIKEKIKIEKKKIEKKKIESDKKSYEDRSKSLODITKEYEKL	EOLNE	LNEIYOSKFNNNIOLTNFEKMMGRRYSYKVEKLTHHNTFAS i: : : KSDIEDNNAMAIDHO		SKHNLEKLTKALKXMEDYSLKNIVEKELKYYKNLISKIENEETL :: :: :: :: :: :: :: :		VENTO ELLO ENTINOEN - REPORTEDENTA PORTE 1 1 1 1 1 1 1 1 1	ILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK	SRTCD	KNIKTEGOSDNSEPSTEGELTGGATTKPGQQAGSALEGD	LTLEHMETERLELAQKLNENYEEVKSITKERKVLKELQKSFETERDHLRGYIREIEATGL	EQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS	: : : : : : : CARTINET : : :	HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS-	: : : : : : : : : : : : : : : : : :	LSQLFMEIYEKEMVCNLYKLKDN	:: : :	SMOPLSLTPODKPEVSANDDTSHSTNLNNSLKLFE	SKOEOSLNWKEK		GENERAL TENTENDOTE IN	TANIDA I	DESCRIPTION AND AND AND AND AND AND AND AND AND AN	KITTIKE-	ELKOPKEHRKAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEALQIERDO	NOW THE THE WIND WAS A STATE OF THE SECOND AS	LKENTKEI	LNIEKKKLSYLSSGLHHLIAELKEVIKNKYJONSPSENNTDVNNALESYKKFLPEGTDV	: : : : : : : : : : : : : : : : : :	ATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDD	: Enlre	GQVVT
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SEKTDKLSNMQ-------KDLENSNAKLQEKIQELKANEHQLI------TLKKD 1838
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                                                                               NSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTD 1375
                                                                                                                                                                                                                         35 LSTDY - - NHNNLLTKFLSTGMVFENLAKTVLSNLL - - - DGNLQGMLNISQHQCVKKQCPQ 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                       nan; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; cipheral nervous system; neuropathy; central nervous system; CNS; sheimer's; Parkinson's disease; Huntington's disease; haemostatic; obtrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; emokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                    6 INFANDVLGYYKILSEKYKSDLDSIKKYINDK-----QGENEKYLPFLN-NIETLYKT 1427
                                                                                                                                                                                                                                                                                                28 VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNY---LKTIQDKLADFKKNNNFVGIAD 1484
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Zhang J;
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ig J, Wang Z, Wehrman T, Xu C, Xue AJ,
io QA, Zhou P, Goodrich R, Drmanac RT;
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9-JUL-2000; 2000US-055317.

9-JUL-2000; 2000US-0598042.

9-JUL-2000; 2000US-0620312.

3-AG-2000; 2000US-0653450.

4-SEP-2000; 2000US-0653191.

9-OCT-2000; 2000US-063314.
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PSDB; AAI60039.
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Immunosuppressant and cytostatics activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as lateral and speripheral nervous system diseases, such as lateral alsolations of disease, Huntington's disease, amyotrophic utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disquosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constants. 82; Note: The sequence data for this patent did \mathbf{n}^{d} form part of the printed specification. LSRTCDRLABVEEKLKEKSQQLQEKQQQ---LLNVQEENSEMQENSKINEIENLKNELKNKE 1195 1024 LESVIAEKEQL---KTDLKENIEMTIENQEELRLLGDELKKQ-QEIVAQEKNHAIKKEGE 1138 336 AKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSİNLLREIDESVCSESDVFSN 498 557 --KEIKEIAKTIK--- 362 491 913 MEQLKEQLENRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESLQIERDQL 972 558 LDEFEALERKTKKDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKEDQIKK 617 ELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMD LIDGYEEI-----PFNLKINFYFDL--LRAKLNDVCANDŸCQI-----PFNLKIR-ANE ---- LKKLVFG---YRKPLDN------IKDNVGK -TID-KNKNATKEEEKKKL YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKN--ENIKELLDKINEIKNPPPANSGNT ----FNIDSLFTDPLELEY ----YLREKNKNIDISAKVËTKESTEPNEYPNGVTYPLS FEOKYKMVLEENERMNOEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE INEIKEKIK-----IEKKK----IEKKK---IESDKKSYEDRSKSLNDITKEYEKL ILKN----VELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK-------NSFGDLINPFDY-TKEPSKNIYTDNERKKF LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH----NTFAS----YEN ---SKHNLEKLTKALKYMEDYSLRNI-------VVEKELKYYKNLISKIENEIETL VENIKKDEEQLFEKKITKDEN----KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL Length 2688; Indels 559; with nootropic DB 22; 616; Juery Match 5.3%; Score 444.5; DB, Sest Local Similarity 18.4%; Pred. No. 4.6e-114atches 345; Conservative 350; Mismatches 6 MEDYIKKNKKTIENIN-----ELIEESKK----encoded polypeptides (AAM38642-AAM42213) ---DKNKKIEEHE-----126 ADLKHRVRNYLLTIKELK---YPQLFDLTNHMLT-YN-----DINNALNEL---2688 AA; PNTLL---rdv----Sequence Query Match 439 1139 337 733 363 793 413 853 453 492 167 214 238 618 279 536 582 637 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ò q a 셤 g ò g ò g δy g ò g g å g ò g ò ò g à ò 8 ò ò

1513 QEETINELRVNLSEKETEISTIQKQLEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVN 1572 ----KCLLNY-- 1559 1354 1196 LTLEHMETERLELAQKLNENYEEVKSITKERKVLKELQKSFETERDHLRGYIREIEATGL 1255 SKQEQSLNMKEK-----DNETTKIVSEMEQFKPKDSALLRIEIEMLGLSKRL---- 1454 1299 HTKLQEEI----PVLHEEQELLPNVKKVSETQETMNELELLTEQSTTKDSTTLARIEMER 990 LEEDINKLK-----KTLQLSFDLYN-KYKLKLERLFDKK-----KTVGKYKMQIK ---QLESKLNSLNNPKHVLQNFSVFFNKKK-----EAEIAETEN ELKOFKEHRKAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEALQIERDQ 1077 TLENTKILLKHYKGLVKYYNGESSPLKTLSEESI-QTEDNYASLENFKVLSKLEGKLKDN 1633 LKENTKEI-----VAKMKESQEKEYQFLKMTAVNETQEKMCEIEHLKEQFETQKLNLEN LNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDV 1850 KANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQKLHENLEEMK -----LKLERDQLKES---LQETKARDL -------ELSTGMVFENLAKTVLSN------LLDGNLQGM BEIRIVAKERDELRRIKESLKMERDQFIAT -- LREMIARDRONHOVKPEKRLLSDGQQHL EQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS --LSQLFMEIYEKEMVCNLYKLKDN-------DKIKNLLEEAKKVSTSVKTLSSS 1355 LRLNEKFQE--SQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRE----TLAKIQESQ SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFE-----NILSLGKNKNIYQELI 944 GQKSSENFYEKILKDSDTFYN----ESFTNFVKSKADDINSLNDESKR------KK -VGAESNTITTSONVDDEVDDV-1730 KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMOKDLEHSNDAL -----IIVPIFGESEEDYDDLGQVVTGEAVTPS----VIDNILSKIE----1317 SRENKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV 1437 IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKN-----NNFVGIADLSTDY HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS-----1279 --NEYEVLYLK-----PLAGVYRSLKKQLENNVMTF----NVNVKDILN------KNIKTE----GQSDNSEPSTEGEITGQATTKPGQQAGSALEGD QTKEELKIAHIHLKEHQETIDELRRSVSEKTAQIINTQDLEK-LNISQHQC--VKKQCPQNSGCFRHLDEREEC------ATVVSESGSDTLEQSQPKKPASTH-----SVMKERDNLRRVEET - - - - - -NHNNLLTK - - - - -KLTLLKE--1256 (1408 1034 1377 1945 2054 1136 1910 2112 1573 1196 069 196 847 893 1241 qq pp g g qq g g g g Db a δ g Óγ g ò qq δλ g ò g ò δ Öλ à ò ò q ò ò g $^{\circ}$ ò δ QΫ́

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 KNINTCLEYLQNDNYQYDIYSLKYFLHNYDYKETEIITNFKEKEKSLC-PFISVESKNIL 630
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                                                                                                                                                                                                     SMGFGTPHSKNEN---ENENERLYRR------NVEFNDA------DIYKKNGNI 458
                                                                                                                                                                                                                                                                                                                                                                                    KELLDKINEIKNPPPANSGN----TPNTLLDKNKKIEEHEKE------- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----YLREKNKNIDI-SAKV-----ETKESTEPNEYPNGVTYPLSYNDINNAL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NELNSFGDLINPFDYTK -- EPSKNIYTDNERKKF-INEIKEKIKIEKKKIESDKKSYED- 476
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        SQSNIKSYLHIFLTFPKLSLSNTYMNEDIITSTLQQKEYSVIF----FICSLCN----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               688 KIERKKEKNNNEMKIEINKEKNFIDNTILHPVILYNVNRLLLDFFYDKISKASIQTLIIF 747
                                                                                          --IITYEDIHKYVNCCLSINLFKLFFFF----KKNYHTNDNRNYYEHNIKMLSGSLHYF
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                                                           YLIDGYEEINEL-----LYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANE----
                                                                                                                                                                   LDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENI--NELIEESKKTID-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes proteins and their fragments (1) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (1) and polyclonal antisera or a monoclonal antised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of the plasmodium chromosome 2 and the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
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                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic. immunosuppressant and cytostatic activity. The polynucleotides are useful im gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous Injuries, peripheral nervous states, peripheral nervous factorial experiences, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chamcactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and contractions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                     Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KEIKEIAKTIK--- 362
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Yang Y,
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6.5e-11;
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                                                                                                                                                                                                                                                hen R, Ma Y,
Xu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 2242; 10078pp; English.
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18.8%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, us such as central nervous system injuries
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Wehrman T, Xu
Goodrich R,
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200005-0598042.
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Wang Z, W
Zhou P,
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Wang
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19-OCT-2000;
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Wang J, 1
Zhao QA,
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949 KSDIHDT-VNMNIDTQ-----EQLRNALESLKQHQETINTLKSKISEEVSRNLHMEEN 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990 LEEDINKLK------KTLQLSFDLYN-KYKLKLERLFDKK-----KTVGKYKMQIK 1033
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581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KNIKTE----GQSDNSEPSTEGEITGQATTKPGQQAGSALEGD-----SVQAQAQ 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFE-----NILSLGKNKNIYQELI 943
                                                                                                    YN-----DINNALNEL---------NSFGDLINPFDY-TKEPSKNIYTDNERKKF
                                                                                                                                      FEOKYKMVLEENERMNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE
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                                                                     ELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMD
                                                                                                                                                                     INEIKEKIK-----IEKKK-----IESDKKSYEDRSKSLNDITKEYEKL
                                                                                                                                                                                                                                                                                             536 ---SKHNLEKLTKALKYMEDYSLRNI-------VVEKELKYYKNLISKIENEIETL
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                                                                                                                                                                                                                                  LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH----NTFAS---
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
                                                    1826 KANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQELHENLEEMK 1885
                                                                                                                                                                                                                                                      1706 KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMQKDLEHSNDAL 1765
                                                                                                                                                                                                SVMKERDNLRRVEET-------1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
                                                                                                                                                                 SRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI
                                                                                                 --NEYEVLYLK-----PLAGVYRSLKKQLENNVMTF-----NVNVKDILN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum chromosome 2 related protein SEQ ID NO:152.
                                  --IIVPIFGESEEDYDDLGQVVTGEAVTPS----VIDNILSKIE--
                                                                                                                                                                                                                                                                                                                       1437 IHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKN 1476
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antimalarial; malaria;
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
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52; parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many 336 396 588 628 685 625 745 121 KELINNLNDISDELKNCIEQVNSVSRNMANVEKEKENIINELQILRMKNDTMRKRISKFV 180 286 NELDVIKKKLNDEEFLKEEEKKKNIDMVYKIKEYEIQIKEKENEIDSLKKNEQNLHVLKN 510 647 803 861 --KEEMGL 729 862 NLYKLKDNDKIKNLL---EEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTN 918 ELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDN----I 231 232 KD-----NVGKMEDYIKKNKKTIENINEL---IEESKKTIDKN---KNATKEEEKKKL 278 -----DILKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHE 351 KEIKEIAKTIKFNIDSLFTDPLELEYYLREK--NKNIDISÄKVETKES--TEPNEYPNGV 407 457 ----KKKIESDKKSYEDRSKSLNDITKE 487 Gaps ELILKKKNY-EELRLKINHL----ECVERDSVKIN-SEKEKGEKVIYELKEKLDNDEKII -----EEAHNLISVLE------KRI----EQEKVLKFKLYTLNNDIFSKNEKLNDMQKKLNDV-NEKYKNIVECLNNYKTEHK--EQIE 337 NEQLIKDIKDENEKMNEHVNKLONELIKRELONKCISKDIĘFCKKEKEDKIKNLEDDLLE HNLEKLTKALK----YMEDYSLRNIVVEKELKYYKNLISKIENEIETLVEN----IKKD 686 NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALĖGDSVQAQAQEQKQAQPPVP -DIVNDCEEKLKQAK----746 VPVPEAKAQVPTPPAPVNN--KTENVSKLDYLEKLYEFLNŢSYICHKYILVSHSTMNEKI · · · · · · NDLMKDME 488 YEKLLNEIYD-----SKFNNNIDLINFEKMMGKRYSYKVEKLTHHNTFASYENS----K EEQLFEKKITKDENKPDEKILEVSDIV----KVQVQKVLLMNKI-----DELKKTQLILKNV---ELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLI LKQYKITK - - EEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC Indels 354; Query Match 5.1%; Score 431; DB 21; Length 980; Best Local Similarity 23.1%; Pred. No. 5.4e-11; Matches 263; Conservative 177; Mismatches 343; Indels 354 TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIK-687 KKKEEINKLVEEKSKLEHSH-----VKIQNEMSLLVEQNEKL 648 --INNKKLTTATNMANNNMLMDENLKEKD--KKI----279 YQAQYDLSIYNKQL------EIQNKEME------980 AA; Sequence 176 7 61 238 408 397 307 181 352 287 458 538 451 589 511 629 999 626 q g q ŏ g ò a g òγ g ò g οy ò g à ò g δ . q δ q ò ò ò q ö g ŏ

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity Y-KMQIKKLTLLKEQLESKLNSL----NNPKHVLQNFSVFFNKKKEAE-IAETENTLEN 1080 979 NSLNDESKRK-----KLEEDINKLKKTLQLSFDLY--NKYKLKLERLFDKKKTVGK 1027 ------KKKNEEE----KERNEET New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess LINNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDI 814 EHQKEDRKRKDKKKKGHSSDKEEKYNKKEKTKEKSSNILFDEEYIIQLEELRDTGENCFI Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. STIAIKDMEEIKKDMEKYEEEKKKNEEERKKNEEERK----KNEEERKKNEEE---1081 TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDN-----YASLENFKVLSKLEGK Claim 20; SEQ ID No 36660; 103pp; English. Novel human diagnostic protein #6292. AA. ABG06301 standard; Protein; 2017 YT; 2001WO-US08631 2000US-0540217 2000US-0649167 (first entry) Tang WPI; 2001-639362/73. Liu C, (HYSE-) HYSEQ INC N-PSDB; AAS70488 WO200175067-A2. GNI - - - -Homo sapiens. 30-MAR-2001; 31-MAR-2000; 23-AUG-2000; biodiversity 13-FEB-2002 Drmanac RT, 11-OCT-2001 ABG06301; 1028 730 874 919 779 RESULT 34 ABG06301 g qq ò g δ Q δy

Page 29

Oy 753 AQVPTPPAPVNNKTENVSKLJ Db 953PKTLDSVTELASEV. Qy 794VSHSTMN Qy 794VSHSTMN Qy 794VSHSTMN-TTQLE Qy 827FNIQNNIPVMYSMFDSL, Qy 827FNIQNNIPVMYSMFDSL, Db 1067 VQSLNIENGSEKHDLS)	Qy 884 TSVKTLSSSSMQPLSLTPQDD 1112 KQIDQLSKDEVGKLTQITQQ Qy 939 YQELIGQKSSENFYEKILKD Db 1169 VPAVLNEKTRENSHLK	Qy 996 KLKKTLQLSFDLYNKYKLKL. :::: Db 1222 MFRETIQNLSRITEKDIETI Qy 1028 YKMQIKKLTLLKEQLESKLN. Qy 1028 YKMQIKKLTLLKEQLESKLN. Db 1282 LKQQVKKMEEMQQVMT. Qy 1088 YKGLVKYNGESSPLKTLSE Qy 1088 YKGLVKYNGESSPLKTLSE Qy 1335 YTGLIQSYEQNETKLKNFGQ	OY 1148 -SGLHHLIAELKEVIKNKNY Db 1392 PQSAECLRASKSEVL QY 1204 SDTL-EQSQPKKPASTHVGA (11:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:1:	Qy 1320 NKRENEKNYLESDLIPYK 1	Db 1758 MYSAELEKOKOLIAEWKKXTR RESULT 35 AAU00669 ID AAU00669 standard; Protei XX AC AAU00669; XX DT 07-SEP-2001 (first entry XX
and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.WIPO.int/Pub/published_pct_sequences. Sequence 2017 AA; Sequence 2017 AA; Sequence 2017 AA; Sequence 2017 AA; Sequence 2017 PA; Pred. No. 2.2e-10;	AACCHES 350; CONSERVATIVE 32, 24 SYQELVKKLEAL; 163 SYRNQLQQKEVEISHLKARQIAL; 73 VASGGSGGSV, 1	120 SDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKY	370VESTKKMEQLEDKIKDINK-KLSSAENDRDILRREGEGLNV 409 288 YNKQ-LEEAHNLISVLE	428 DLINPED-YTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYE	
88888888	7 A A A A A A A A A A A A A A A A A A A		99 09 09 09 09 09 09 09 09 09 09 09 09 0		6 6 6 6

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AESNTITTSQNVDDEV---DDVIIVPIFGESEEDYDDLGQV 1259
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                                                                                                 ELEKDEEIKSLQKTIEQIKTQLHEERQDIQTDNSDIFQETK 1066
                                                                                                                                                                                                                                                        NSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKH 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:: : || :| || |-----SESSELLQQELEELRKSLQEKDATIRTLQENHRL 1441
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SKAETERLVKGIKEREL------EIKLLNEKNISLT 1111
                                                                                                                                                                                                                                                                                                                                  IDALSOKCOTLLAVLQTSSTGNEAGGVNSNOFEELLQERDK 1281
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                                                                                                                                                                                                                              DKP-EVSA----NDDTSHSTNLNNSLKLFENILSLGKNKNI 938
                                                                         DSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDI---N 995
                                                                                                                                                      LNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVS
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LDYLEKLYEFLNTSYICHKYIL-
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Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 YQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum chromosome 2 related protein SEQ ID NO:75
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence encodes a Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae and Plasmodium ovale antigen which may be unin the diagnosis of malaria and as a vaccine against malaria.
                                                                                                                                                                                                                                                                                                                                                Prodn. of antigens of Plasmodium species, esp. of falciparum recombinant DNA methods giving polypeptide(s) for protecting against malaria or for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 424; DB 6; Le
Pred. No. 7.3e-12;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 GGSVASGGSVASGGSGASGRRTNPSDNSSDSDAKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheung A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18218 standard; Protein; 2010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 49pp; English.
                                                                                                                                                                                                                                                                McGarvey M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 5.0%;
Local Similarity 91.0%;
hes 91; Conservative
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                                                                                                                                                                                                                                                                                                 WPI; 1985-223371/36.
                                                                                                                                                                                                                                                             Mach B, Perrin L,
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CARUCCI D.
GARDNER M.
VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA;
                                                                                                                                                                                                                              (BIOJ ) BIOGEN NV
                  Malaria; vaccine.
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN50354
                                                    Plasmodium spp.
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                                                                                                                                                          20-FEB-1985;
                                                                                                                                                                                           20-FEB-1984;
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                                                                                     WO8503725-A.
                                                                                                                        29-AUG-1985.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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(CARU/)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a plasmodium vivax merozoite surface protein (MSP) C-terminal region. The C-terminal region of the merozoite surface protein has a strong antigenicity in malarial diseases. For diagnosis of malaria, recombinant proteins with hanced antigenicity, obtained by addition of fusion proteins to surface protein C-terminal regions, can be reacted with serum or blood of a Plasmodium infected patient. Antigen-antibody composites will be formed, and these are detected by Enzyme Linked Immunosorbent Assay (ELISA). The recombinant antigens provide a quick and reliable diagnosis of malaria, with good sensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene encoding merozoite surface protein of Plasmodium vivax, useful for producing protein for diagnosis of malaria and for vaccination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1425 YKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIAD 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1485 LSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCF 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECT 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S KKNEVKSSGLLEKLMKSKLIKENESKEILSQLLNVQTQLLTMSSEHTCIDTNVPDNAACY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merozoite surface protein; malaria; blood; serum; diagnosis; vaccine; antigen-antibody composite; Enzyme Linked Immunosorbent Assay; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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Plasmodium vivax merozoite surface protein C-terminal region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Storage-specific, late schizont merozoite malaria antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 424.5; DB
Pred. No. 1.6e-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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25-APR-2000; 2000KR-0022041.
20-MAY-2000; 2000KR-0027305.
                                                                                                                                                                                                           15-NOV-2000; 2000WO-KR01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1991 (first entry)
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                                                                                                                                                                                                                                                                                                               (HUMA-) HUMANBIO CO LID
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N-PSDB; AAS00655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA;
                                                                                                       Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and selectivity.
                                                                                                                                        WO200136587-A2.
                                                                                                                                                                         25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
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RESULT 36

EX BX SX B

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Gaps 84

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Length 102; Indels

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Shaw A;

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The process of the human malarial parasite, plasmodium falciparum. Also described are: (1) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against to the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, and the identification of drugs to treat or prevent P. falciparum infection, or they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the vecine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many drugs. Ana/10078 to Ana/10287 and Analasis2 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                   The present invention describes proteins and their fragments (I) encoded
                                                                                                                        Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
               Venter JC;
                                                                                                                                                                                                                                          Disclosure; Page 177-182; 577pp; English.
            Gardner M,
Hoffman S, Carucci D,
                                                                  WPI; 2000-365347/31.
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2010 AA; Seguence

87; : | ::|: | ::| | ::| | 1000 ENCMNTIDILYNDVKKNTKIDDLENIDIPIITNDKEEYHVNNSIISVLKKHNSSVYKLKK 1059 60 TAVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSD 119 854 334 394 TKES-----TEPNEYPNGVTYPLSYN-DINNALNELNSFGD-LINPFDYTKEPSKNIYT 445 446 D---NERKKFINEIKEKIKIEKKK-----IESDKKSYEDRS-----KSLNDITKEYE 489 Gaps SDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHG-----FKYLIDGYE 172 EINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFG----YRKPL 228 335 NTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDIS-AKVE 393 2 KIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGY--SLFQKEKMVLNEGTSG 59 796 LNEFSKEFKLFKFLNKNVENIDNTFNSITNIYNKYYIN-MVVHRKDCFEKKQIHSKEHMM ENSLMLKTLKTKKHHYIKKLRHHIIHNSDVYKILN--NYYKDEIFIVYDITK-----WT 229 DNIKDNVGKMEDYIKKNKKTIEN ------INELIEESKKTIDKNKNATKEEEK 276 KKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIK-NPPPANSG Query Match
4.9%; Score 414; DB 21; Length 2010;
Best Local Similarity 20.0%; Pred. No. 7e-10;
Matches 347; Conservative 283; Mismatches 588; Indels 516; 855 899 173 g ολ g ò g ŏ qq οy g g qq ολ οy ò g ò

Qy Db	490	KLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNL 540
Oy Db	541	EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVE-NIKKD 588 :: : : :
Qy Db	589	EEQLEFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLI 637
Qy Db	638	LKNVELKHNIHV-PNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIK 693 :::: :
δ.	694	AGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKA 7
oy ea	754	QVPTPPAPVNIKTENVSKLDYLEKLYEFLNTSYICHKYILVS 795
go :	1305	SLID
Oy Dp	796	HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLS-QLFMEI 854 : : :: :: : : : : NFIINVRLYEKYNKENKTTKCFIPRIILYLTHQSSILSFQSCVGI 1400
ò d	855	VCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKP 905
Qy Vy	906	ASETSLELITITATA TARATAN LENVISNNERSYCYSNAYN L STNLNNSLKLFENILSLGKNKNIYQELIGQKSS
QQ	1459	
Oy Dp	957	KDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYN 1009
ΟŸ	010	PERLFDKKKTVGKYKMOIKKLTLIKEQLESKLNSLNNPKHVLQNFSVFFNK 106
qq	1566	NKKYESYLPKCLNKIHDFK-NLFYLLCYKNNNIQDLIQLYDICLNNNY 1612
λ O	1066	KKEAEIAETENTLENTKILLKHYKGLVKYNGESSPLKTLSEESIQTEDNYA 1117 :: : : : : THIKKNMQLKEĞKKHGKRNPYGYFVKFTFNNSVPLKLKKNKLIKKYN 1659
Qy	1118	KLKDNLNLEKKKLSYLSSGLHHLIAELKEV :
qq	1660	DN - NYHNDKNNY - SDNIFYDNHDINN - NNNNNNNNNN
Oy Dp	1178	VNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEV 1237 : : : : : : NNICLKNNKNNIMHEDINANKRESLKKKKKKKKKNCIQKNNNICERK 1756
Qy	1238	IVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK 12
qq	1757	KSNIHNNSSKYIFNTVRFFKMKDIAKINTNKKCDBNSISCINNMRE 1802
Oy.	28	AGVYRSLKKQLENNVMTFNVNVKD-ILNSRFNKRENFKNVLESDLIPYKDLTS 13
QQ	1803	KRNIFKNLNRNILNFNNSNNDKYMNYIYNSTNYTYGKNYKRINKKDVH 1850
Qy Dp	1342	SNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIK 1401 :: : : : : INNILLHTYK-QHKKKKSTIISSDNNNNNNNAEDDISSRKLKFKDIKGNTK 1901
٥ý	1402	KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHL
qq	1902	

92;

523;

559; Indels

Venter JC; Venter JC; Venter JC; infection; ins the human malaria the human malaria the human malaria the human malaria the comprision glish. teins and their the normalian the sequences (il) se	Matches 363; Conservative 262; Mismatches				90 -ICKLLYYNIRPIFIFDGNPPELKR	QY 230 NIKDNVGKMEDYIKKNKKITEN QY 230 NIKDNVGKMEDYIKKNKKITEN DA 149 SMKCKNKKNINGNNTFDRATNIPDNKFNNFNKGNPNKGNPNKGNPNKGNPNKGNPNKGNPNKGN	C#1	304		Qy 360 TIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKE	Db 324 KNKENINNIYLDDDDEKEDIQNKNGVYNNDDIDEQIIRRK	Qy 410PLSYNDINNALNELNSFGDLINPFD)	Db 384 MRRPVDIIDISNYNTEMLEISETLKVHENKFKQHLNVLDF	Qy 448ERKKFINEIKEKIKEIKE	Db 444 DDLIEGGEKKSFINLINVDSCYSSSNSRLENDENIERGRI	475	504	504	DD 504 LDTSNIFLEGKDEKKVYYVNKEEIKLFLFKEINKEIF Qy 562 KELKYYKNLISKIENEIFTLVENIKKDEEG	DD 616 KEEWYTDNRIKAIKSKDDMDVFSQVQLETYVRMIKTDFE-	Qy 609 LEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELK	DD 674 LINKDLSKNTDNINIKDYNVLQKKKSKKKKKFLNDILNY	QY 659 QEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEC	Db 734 EDIKNQIDFVTQECYRNNDIIRDTHDKSDIFKN]	Qy 717 PCQQAGSALEGDSVQAQAQEGKQAQPPVPVPVPEAKAQVI	Db 774 KYEIYNLELEQEEINEKKNYNKNND	Qy 772 LDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITH	Db 814 KDLLLDDSQIFGDSLLADIKEYNYTA	Qy 832 NIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLF	Db 845NENKSLYEDGENFITRNEPITNEYEE	OY 870 DKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEV-5		DD 946 -IXXXXEKXSPRIC'LLDEFERSUDIEN
OY 1458 KELNYLKTIQDKLADFKKNNNFVGIAD DD 1936NKNNOIIG DY 1518 DGNLQGMLNISQHQCVKQCPQNSGCF AAB18195 ID 1967 DKKIKKRKKKLQKKN KKAB18195 XX AAB18195 AAB18195 XX AAB18195 XX AAB18195 XX AAB18195 XX O7-NOV-2000 (first entry) XX AB18195 XX O7-NOV-2000 (first entry) XX O7-NOV-2000 (first entry) XX WACOOUS5728-A2. XX WACOOUS5738-A2. XX CARUN/ CARUCCI D. XX WACOOUS5738-A2. XX	1458 KELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLL	1936NKNNQIIGYSIKYDKNVVSENSCSDVITSLK	1518 DGWLQGMLNISQHQCVKKQCPQNSGCFRHLDEREEC-KCLLNYKQEGDKCVENP	1967 DKKIKKRKKKLQKKNYENENIVCLDCLISYLKKMLRIYGNP	36 TIOS	1195 standard; Protein; 1516		Plasmodium falciparum chromosome 2 related protein SEQ ID	Plasmodium falciparum; chromosome 2; human malaria parasite; antimalarial; malaria; protozoacide; infection; insecticide.		_		05-NOV-1999		(HOFF/) HOFFMAN	(GARD/) GARDNER M (VENT/) VENTER J	Hoffman S, Carucci D, Gardner M, Venter		Proteins encoded by chromosome 2 of the human malarial parasite,	diagnosis of P. Talciparum infecti	o bisciosure; rade 120-124; 3//pp; English.	ine present invention describes proteins and their insymments (1) encoused. by chromosome 2 of the human malarial trassite, Plasmodium falciparum. also described are: (1) and active sequences (11) and (2).	vaccines against P. falciparum infection comprising (1) and (1). (1) and (1) are useful for the development of vaccines against	P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to imminogens comprising the seminance of (I) are	useful in the detection of infection with P. falciparum. Furthermore, (1) (especially when they are rifins or secreted or membrane proteins)	can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in	P. falciparum Sequencing of the Plasmodium right consone 2 and the subsequent identification of proteins encoded by it will help to expand	our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for	vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurrence of malaria in many	parts of the world, and there is drugs. AAA70078 to AAA70287 and	and protein sequences given in specifically mentioned within the	Sequence	Query Match 4.9%; Score 411.5; DB 21; Length 1516; Best Local Similarity 21.3%; Pred. No. 6.5e-10;

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P-QLFDLTNHMLTLCDNIHGFKYL-IDGYEEIN----ELLYKLNFYFDLLRAKLN 193
                                                                                       229
                                                                                                                                                                                                                    KNKKNDNSNNIEDKTNTPNKTNTQNKSNTPNKINADISKSSLIQIYDDIK 208
                                                                                                                                                                                                                                                                                                                                                               RIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK-IEEHEKEIKEIAK 359
                                                                                                                                                                                                                                                                                                                                                                                           ::| |:|| |:|| |::|
KLDNRNKDENNLSYSINYNKVQD----VNNNNDDDK--DKDKENINEVRRDQKNYVY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFEKMMGKRYSYKVEKLTHHNTFASY -- ENSKHNLEKLTKALKYMEDYSLRNIVVE 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYKNLISKIEN-----EIETLVENIKKDEEQLFEK-KITKDEN--KPDEKI 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JIVK----VQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYK-----QENK 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLIVLKKEIDKLKVFMPKVESLINE--EKKNIKTEGOSDNSEPSTEGEITGQATTK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LDDSQIFGDSLLAD-----IKEYNYTAD------NLDN 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NNENKSLYEDGENFITRNEPITNEYEEKNNIIYISDEOKYNEEDIIFK 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEV-SANDDTSHSTNLNNSLKLFEN 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRK 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNSLVEHVGNVPVSVKDVLTICNDDLSKIKNKIFMITDFGPVLFLGEQDGDMGTV
                            -NLKIRANELDVLK---KLVFGY--RKPLD
                                                                                                                                                                                ----DNVGKMEDYIK-----KNKKTIEN-----INELIEESK-----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIDSLFTDPLELEYYLREKN---KNIDISAKVETKESTEPNEYPNGV--TY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNDINNALNEL-----KNI-YTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IKNQIDFVTQECYRNNDIIRDTHDKSDIFKNIKIDNN------K
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                                                                                                                                                                                                                                                                        NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLE----
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                                                                                           ADYCQI-PF----
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KK-----LKKNNIEINDEMNDDIK--LLLNFFGIPYIQSPCEAEAQCSYLNNKNYCDAI 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT 1036
                                                                                                                                                                                                                                  1096 NGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIA 1155
                                                                                                                                                                                                                                                                                                                                                     ELKEVIKNKNYTGNSPSENNTDVNNALE--SYKKFLPEGTDVATVVSESGSDTLEQSQPK 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --EDYDDLGQVVTGEAVTPSVIDNILSKIE--NEYEVLYLKPLAGVYRSLKKQLENNVM- 1305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLNNI-ETLYKTVN---DKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLAD 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1301 CGCDYTIGVHGIGIVNA-LEIIKAFPN------FEDLKILKDIVSNPFRKIDKNMYNE 1351
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                                                                                                                   LLKEQL-ESKINSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYY
                                                                                                                                                     LSKDYISDVDKNHVNNIYNIERGEDERENEFVENKIQSTESHKSNEFICTEN-----
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989 KLEEDINKLKKT---
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CARUCCI D.
GARDNER M.
VENTER J C.
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the present invertice usersities proteins and utelf iragments (1) encoded according to the human malarial parasite, Plasmodium falciparum.

Also described are: (1) nucleotide sequences (II) encoding (I); and (2) accines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against C. (I) and (II) are useful for the development of vaccines against constitution in the detection of Infection with P. falciparum Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum (I) especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum (I) especially when they are rifins or secreted or membrane proteins) confection, or they can be used to identify drug resistance in the complexity of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand contraction of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for complexity of the parasitic resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many carefines of the world, and there is a pressing need for vaccines and enew carefines of the world, and there is a pressing need for vaccines and mosquito drugs. AAA70078 to AAA70287 and ABAB1814 to AABA1835 represent nucleotide sections and protein sequences given in the present invention, but which are not specifically mentioned within the specification. 105; present invention describes proteins and their fragments (I) encoded NVGKMEDYIKKNKKT-IENINE----LIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIY 288 NV-----FISSYKKTNIININENSIYLIDSSDKENDRPMSSKRKRESK------ 232 293 TNMKRKNILLPHTGNKSESIRVIYASCLSSNKIYLRNINMCYDVVVFIKILRDLHF--PI 350 129 KHRVRNYLL--TIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFD 186 ELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDL--IN 431 |: :| || :: | || 351 MLKG--RKIDKYIDNIINIQKKVYSEEMEKIDDEKRFTSVESINNSFN-INNMENIFRIQ 407 PFDYTK-----EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITK 486 ----MM 513 Gaps 131 INETYLSLHIKDVIHNLYVSNYIVYLNYLVLFNPVHISKIKKNIL-IQIPMDIILKVLCP L----LRAKLNDVCANDYCQ---IPFNLKIRANELDV--LKKLVFGYRKPLDNIK----D -----PANSGNTPNTL-----LDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPL parasite, and in the 4.8%; Score 408.5; DB 21; Length 2539; ilarity 19.1%; Pred. No. 1.6e-09; Conservative 314; Mismatches 619; Indels 761; EY-----FKLLNEIYDSKFNN-----NIDLTN-----FEK-----NKQLEEAHNLISVLEKRI------DTLKKNENIK-ELLDKINEIKNPP-Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines Venter JC; Disclosure; Page 126-133; 577pp; English. diagnosis of P.falciparum infection -ΣÌ Gardner à Carucci WPI; 2000-365347/31. 2539 AA; Similarity Matches 400; Hoffman S, Sequence Query Match Local 187 289 234 190 374 487 465 512 g δλ οp Db g Q ò 줨 δ ò Вþ ò οy δ δλ 合 ò

	1348	1372	Qy 1427 TVNDKIDLFVIHL Db 1735 DVKRKRYISLYMYNKKG	Qy 1466 IQDKLADFKKNNNFVGIA : : Db 1792NNIIDMYKRNNFIYKDI			QY 1586 KCTEEDGSNGKKITCEC DD 1961 NNKDNQHTSTKKKIOKKV	RESULT 40 AAE00425 ID AAE00425 standard; Prot.	XX AC AAE00425; XX XX 19-JUN-2001 (first ent		EST; therapy; st Plasmodium falci			XX XX PD 19-APR-2001.	,	YX (KEKE-) KES & DEV INST XX PI Long DM, Metz AM, Lov- XX DR WPI; 2001-266411/27.	DK N-PSDB; AADU3/29. XX XX Telomerase reverse tran
525 LPLLCLYICKQNIKAQEENKTKIKYIILKGCKQMENVRIIHPLVNVLRKCFKYIKIKYLK 584 514 GKRYSYKVEKLTHHNTFASYENSKHNLEKLTK- 545	546 ALKYMEDYSLRNIVVEKELK-YYKNLISKIENEIETLVENIKKDEE 590	591 QLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKİDELKKTQLILKNVELKHNI 647 	** 648 HVPNSYKQENKQEPYYLIVLKKEIDKLKVPMPKVESLINBEKKNIKTEG- 696	697TGOATTKPGQQAG 722 :::::::::::::::::::::::::::::::::::	SALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLD : : :	774 -YLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKI-TKËEESKLSSCDPLDLLFNIQN 831	832 NIPVMYSMFDSLNNSLSQLFMEIYEREMVC	869NDKIKNILEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNN- 921 1028 YQKDIXNYYLLNILLLVGVKIXIRQHŅKLNKESEXNVNSQNL 1069	922SLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFT 968 1070 IGSKSKSSKIYMVHFITSEISFNKKKILRPFYKIQKKINNKYKRIIMNQSAHINIKESKN 1129	969 NFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015 : : : : : :	1016 ERLFDKKKTVGKYKMQIK	1054HVLQNFSVFFNKKREAEIAETENTLENTKILLKHYKGLVKYNGESSPLKTL 1105 : : : : : : : : : : : : :	1106 SEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIK 1162 :::	1163NKN	1188 FLPEGTDVATVVSESGSDTLEQSOPKKPASTHVGAESNTIT 1228	1229 TSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNIL-SKIENEYEV :	1284 LYLKPLAGVYRSLKKOLE 1301 1516 CCMNKLTKENMEMNNVIITKNNNNDNNNENNENNENNENNENNENNENNDNNNNNN 1569
do Qy Db	Qy Db	Oy Db	O O	oy og	φ. _d	Oy Dp	Oy Db	oy D	O.y D.b	Q.	oy D	Qy Db	Q D	Oy Db	Oy Dp	Oy Dp	දු පු

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:LESEK---YKSDLDSIKKYINDKQGEN-EKYLPFLNNIETLYK 1426
:::|:|:|||||||
:KIDDTLNVHKEEIDTSKQHTDEKICKKIQKY-----LYL 1734
NISQH----- 1530
                                                                                                                                                                                                                                                                                                                                                                   ------EAKVLNYTYEKSNVEVKIKELNYLKT 1465
                                                                                                                                                                                                        GRDTNNKNIQKKKKKEEEKKQISYNISSKHNSILNNRMKY--- 1791
                                                                                                                                                                                                                                              AD----LSTDYNHN-----NLLTKFLSTGMVFENL 1508
                                                                                                                                                                                                                                                                                                                                      DIDEYILKDEIKFDKLSISDFRYYEYVTFISSLYLAFYILTFD 1905
                                                             -- DPY -- KFLNKEKRDKFLS------SYNYIKDS 1371
                                                                                                                                                                                                                                                                    inscriptase genes and proteins from Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               se reverse transcriptase full length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                : | :: | |:| VSFSDVCEIYVDGPNFENKNYDDNIFYTN-KGITF 2013
                                                                                                                                                                                                                                                                                                                                                                                                                               CTKPDSYPLF------DGIFCSSSNFLGISF 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nscriptase; TERT; ever shorter telomere; cancer; malaria; vaginal candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              = Asp, Gly "Encoded by GWT"
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94; falciparum and Candida albicans are used to detect infections of these 265 DFFSEDRKEKSSSVGYDXKKKNXSNIKRFHNKINRTKEEKKKK-------WNKIIIN 362 AHNLIS-----VLEKRI--DTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLD 342 472 KTKILKY----VYNYFKEFINNVIN--TKFGKIYRKF------FPRKHILNKI 512 KEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKR 516 SDNSSDS--DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHG-FKYLIDG 170 253 294 414 343 KNKKIEEHEKEI-KEI-AKTIKFNIDSLFTDPLELEYY----LREKNKNIDISAKVETKE 396 415 HNNFIDEYKQKICKQIKCSTKKNDISHIITSRKENHLFHVQKLENNYKHPNINKQL---R 471 STEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEI 456 Gaps The invention relates to identification and use of telomerase reverse transcriptuse (TERT) genes and proteins isolated from Plasmodium falciparum. Candida albicans and rice. TERT gene is also called as ever shorter telomere (EST) gene. TERT gene is are used to detect P. falciparum and C. albicans infection in mammals. They are also used to diagnose the state of an infection in a patient and the relative amount of the pathogen in a cell, tissue, organ or organism. The potential binding partners and modulators of the activity of TERT genes and proteins are used to inhibit or promote growth of the pathogens and hence are used to treat e.g. stomach cancer, malaria and vaginal candidiasis in LVFGYRKPLDNI -----KDNVGKMEDYIKKNKKT -- IENINELIEESKKTIDK --------N--NATKEEEKKKLYQAQYDLSIYNKQLEE YEEINELLYKLNFYFDLLR------AKLNDVCANDYCQIPFNLKIRANELDVLKK Length 2184; The present sequence is Plasmodium falciparum TERT full length Indels Score 402.5; DB.22; Pred. No. 2.5e-09; Best Local Similarity 20.4%; Pred. No. 2.5e-09; Matches 362; Conservative 268; Mismatches 585; Page 104-111; 138pp; English 4.8%; pathogens in mammals 2184 AA Claim 10; Sequence Query Match protein. mammals 254 295 148 220 997 313 363 513 171 397 457 qq g ŏ q δ g qq В qq ò ò g ò ò οy ò

1091 1134

KLIHRIKNIIIKQNSGIVKNKDKTFLHLIKNKSNKNNNNK-KKNKNNYNNNNINN--NNN 1005 1252 DYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMT-FNVN 1310 ADDINSLND------ESKRKKLEEDIN--KLKKTLQLSFDLYNKYKLKLERLFDKKK 1023 VKD-----ILNSRFNKREN----FKNVLESDLIPYKDLTSSNYVVKDPYKF 1352 1395 SDLDSIKK-YIND-KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSN 1452 1024 TVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKI 1083 NLNLEKK--KLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALE-SYKKFLPE 1191 1353 LNKEKRDKFLS----SYNYI------KDSIDTDINFANDVLGYYKILSEKYK 1394 : ||: | : | | | ||||:||: KIYIYKI---KNIIEKRNFMLKLNSINH-------FISKKLRIN------GTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEE |: : : ||| : : : |||
1243 CYEHINHNYLFK-ILKNFFDNI-----NNFEFIYL--FKRSFRLYNKNLNNSFLSYYPVN LQVDKRDIF#TIITVIRYYYLNIYFSIKEFKLNRKNIFYFQIFQENQMKGVY--LSVRDK LAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCV ENPNPTCNENNGGCDAD --- AKCTEEDSGSN ---- GKK ITCECTKPDSYPLFDG I FCSSS FLNTSYICHKYILV-----SHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI--QN KIKT----NKYIFIKKMKKKSTNKCINNKFSKKCIPKKKKN------LYNITRHN ----IKNLLEEAKKVS TSVKTL-----SSSSMQPLSLTPQDKPEV-----SANDDTSHSTNLN 889 FALKKMYIHMRMAKEEKSNIKLERAFKHFFIFAQEKEHILKYFSSHFFQNRKINYGKRFN NSLKLFENIL-----SLGKNKN-IYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSK LLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK-----VLSKLEGKLKD-1453 VEVKIKELNYLKTIQ----DKLADFKKNNNFVG-IADLSTDYNHNNLLTKFLSTGMVFEN GDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLY - -NIPVMYSM - - FDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK ------NNSWNECYVKDI 756 NFCLYHQIFRNKKL----1058 792 949 1345 1508 1568 727 781 832 884 975 1084 1092 1192 1205 1311 1621 1577 921 1135 1522 δ g qq Dp ò g δy d ŏ g ŏ g δy g ŏ Dp δ Op ò ŏ q ò δ q Qy q δy a οy q ò g οy g ò g 556 563 615 999 620 DNLNNSFKIKTTLFNKLRRKYFNKIKKINIAIQKRHLMNRL----IYFLFN----YFIMP 722 LKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALE 726 ----FTK-----IS 755 YSYKVEKLTHHNTFASYE-----NSKHNLEKLTKALK-----YMEDYSLRNIVVEKE ------KVLLMNKI-----DELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIV LK-YYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQ--LIRRF----FFLTKSEQTLH---KTIFFDRKIWNH-----

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73 KNMTINIMLLQNENKKIIKETCYIKNVTNKIYHTLFLVINKHYHNILCSLSFENNSFEI 132	217 LKKLVFGYRKPLDNIKDNVCKMEDVIKKNKKTIENINELIEESKKTIDKNKNATKEEEKK 276 133 IN	277 KLYQAQYDLSIYNKQLEBAHNLISVLEKRIDTLKKNENIKEL	177	319 LDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYY 378 :	379	273 NEEKNEKINEEKNEDTUKDPYEKENDNIPLGDHHSVQYNIFTFSILNK 321	435 YTKEPS-KNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYE	322KEPDLKKIQFSNIILPIKKMIICPYDEKIIILLSHKSIVYIITNKNNDDLKNMF	490 KLLNEIYDSKFUNNIDLTRFEKMGKRYSYK -VEKLTHYFF 530 1 :	531	436 KSRNLYISFKTKEIVCFKIRYYEIPLTVFKKIQTTEGNYIDAKYLFRKRPRYINTNHNQS	542 KLTYKALKYMEDYSLKNIVVEKELKYYKNLLSKIENZETLVENI D8D :	586 KKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLANKIDELKKTQLILKNVEL	200 ONNUINTELEDGETUNDERNN NUORANOEOA TIANTENNAN TAMBARATATATATATATATATATATATATATATATATATATA	044 KHNIHYPNSYKQENKQEPYILIVIKAELOKLKVVMPKVESLINEEKKNI 09Z 	693KTEGQSDNSEPSTEGEITGQATTKPGQC	651 HLYFLKKKKKKKKKKNDENVIKLLDFVSI	746 VPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSY	683INLHKYILNNITSFYIMSKYLFVLLDNGLLYYTKKN	734 ICYYKNINKIVDIKIINEHDIYYMDKKHILKNHSLKNNYLNIINTKEKI-QSYNIF	815	789 SMLENCTCIFLSLNDGSFYFINITKHKILLY;ENLQNFSNLGHNQIYCNFKKN	867 KDNDK.KNLLEEAKKVSTSVKTLSSSSMOPLSLTPORKPEVSANDDTSHST 917 1 1 1 1 1 1 1 1 1 1	918	901 NILYKNKEKNQNGNENIINMKRQKESSNYILYNFYLKTLNKDYVCLLCSDK 952	962FY	1060 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 1081 - 10	1013 VENYHYDDDDDDNKSYPLYTRNIFFCSIKNTNIVYAKCIGNYMIVADYYLNITFYYIKDN 107
<u>а</u>	O _Y	- K	qa	yo .	Qy	qq	Qy	ପ୍ର	Qy da	δy	q _Q	ò á	Q V (3 6	δο Q	QY	qa	QY	Q (λ d —	Qy	qa	Qy	Qy	qa	Oy do	Qy	q _O
	RESULT 41 AAB18265 LD AAB18265 standard; Protein; 2013 AA.	AAB18265;	DT 07-NOV-2000 (first entry) XX DE Plasmodium falciparum chromosome 2 related protein GEO TD NO.122	Plasmodium falciparum; chromosome antimalarial; malaria; protozoaci	XX OS Plasmodium falciparum.	XX PN W0200025728-A2.		05-NOV-1999;	05-NOV-1998; 9 (HOFF/) HOFFMAN	PA (CARU/) CARUCCI D. PA (GARD/) GARDER M. PA (VENIT/) VENTER J C.	XX PI Hoffman S, Carucci D, Gardner M, Venter JC;	AX DR WPI; 2000-365347/31	PT Proteins encoded by chromosome 2 of the human malarial parasite, PT Plasmodium falciparum, useful as antimalarial vaccines and in the PT diagnosis of P.falciparum infection .		AA The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum.					cc r. tattipatum: sequencing of the frammodum chipunosome a muu che CC subsequent identification of proteins encoded by it will help to expand CC our understanding of parasite biology, a process hampered by the	COMP Vacc		CC and protein sequences given in the present invention, but which are not CC specifically mentioned within the specification. XX	Sequence 2013 AA;	Query Match Best Local Similarity 19.5%; Pred. No. 32e-09; Matches 366: Conservative 235: Mismatches 593: Indels 684: Gaps 85:	LCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAK 191	Db 15 ISDNIFCFLKDGYICFMNLLNNEKKYLYITCSQDBGYVAQYYFDVVKCRYEKKEEDCN 72 Ov 192LNDVCANDYCOIPFNIKIRANELDV 216	

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1127 NHNMQNMAQRFFFLKRKKLKNKTEFNDNMIKEDKLEEKINEDFVITEEGEKKSNKKI-KN 1185
                                                                                                                                                                     : : || :|| :|| 1416 KNFFEDIVCMEKKYIENNKNNNEKMNIKVDININMNMPTHYNIILKNKIILLINDVEKTKCI 1475
 ---KLER----LFDKKKTVGKYKMQIKKLTLLKEQLESKL--NS 1048
                                  1073 FNNYYMSSGETPSSFFVSHKLEEPCVYKMKKKKEKQKYTCN-----MKEESESKIDYST 1126
                                                                                                                                                                                                                                                                                                                             1306 KKNFLLLRNNIKEDEEAIIKQKEKDHSTICNPKLIQNQQNDQTYNTKCVEENVFNVTINS 1365
                                                                                                                                                                                                                                                                                                                                                                     DDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN---ILSKIENEYEVLYL-KPL 1289
                                                                                                                                                                                                                                                                                                                                                                                                        1366 NEHISFYLSKWIIEDNNTSY-----YINDSLIKNMNIVFLKIKNDISQNYTNRKR 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----YKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSS----Y 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IETLYKTVNDKIDLFVIHLEAKVLN----YTYEKSNVEVKIK-----ELNYLKTIQDK-- 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LADFKKNNNFVGIADLSTDY------NHNNLLTKFLSTGMVFENLAKTV 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1642 ILNKIDFLSAFKKNLYVVNFYNNQTGYKFCNYISYPSNKSNHLSNEKSNFSSYNNLSSY- 1700
                                                                        1049 LNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEE 1108
                                                                                                                                            SIQTEDNYASLENFKVLSKLEGKLKDN ---- LNLEKKKLSYLSSGLHHLIAELKEVIKNK 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1476 EPONNNHNINNKEIEFKQISNMD----KLNEEKTYILKDKNYIIHNKNTNYFFDNETIIF 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plus end-directed microtubule motor activity; chromosome congression; microtubule binding activity; chromosome movement; mitosis; cell proliferation; tumor; metastasis; vascular malfunction; inflammatory disease; immune disease; anglogenesis; hypertension; restenosis; fungal infection; selective herbicide; fungicide; insecticide; plant growth regulator; activator; cancer cell marker.
                                                                                                                                                                                                                                                                                             ------DVATVVSESGSD-----TLEQSQPKKPASTHVGAESNTITTSQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1366 NYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of centromere-associated protein-E (CENP-E)
                                                                                                                                                                                                                                                                                                                                                                                                                                            1290 AGVYRSL----KKQLENN-----VMTFNVNVK-----DILNSRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          centromere-associated protein-E; ATPase activity;
                                                                                                                                                                                                                     1165 N----YTGNS---PSENNTDV-----NNALESYKKFLPEGT-----
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 1008 YNKYKL---
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87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1113 FPITPLSDSLPPSKLVEGNSQDPIEINDYHNLIALATERNNIMVCLETERNSLKEQVIDL 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- KKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEY 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ADLKHRVRNYLLTIKELKYPQLFDLTNHM---LTLCDNIHGFKYLIDGYEEINELLYKLN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963 VTCLSEYKFLPNEVECLKNQISKASEEIMLLKQEGEHSASIIS--KQEIIMQEQSEQILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKVEKLTHHNTFASYENSKHNLEKL--TKALKYMEDYSLRNIVVEK------ELK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 FYFDL----LRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLRSENLELKEKMEDT-SNWY-----NQKEKAASL-----FEKQLETEKSNYKKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 E-DYIKKNKKTIENINEL------NKNATKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903 EADLOKELOSAFNEINYLNGLLAGKVPRDLLSRVELEKKVSEFSKOLEKALEEKNALENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1173 NTQLQSLQAQSIEKS--DLQKPKQDLEEGEVKLLLE-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2954;
                                                                                                                                                                                                                                   Centromere-associated protein-E and related nucleic acid
                                                                                                                                    Wood KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.7%; Score 393; DB 20;
Best Local Similarity 19.3%; Pred. No. 9.3e-09;
Matches 341; Conservative 325; Mismatches 583;
                                                                                                                                    Sakowicz R,
                                                                                                                                                                                                                                                                           Claim 5; Page 66-67; 77pp; English
                                                                                                                                  Cleveland DW, Goldstein LSB,
                98WO-US19231.
                                                     97US-0058645.
                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                       WPI; 1999-229233/19.
N-PSDB; AAX26819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer cells.
                                                     11-SEP-1997;
                10-SEP-1998;
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0y D	566	YYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIV 615 :: :: :
οy	616	HNIHVPNSYKQENKQEPYYL 664
QQ	1321	ANQEKVSLGEVNSLQSEMLRGERDELQTSCKALVSELELL-RAHV-KSVEGENLEITKKL 1378
γο	665	TEGEITGOATTKPGQQ 720
g	13/9	
ογ ·	721	QPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYE 780
g	1435	KAAEERL
ð	781	Д
<u>a</u> ,	1400	
λo i	823	LDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEE 878
α ,	1521	
Ši i	α / α	927
QQ	1556	ILKENIDTTLKHHSDTQAQ-LQKTQQELQLAKNLAIAASDNCPITQEKETSADCVHPLEE 1614
δ	928	GKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADD 977
Q Q	1615	KILLLTEELHQKTNEQEKLLHERNELEQAQVELKCEVEHLMKSMIESKS-S 1664
70 4	978	101
a a	1992	LESLOHEKHDTEQOLLALKOOMQVVTOEKKELQOTHEHLTAEVDHLKENIELGLNFKNEA 1724
οy	1012	SVFFN I
QQ	1725	QQKTTKEQCLLNENKELEQSQHRLQCEIEELMKSLKDKESALETLKESEQKVINLN 1780
οy	1065	KKKEABIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKV 1124
qq	1781	QEMEMVMLEMEELKNSQRTVIAERDQLQDDLRESVEMSIETQDDLRKAQEA 1831
ΟŻ	1125	LSKLEGKLKDNLNLERKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNN- 1180
g	1832	LQQQKDKVQELTSQISVLQEKISLLENQMLYNVATVKETLSERDDLNQSKQHLFSEIETL 1891
οy	1181	STHVGAE 1223
QQ	1892	SLSLKEKEFALEQAEKDKADAARKTIDITEKISNIEEQLIQQQATNLKETLYERESLIQCK 1951
δy	1224	S
QQ	1952	EQLALNTEHLRETLKSKDLALGKMEQERDEAANKVIALTEKMSSLEEQINENVTTLKE 2009
ò	1277	LAGVYRSLKK
Dp	2010	GEGEKETFYLQRPSKQQSSSQMEELRESLKTKDLQLEEAFKEISEATNEIKNLTAKISSL 2069
οy	1314	ILNSRENKENFKNVLESDLIPYK-DLTSSNYV 1345
QQ	2070	ERENLRHSKQQLVS
δ	1346	z
QQ	2130	ASLAEEIKILTKE-MDEFRDSKESLQEQSSHLSEELCTYKTELQMLKQQKEDINNK 2184
γ	1404	ÍADKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHL-EAKULNYTY-EKSNVEVKIKELN 1461
QQ	2185	LAEKVKEVDELLOHLSSLKEOLDOIOMELRNEKLRNYELCEKMDIMEKEIS 2235

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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. C Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

C vaccines against P. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against comprising the sequences of (I); are useful in frection. (I) and polyclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, and the identification of fargs to treat or prevent P. falciparum complexity of the plasmodium chromosome 2 and the infection, or they can be used to identify are resistance in cour understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite biology, a process hampered by the complexity of the parasite infection, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new cross the world, and there is a pressing need for vaccines and new can protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                       2296 AHKHCMINIKESLSSTLSRSFGSLQTEHVKLNTQLQTLLNKFKVVYRTAAVKEDHSLIKD 2355
1462 YLKTIQ-----DKLAD----FKKNNNFVG--IADLSTDYNHNNLLTKFLSTGMVFE-- 1506
                         2236 VLRLMQNEPQQEEDDVAERMDILESRNQEIQELMEKISAVYSEQHTLLSSLSSELQKETE 2295
                                                                             ---ISQHQCVKKQ 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum chromosome 2 related protein SEQ ID NO:37.
                                                                                ----NTAKTVLSNL------LDGNLQGMLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gardner M, Venter JC;
                                                                                                                                                                                       1537 CPQNSGC--FRHLDEREECKCLLNYKQEGDK 1565
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                                                                                                                                                                                                                                                                                                       AAB18180 standard; Protein; 2295 AA
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200025728-A2.
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AAB18180
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SQ 'Sequence 2295 AA; Query Match 4.6%; Score 388.5; DB 21; Length 2295; Best Local Similarity 19.9%; Pred. No. 1.1e-08; Matches 370; Conservative 282; Mismatches 591; Indels 615; Gaps 98;	178 LYKLNEYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNV 235	57 GENDELSSYVPREVDEKKKNKKDIDSKENSKSGNNIYNKDNTKNNEDVN 106 283 YDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLD 342 ::::: : : 342 ::::: : :	KNKKIEBHEKEIKE-IAKTIKFNIDSLFTDPLELEYYLREK-NKNIDISAKVETKESTEP :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	401 NEYPNGVTYPLSYNDINNALNELNEFGEDLINPFDYTKEPSKNIYTDNERKKFI-NEIK 457 208	245 ENIYIRHPIVSLERWYNNFKLIETCFDKNNPIYYIDENK-IYSYKVNYKLMLNLESSENF 303 501 NNNIDLTNFEKMMGKRYSYKVEKLTH	HILEKLIKALKYMEDYSLRILVOKKELKYYKNLISKIENEIETLVENIKKDEEQL HILEKLIKALKYMEDYSLRILVVEKELKYYKNLISKIENEIETLVENIKKDEEQL HILL HI	593 FEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNS 652 1 : : :: ::	653 YKQENKQEPYZLIVLKKEID-KLK-VFMP-KVESLINEEKKNIKTEGQSD 699 	700NSEPSTEGELT	742 PPVPVPVPDEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICH 789	790 KYILVSHSTMMEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSL 847 : .	848 SQL-FMEIYEKEMVCNLYKLKDNDKIKNLLEEBAKKVSTSVKTLSSSSMQPLSLTPQDKPE 906 ::	907 VSANDDTSHSTALLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKIL- 956 	-KDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL ::	1016ERLFDKKKTVGKYKMQIKKLTLIKEQLESKLNSLNNPKHVLQNFSV 1061

Y 604 PDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYY 663	704 673 748	1	974 PYNSNNVISYTNNKGHKNFDINKLKKTLQLSFDLYNKYKLKLEELFDKKK	OY 1024 TYGKYMOIKKILLKEQLESKINSLNNKHVLQNFSVERNKKE 1068 1	QY 1080NTKILLKHYKGLVKYYNGESSPLKTLS-EESIQTEDNYASLENFKVLSK 1127 DD : 	QY 1175 NTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVD 1234 Db 1266 NTNIMNQIDTKDQISKNLHDLSTNNNMDQKHGALQKMHMNEKTNQD 1311 QY 1235 DEVDDVIIVPLFGESEEDXDDLGQVVTGEAVTPSVIDNIL 1274 DD 1312 KPLNDEEIL-IENRDDONVNKINCKVINKKNSCAYTKMVSFFKTPIIIFFFLLCLNEKVL 1370	OY 1275 SKIENEYEVLYLKPLAGVYRSLKRQLENNVMTFNVNVKDILNSRFNKRENFRNVLES 1331
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PN W09949048-A1. XX PD 30-SEP-1999. XX PF 25-MAR-1999; 99WO-AU00213. XX XX XX XX XX XX XX XX XX XX XX XX XX	PA (MENZ-) MENZIES SCHOOL HEALTH RES. XX PI Kemp DJ, Trenholme KR, Gardiner DL, Holt DC, Cowman AF; XX DR WPI; 1999-591099/50. XX PT New proteins useful for treatment of Plasmodium infections in humans, PT especially malaria.	PS Disclosure; Page 90-115; 150pp; English. XX XX XX XX XX CC Cone (see also AAZ20056) on chromosome 3 of Plasmodium falciparum. CC gene (see also AAZ20056) on chromosome 3 of Plasmodium falciparum. CC gene (see also AAZ20056) on chromosome 3 of Plasmodium falciparum. CC dene on chromosome 9 gene of P. falciparum. CLAG9 facilitates CC asexual gene 9 (CLAG9) protein (see AAX31945) encoded by the clag9 CC gene on chromosome 9 gene of P. falciparum. CLAG9 facilitates CC cells. The identification of clag genetic species, and the CC products encoded by them, enables a range of therapeutic agents to CC products encoded by them, enables a range of therapeutic agents to CC be rationally designed and/or identified that are useful for the CC exacerbated by infection with plasmodium spp., e.g. malaria, CC especially in humans.	SQ Sequence 4134 AA; Query Match A.6%; Score 387.5; DB 20; Length 4134; Best Local Similarity 21.1%; Pred. No. 2.4e-08; Matches 357; Conservative 245; Mismatches 525; Indels 567; Gaps 93;	QY 134 NYLLTIKELKYPQLEDLTNHMLTLCDNIHGFKYLIDGYEBINELLYKLNFY 184	222 FGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNA 229 TIPKPKDYTKDKLESNKSNOVEKKENDONVDKKLITTMNNINTNLSEKKKVIND 270 TKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPP	330 PANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNI	429 LINPEDYTKEPSKNIYTDNERKKINEIKEKI-KIEKKKIESDKKSYEDRSKSLNDITKE 1

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3399 AIKKPEAIAEIQELADKK------
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                                                                                                                                                                                                                         epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
1428 VNDKIDLFVIHLEAKVLNYTYEKSN-VEVKIKELNYLKTIQDKLADFKKNNNFVGIADLS 1486
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                   ---IKLMLIPLN-----SYKQNNDLKSALEELNNVFTNKEA----QKESSPIG----
                                                                                                                                                                                                   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5080
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4.6%; Score 387; DB 23; I
Best Local Similarity 20.9%; Pred. No. 2.2e-08;
Matches 314; Conservative 231; Mismatches 592;
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antibacterial;
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|ISNTPDATLEEKAEA------NRLLQ---NVLTSTSDEIANVDHNNEVDQALDKA
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences ((II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) and infection, or they can be used to identify dry resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand
                                                                  1312
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   ---EDYDDLGQV 1259
                                                                                                                                -DILNSRFNKRENFKNVLESDLIPYKDLTSSNYV----VKDPYKFLNKEKRDKFLSSYNY 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum, chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                           ------DKINDISSRATNEEKQIFVSKLKALINRTHKQIDEAETFVSVETIVRNFKVE
                                                                                                                                                                 3544 ADKLNSIVRKKAKAKASKEIELEADHVKQMINANLSASTRVKQNARTLINEIVSNALSQLNK
                                                                1260 VTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLEN----NVMTFNVNVK--
                                                                                                                                                                                               IKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKT
                            3436 NELEGALKSAINHIHQSQNNESVSAALKESISLIDSIEIQAHKKLEAKAYIDGYSD----
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and in the
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vaccines
 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESE-
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Plasmodium falciparum, useful as antimalarial
diagnosis of P.falciparum infection
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CARUCCI D.
GARDNER M.
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our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 TKESTEPNEYP-NGVTYPLSYNDINNALNELNS-----FGDLINPF---DYTKE
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                                                                                                                                                                                                                    ESEEDYDDL---GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNV 1304
GEFFFDEVEEKFDEKMGEFFFDEVEEKFDEKMGENIFEEIPK----KDDVEIEETYSEK 723
                                                                                                                                                                                                                                            941
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                                                                                        DNIYSGDNIYSG-----DNIYSG-DNIYSGDNIYSGNIYSG-----DNI
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                            LERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET
                                                                         ENTLENTKILLKHYKGLVKYYNGES----SPLKTLSEESIQTEDNYASLENFKVLSKLEG
                                                                                                                        KIKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYK-KFL
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

C (I) and (II) are useful for the development of vaccines against D. falciparum infection or a monochonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, attibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum of infection, or they can be used to identify drug resistance in sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AaA70078 to haA70287 and AAB18135 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                                                                                                                      Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
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can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. 72; secreted or membrane proteins) TFYNESFTNFVKSKADDINSL -- - NDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER 1017 : | | | | | : : | | : | : | 328 IINKKKDRSRDTYEDESREGAYGENTTEDLNEDTQEGHKNKKKEILMNILYNDINIKKN 328 356 EIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND 415 471 268 723 427 781 900 240 DYIKKNKKTIENINEL----IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEA 295 296 HNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIK 355 ----INYNKKYEN 124 472 KSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFE-----KMMGKRY---SYKV 521 EKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETL 581 619 VQKVLLMN------KIDELKKTQLILKN-VELKHNIHV-----PNSYKQENKQEPYYL 664 :| :: | :: | :: | | :: | | DEKDFF#DRNFKGKKKEIDIKKNQQV#KNMLNIKNNENIDVYNDKDNFINIDDKCPSGYF 416 IN----NALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDK VENIKKD------EEQLFEKKITKD------ENKPDEKILEV--SDI-VKVQ 724 ALEGDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKT--ENVSKLDYLEKLYEF 665 IVLKKEIDKLKVFMPKVESLINEEKKNI-KTEGQSDNSEPSTEGEITGQATTKPGQQAGS -----KDKIKEY----DYLDNEKOKNVNKMIHPKDGNNNNNNILLSQ----------NSSTILSHVVQEDYADGIKKF 782 LNTSYICHKYILVSHSTMN-EKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMF NKNSFYNN---LENRKLININNIYDKYKI------ILSEIKSG-----DSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLT PQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSD -------CDK------LDIK Length 2206; 515; Query Match
4.5%; Score 379.5; DB 21; Length
Best Local Similarity 19.9%; Pred. No. 2.6e-08;
Matches 294; Conservative 214; Mismatches 451; Indels DGGDTFEENINVL-----KKKKKKKNSDT-----(especially when they are rifins or ------: | : | | : | : | ------2206 AA; Seguence 269 92 125 168 522 217 582 329 841 483 901 961 428 518 8×866666666668×8 δ ద ò g ò g δ g οy QQ ογ q οy QQ δ QQ δ g ò qq οy g g ŏ ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system, and a localised neuropathies and central nervous system diseases, aunch as lateral sclerosis, and SNy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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Zhang J;
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Yang Y,
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18.9%; Pred. No. 3.1e-08;
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Xu C, Xue AJ,
, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-0488725.
2000US-0552317.
2000US-0598042.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wang 2, F
Zhou P,
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                                                                                    03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                    25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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QA,
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infection, or they can be used to identify drug resistance in subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their fragments (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).
(I) and (II) are useful for the development of vaccines against antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of integs to treat or prevent P. falciparum
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                                                                                                                                                                                                                                                                            chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
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and in the
                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related protein SEQ ID NO:129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines
QY * 1391 EKYKSD---LDSIKKYINDKQGENEKYLPFLNNIETLYKTVND 1430
                       | | : : | | : | : | : | : | ETSKIETQIMDIKPKRISSADPDKLQTEPLSTSFEISRNKIED 1558
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                                                                                                                                AAB18272 standard; Protein; 2500 AA
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antimalarial; malaria;
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
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1243 AHLNFGRSYSD------PFPFHSPNTSILEFCCSRYFSSNFPFEKTMIQ 1285
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| 1920 LNGGHTFVEDQKKGKEYKKEEREHIVQGEIKEKEK----YTLGGRERGSRRSKESDSFRG 1975
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1128 QCLIDKNVRN-----EQLSDATLNRYFLECSQRNTESLCNESLSDPYMNNDNSHSQYSNS 1182
                                       1117
                                                                                                                                                                                                                                                                                                                                                              -NKNVVKNEN----VVEKNSRFIKKEHNISMLNVPNYYENNTRGKDITNNNNISGDPLVNG 1422
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                                                                                                            SDSD-AKSYADLKHRVRNYLLTIKELKYPQLFDLTN-HMLTLC-----DNIHGFKYLID 169
                                                                                                                                                                                                                                                                                                                                                                                                  334 GNT----PNTLLDKNKKIEEHEKEIKEIAKTIKFNI-----DSLFTDPLELEYYLR--- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590 EQLF----EKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKH 645
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                                                                                                                                                                                                                                                                           ------LDKINEIKNPPPANS
                                                                                                                                                                                                                                                                                                                                                                                                                         YETENDNISSENPNVDDLSGHIQNNDNSFNSSSSNVPLNVNPTNIENSNILPLSIEGTNS
                                                                                                                                                                                170 GYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLD
                                                                                                                                                                                                                1286 N-EQVQESLYISNNFI-----KANHV------ERIKITHIDTFTS-----N
                                                                                                                                                                                                                                                      N--IKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSI
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                                     SGGSGGSVASGG---SVASGGSVASGGSVASGGSGNSRRTNPSD
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Gaps

QCVTHESYQELVKKLEALEDAVLTGYSL --- FQKEKMVLNEGTSGTAVTTSTPGSKGSVA 74

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*Match 4.4%; Score 372; DB 21; Length 2500; Local Similarity 20.5%; Pred. No. 6.3e-08; les 328; Conservative 231; Mismatches 574; Indels 466;

Query Match

Matches 18

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γo	-DTFYNESFTNFVKSKADDINSLNDESKRKKLEEDLINKLKKTLQLSFDLYNK-YK	8888	specification in the couple	specific aut in the remov coupled to a
Q D	NNKKKDHYYVDKYHYINKYYP 	3 %	produc	producing 1y
δy	1013 LKLERLEDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKK 1067	ÖS	Sequence	ice 1
QQ	EKYSRKFNYNHSSGSYHNAQKYDSLRYEQKEKPYKITENNKKNEGNEILKKYSIENEEKN	ÕĂ	at Ca	ch 1 Simi
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QQ	2202 NYDKEQNENCILDKDTQCNVNTKEKNNLDNKKSFPSNIKVKLEEEEKSDD 2251	Qy	232 K	KDNVGKM
δ	1120 ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN 1179	QQ	82 F	RDDVTLI
qq	2252KRDDKKNDNTR-EKNNLDNKKSFPSNIKVKLEEEEKSDDKRDDKKNDNTREKN 2303	Qy	290 K	KOLEEAH
Οy	1180 NALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDD 1239	QQ	142 0	OOLEEAC
qq	2304 N-LDNKKSF-PSNIKVKLEEEEKSDDKRDDKKNDNTREKNNLDNKKSF 2349	Qy	350 F	HEKEIKE
δλ	1240 VIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVL 1284	QQ	182	-ERSLRE
q	2350 PSNIKVKREKEEKSDEMKDDKKNDDKKNENTREKNNLDNKKLFPSNIKVKLEKEEKSD 2406	QY	410 F	410 PLSYNDI
οχ	1285 YLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTS 1341	qa	219	GIEDV
QQ	2407 EMKDDKKDDKKDHKKDHKKNDKKIDKKIDKKNDKKNDKKNNKKNNKKVEK 2460	Qy	470 I	470 DKKSYED
δλ	1342 SNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFAN 1380	qa	261	QYASSEA
QQ	2461 KNEIKNDKKNNKKNNKKVAKKNEIKNEIKDEIKÖEN 2496	Qy	519 1	Y-KVEKI
000	[5]	QΩ	318	318 YTKLEE-
AAW(AESOLI J. AAW02258 TD AAW02258 standard: Protein: 1411 AA.	QY	560 1	VEKELKY
××	DAMO2258.	qa	365	VELSEK
X	00.wab_1007 /first ontwit	Qy	610 F	EVSDIV-
X		qu	425 E	ETERQLO
X OE	Nucleolar/endosomal auto-antigen pi62.	Qy	649 1	VPNSYKC
KK	Auto-antibody; p162; rheumatic disease; antigen; diagnosis; gene therapy.	qa	485 F	КТКООНС
SS	Homo sapiens.	δλ	688 I	EKKNIKI
X M	DE19515514-C1.	q _Q :: .	545	1:::: 545 EREDLY?
X G	12-SEP-1996.	QY	742	\d\d\dd
PF X	27-APR-1995; 95DE-1015514.	qa	1 965	596 ENLHDQV
PR S	27-APR-1995; 95DE-1015514.	QY	802 1	KILKQYF
AX PA	(PRIV-) PRIVATES INST IMMUNOLOGIE & MOLEKULARGEN.	qa	645 F	KAKTELI
PI	Renz M, Seelig HP;	Qy	862 1	NLYKI
X X 2	WPI; 1996-403153/41. N-DSDR: AATFR751	qa	705	SQLESHI
XX	lar-endosomal auto-antigen - useful for exact	Qy		LNNSLKI
FP F	<u></u>	qq i		LNTDLE
PS	Claim 1; Fig 2; 15pp; German.	λ	817 1	ETLSOE!
\$ 88	Transformed cells can be cultured to produce the antigen p162, for use	3 6		
ខ្លួ	in exact (differential) diagnosis of rheumatic disease, i.e. they can detect, in immunoassays, Western blots, etc., rheumatism-	δŏ	1014	:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----QEPYYLIVLK-----KEIDKLKVFMPKVE---SLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTEGQSDNSEPSTEGEITGQATTKPGQQAGSALE-----GDSVQAQAQEQKQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHNLI SVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIES
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                                                                                                                                                                                                                                                                                                                                                                                                                Indels 382;
                                                                                                                                                                                                                                                                                                                  4.4%; Score 370; DB 17; Length 1411;
nilarity 17.8%; Pred. No. 3.9e-08;
Conservative 270; Mismatches 574; Indels 382.
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                                                                                                                                                                              -----TAKATLE 1088
                                                                                                                                                                                                     1209 QSQPKKPASTHVGAES-----NTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVT 1261
                                                                                                                                                                                                                                                                                       1149 SH-------KLESIKEITNLKDAKQLLIQQKLELQGKA------DSLKAAVEQ 1188
                                                                                                                                                                                                                                                                                                                                                 1189 EKRNQQILKDQVKKEEEELKKEFIEKEAKLHSEIKEKEVGMKKHEENEAKLTMQITALNE 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIAD---L 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1299 CLKGEGEIEKLOTKVLELORKLDNTTAAVOELG------RENOSLQIKHTQAL 1345
                                  NKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK 1123
                                                                                                                                                                                                                                                                                                                        RENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFAND 1381
                                                                                                                    LENKLOQOLTQAAQELAAEKEKISVLONNYEKSQETFKQLQSDFYGRESELLATRQDLKS 1051
                                                                                                                                                                                                                                                              1262 GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNK 1321
875 FFEKENQKGKAAILDLEKTCKELKHQLQVQMENTLKEQKELK-KSLEKEKEASHQLKLEL 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
                                                   VLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multivalent protein; immune response; Plasmodium vivax; parasite; protozoacide; vaccine; malaria; recombinant; ViVacl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQC 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------VTVRRHHC--RQC 1377
                                                                                                                                                                 1124 VLSKLEGKL---KDNLNLEKKKLSYLSSGLH-----
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N-PSDB; AAH47058.
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the inventor in transcript of conservative substitutions, derived from more standiate an immune response to substitutions, derived from more than one stage in a life cycle of a Plasmodium vivax parasite. (I) is comprises antigenic than one stage in a life cycle of a Plasmodium vivax parasite. (I) is specifically a protective immune response that confers increased resistance to infection by Plasmodium parasites, such as P. vivax. (I) is especially useful in the treatment, prevention and reduction of malarial infection, as conferring immunity against multiple stages of the malarial parasite. The antibodies produced are useful for the detection or measurement of antigenic epitopes derived from one or more stages in a life cycle of a parasite, particularly P. vivax. The vaccine comprising the recombinant proteins, is cost-effective, health-companies of the recombinant proteins, is cost-effective, health-companies of the recombinant proteins, is cost-effective, health-companies of the recombinant proteins, is cost-effective, health-companies of the recombinant proteins, is vaccined and and are in the present sequence represents the amino acid sequence of the recombinant protein vivacine and and and proteins vivax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---IYTDN--ERKKFINEIKEKIKIE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 GSVASGGSGGSVASG---GSVASGGSVA--SGGSVASGGSGNSRRTNPSDNS-SDSDAKS 124
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                                                                                     relates to recombinant multivalent proteins (I) that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 YLD---KVRATVGT-----EWTPCSVTCGVGVRVRRRVNAAYKKPEDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 PLELEYYLREKNKNIDISAKVETKEST------EPNEYPNGVTYPLSYND----INNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 FDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYR-----KPLDNIKDN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK-----ELLDKINEIKNP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107; Score 369.5; DB 22; Length 1807; Similarity 19.2%; Pred. No. 5.5e-08; Conservative 272; Mismatches 684; Indels 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKKI-----ESDKKS-YEDRSKSLNDITKEYEKLLNEIYDSKF-----
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                                        Claim 5; Page 39-45; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1807 AA;
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Db 887 IPMLNGLINSLSESRDTINLYMNLFGNYT	IPMLNGLINSLSLSRDTINLYMNLFGNYTTELIRLGSGQSIDKRQALSKVTELR 940	OI X	9935	standard; Pro
755 VPTP	PAPVNNKTENVSKLDYLEK-LYEFLNTSYICHKYIL ^I USHSTMNEKILKQYKITKEE 813 	XX		
Db 941 KTYTPYGTTNMTAALDEVQKHLNDRV	PYGTTNMTAALDEVQKHLNDRVNREKAIQLVILMTDGVPNSKYR-ALEV 992	DT	19-JUL-1999	(first en
Qy 814 ESKLSSCDPLDLLFNIQNNIPV-MYSMFD	ESKLSSCDPLDLLFUIQUNIPV-MYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDK 871	DE	B. burgdorferi antigen	i antige
DD 993 ANKLKQRNVSLAVIGVGQ	QRNVSLAVIGVGQGINHQFNRLIAGCRPREPNCKFYSYADWNEA 1041	XX XX	Antigenic protein; vac	tein; va
OY 872 IKNLLEEAKKVSTSVKTLSSSS	863	SO	Borrelia burgdorferi	dorferi.
DD 1042 VALIKPFIAKVCTEVERVANCGPWDPWTA	KPFIAKVCTEVERVANCGPWDPWTACSVTCGRGTHSRSRPSLHEKCTTHWVSECEE 1101	Nd >	WO9859071-A1.	
Qy 894MQPLSLTPQD-KPEVSA	MQPLSLTPQD-KPEVSANDDTSHSTNLNNSLKLFENILSLGKNK 936	VV Gd XX	30-DEC-1998.	
Db 1102 GECPVEPEPLPVPAPLPTVPEDVNPRD	GECPVEPEPLPVPAPLPTVPEDVNPRDTDDENENPNFNKGLDVPDEDDDEVPPANEGA 1159	PF	18-JUN-1998;	SN-OM86
937 NIYQ	YNESFINFVKSKADDINSLND	P P P	03-SEP-1997; 20-JUN-1997;	97US-00 97US-00
nort			22-JUL-1997;	0-SD/6
QY 984 ESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER-LFDKKKTVGKYKI	ESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER-LFDKKKTVGKYKMQIKKLTLLK 1039 : :::::: ::	XX PA	(HUMA-) HUMAN GENOME S (MEDI-) MEDIMMUNE INC.	GENOME MUNE INC
OY 1040 EQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTKILLKHYK-	NKKKEAEIAETENTLENTKILLKHYK 1089	X X	Choi GH, Erwi	Erwin AL, H
Db 1264 DSARDRYARPHGSTHVNNNRANENSDIPN	: :	AX DR	WPI; 1999-189980/16	980/16.
Oy 1090GEVKY-YNGESS	GESSPLKTLSEESIQTEDNYASLENFKVLSKLEGK 1131	XX	Now isolated Dorrelia	ove.
Db 1322 AGLALVGCVGFAYNFVAGGGAAGMAGEPA	AGLALVGCVGFAYNFVAGGGAAGMAGEPAPFDEAMAEDEKDVAEADQFKLANGADDQ 1378	T E E	new isolated bolletia products for the diagn	the diagn
1132 LKDNLNLEKKKLSY ::	YS	Sd Sd	Claim 12; Page 125; 27	e 125; 2
Db 1379 PGANGADDQPGARHAFLQ-NTV	PGARHAFLQ-NTVMKNCNYK-RKRRERDWDCNTKKDVCIPDRRY 1429	XX D	This sequence	represe
Qy 1186 KKFLPEGTDVATVVSESGSDTLEQSQE	KKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDV 1240		invention, which is su	ich is s
Db 1430 QLCMKELTNLVNNTDTNFHRDITFRKLYI	QLCMKELTNLVNNTDTNFHRDITFRKLYLKRKLIYDAAVEGDLLLKLNNYRYNKDFCKDI 1489	888	the Borrelia genus, pa	genus, p
Qy 1241 IIVPIFGESEEDYDDLGQVVTGEAVTPS-VIDNILSKI	TPS-VIDNILSKIENE 1280		infection caused by a be used for detection	sed by a
1490	RWSLEDFGDIIMGTDMEGIGYSKVVENNLRSIFGTDEKAQORRKQWWNESK 1540	XX SOS	Sequence 108	1087 AA;
1281	ILNSRFNKRENFKNVLESDLIPYK 133	ā	/ Mat	
1541	IEPQI	ă X	Best Local Similarity Matches 286, Conser	larity 2 Conservati
QY 1338 DLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFA	DPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383 I::	ΟŸ	261 KTIDKNKNATKEEEKKR	ATKEEEKK
1384 GYYKILSEKY		qa	1 KLNDKNREIMLNEVKN-	IMLNEVKN
1624		QY	321 KINEIKNPPPANS	PPANS
1443		qa	49 TLAEIANSSPFESKDLÇ	SPFESKDI
1672	: : : : : : : :	Qy	374 ELEYYLREKNKNIDISP : :	KNKNIDIS
		40	107 NVCDBNDDVGTEDET	RUGTERE

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68;
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KKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLD 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAKVETKESTEPNEY-PNGVTYPLSYNDINNALNELNSFGDLINP 432
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                                                         Indels 378; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a burgdorferi nucleic acids - used to develop gnosis, prevention and treatment of diseases particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                           sccine; Lyme disease; infection; detection.
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994 INKLKKT----LQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSL 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1223 ESN-----TITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNIL 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKD----ILNSRFNKRENFKNVL 1329
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                                                                                                                                                                                                                                                                                   ------SRQQAIKDLNEFLKNN------PNDAQASKTLAQANKIQHLEDLKSKVH 517
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                                                                                                                                                                                                                                                                                                                                SEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQAQQQQQPPVPVPVPVPVPVPAAKAQVPTPPA 760
                                                                                                                                                                                                                                                                                                                                                                474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAKKVSTSVKTLSSS--SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKN 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NK------KAIESFEKAIQIDKNYGTAYYOKG------IAE 821
433 foytkepskniytdnerkkfineikekikiekkkiesokksyedrskslnditkeyekll 492
                                                                                   KTPDNSKYSNNNNTTSLKKISSNSQKESELSPPSQTIIGKIYRPYSYLIKKELYEILDDI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 QANKIQ-HLEDLKSKVHSIKPIDLENTKSRQQAIKDLNEFXKNNPNDAQASKTLAQANKI 614
                                                                                                                                NTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKN-LISKIENEIETLVENIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 QH-----LKSKVHSIKPIDLENTKSRQQAIKD
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                                                                                                                                                                                                 KD--EEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVE--
                                                                                                                                                                                                                                                                                                                                                               430 NEFLKNNPNDAQA-SKTLAQANKIQHLEDLKSKVHSIK-----PIDLENTK-----
                                                                                                                                                                                                                                                                                                                                                                                              761 PVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEE--SKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               936 KNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDIN--SLNDESKRKKLEED
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|::| | | ::| | | |::| | | |::| | | |::| | | |::| | | |::| | | |::| | |::| |::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| 
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llarity 21.3%; Pred. No. 3.3e-08;
Conservative 208; Mismatches 472;
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                                                                                                                                         I ---- IEYNENNNDQTLRELIKKF 1072
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                                                                                     IADLSTDYNHNN -----LLTKF
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MEDIMMUNE INC
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                         FNLEK-LKKNLSGKSNSENILN-----DSQKIENDKQN-TNLSKEKNS----ENIL
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                                                      --RYSYKVEK----LTHH
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alaheimer's, Parkinson's disease, Huntington's disease, amyotrophic cutilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthitits and inflammation, leukaemias and CN.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.
Wang D;
                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 5398.
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2000US-0552317.
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Wang 2, V
Zhou P,
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19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum chromosome 2 related protein SEQ ID NO:173
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CARUCCI D.
GARDNER M.
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                                                                                                                                                                                                                                                                          171 YEEIN-ELLYKLNF----YFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGY 224
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                                                         Length 1788;
                                                                                                                  441;
                                                      4.4%; Score 368.5; DB 22; Length ilarity 19.0%; Pred. No. 6e-08; Conservative 266; Mismatches 551; Indels
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1788 AA;
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                                                         Query Match
Best Local Simi
Matches 295;
SQ • Sequence
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Also described are: (1) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(1) and (II) are useful for the development of vaccines against

(2) falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum of the identification of drugs to treat or prevent P. falciparum of the identification of drugs to treat or prevent P. falciparum of the identification of drugs to treat or prevent P. falciparum of the identification of drugs to treat or prevent P. falciparum of proteins encoded by it will help to expand the subsequent identification of proteins encoded by it will help to expand complexity of the parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification. present invention describes proteins and their fragments (I) encod chromosome 2 of the human malarial parasite, Plasmodium falciparum Page 395-401; 577pp; English. Disclosure;

2380 AA; Sequence

83; EKIVY-----KFLLNNKNFEYIEKQYSSKEDMNELDILVNTYDMKYDKIIEFLKNNGYLK 1199 ----NNNNNIFNN-NIF-----NNNIFNNNMNSCVGVSEKDFISTSIVASF 1024 302 STRKKDFGCPNTRTERIIKVSPFDSDY-VGIGNKNNSVISPHLIKYNHILFLFICVKNIF 876 487 NHMLTLCDNIHGFKYLIDGYE-----EINELLYKLNFYFDLLRAKLNDVCANDYCQI 203 -HEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVT 408 928 YEEEEYEDEGEEYEEEDDDEEED--EEEYGHNNDNODDEGDKNKTTNEKNKKKKNKNN-- 983 EKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIEN----E 577 KTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIÖKLKVFMPKVESLINEEKKNI 692 711 NKCYFLIENIISNVYKHGCYQKLENILNIELNKYLYEDSYİY--LNNRIGNVFVGITQIL 204 PFNLKIRANEL - - - DVLKKLVFGYRKPL - - - DNIKDNVGKMEDYIKKNKKTIENINELI -----RNKKCIDG---FF --LEEAHNLI----SVL EKRIDTL--KKN----ENIKELL-----DKINEIKNPPPANSGNTPNTLLDKNKKIEE-----YFTFLRKNETIDDK -----ERKKFIN-----IETLV---ENIKKDEEQLFEKKITKDEN--KPDEKILEVSDIVKVQVQKVLLMNKIDELK Length 2380; Indels DB 21; Ouery Match 4.3%; Score 365.5; DB|21; Best Local Similarity 18.7%; Pred. No. 1.2e-07; Matches 344; Conservative 264; Mismatches 600; 877 HKYINNLWIEKDYLFLIENLKDILERKIFDYYTFVKR----YPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDN-EESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQ-----EIKEKI --KIEKKKIESDKKSYEDRSKSLNDITKE------YEKLLNEIYDSKFNNNIDLTNFE--152 1200 1085 633 257 1145 694 818 303 409 455 522 578 488 ó g ò g ò g ò QQ ð QQ à qq ò g ò g ò 셤 δ g ò

1542 1603 CLONDNDKNVNNNFKFIENNGTNEIKKELYRNDMYNDGIINFDINNEYFFRNLNNMNECQ 1662 1663 FFKYTLFDKNDNVFDHINNKDNTDYNKYFYKFENLIIFNYDFTLISKIEDF----YQSNR 1718 ESSPLKTL-----SEESIQTEDNYASLENFK-----VLSKLEGKLKDNLNLEKKKL 1143 1972 VILSK--SEY-----VRKKRLRYLEGNDSDFVEDLKTNIEDELYDKYKTYFVKNV 2019 - 1293 1543 DKKKKKNDKTIERNESAENKIEKNIIENNYTIDNDKREFNMDNTIKNEKRESENNNKHME KTEGQSDNSEPSTEGEITG--QATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVF ---KPEVSANDDTSHSTNLNN QYRDYLLRARRLSREENKIS------PKDDSTGKNNTINNNISNNNISNNINNN --LERLFDKKKTV------GKYKMQIKKLTLLKEQ--LESKLNSLNNPKHVLQN ----AETENTLENTKILLKHYKGLVKYYNG ::| ||||:||
YKIFDINKKKKKKEIFYHLYYIYIYYRDILFLLKFVFTLNFCENTK----YKFLKRRENT | : |: | : ::: | | : :::| | XKKKYKDMRVPYINLHMEQGGDKKGNHENIQHRKNNEVDIVYNNRVEDIRENMN-----LESYKK--FLPEGT-----KKPASTHV ----NNIYSNNN------LYGDDNMNYPTSS---TGKGTPRRLFEGSNNDGNNS 2020 YSMRKLFKIALEGSEEKVIKKIYDLGRSDAHLWLFVEYLNVGIYLYKRIYTIYIKLLTVF ESLIYLTNINKKKKKVDISTFLASIEYAVIYVNGNPFDLFKFCNLLVLCYTYYSMPYVKA QTSVLNNNDDHKLGTVYDKNIMNKESVHANGISKELIKNDKTSEKLRKKDEKKKMKKIKK TVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLAD---FKKNNNFVGIA 2200 NSTSSIDMDI------NNYEKGKIDVR-QNIDYNNKKEDNVNSDHIKRKNR---IK KEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDND TLQ------LSFDLYNKYKLK-----SIDTDINFANDVLG--YYKILSEKYKSDLDSIKKYI--NDKQGENEKYLPFLNNIETLYK 751 AKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKIT SLK------LFENILSLGKNKNIYQELIGQ--KSSENFYEKILKDSDTF----1294 NTRGDHNNNOTNDNHYNHHYDDTHNNNNNNSKYKNKNKNKIMYEKERK-----ILSKIENEYEVLYLKPLAGVYRSLKKQLENN----VMTFNVNVKDILNSR----SYLSSGLHHLIAELKEVIKN-------KNYTGNSPSENNTDVNN-------YVVKDPYKF---GAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN-- VNNSNMF ---YNESFTNFVKSKADDINSLNDESKR----871 KIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQD--------LNKEKR----DKFLSSYN----1260 ITKVIFFPVHMKEHDHVMNKNYYNNQY----FNKRENFKNVLESD ----LIPYKDLTSSN----FSVF-FNKKKEAEI-------693 1345 1390 1433 922 1719 1098 1144 1182 1273 1319 2080 1427 2140 1828 1221 1931 963 1871 1353 g g Dp g ò q δ a g qq g g ŏ δλ g ŏ ð ö a ŏ ò ŏ a ŏ qq ò g δ a ŏ a δ ŏ ò

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1083 ILLKHYKGLVKYYNGESSPLKTLSEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
               2247 KTNKQRNNKEKLKRSISLPL---NLKRTVVKII---NLKNKINLNKNIIDAINNDILKGT 2300
  ---HQCVKKQC 1537
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                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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1484 DLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQ--
                                                 P-----QNSGCFRHLDEREECKC----LLNYKQEGDKCVEN 1569
                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 17349
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Calso described are: (I) nucleotide comprising (I) or (II).

Cando (II) are useful for the development of vaccines against or infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in the customer of drugs and the consent identification of proteins encoded by it will help to expand or understanding of parasite biology, a process hampered by the cour understanding of parasite biology, a process hampered by the cour understanding of parasite biology, a process hampered by the cour understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for complexity of the parasitic lifecycle, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many creasitance for the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AABI8144 to AABI8352 represent nucleotide
                                          1220 VGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIEN 1279
                                                                                                       1280 EYEVLYLKPLAGVYRSLKKQL--ENNVMTFNVN-VKDILNSRFNKRENFKNVLESDLIPY 1336
1644
                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                          TEPETDTSAIRQEYKAKLDKLVVDLTVART-----DLVNQETTFAGTKSSYDETIARLEK
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vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum chromosome 2 related protein SEQ ID NO:62.
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CARUCCI D.
GARDNER M.
VENTER J C.
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and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                 72 VRVNQNNNEEKKKEEANYTCVNNKYVTLKNKVHVNKY---VNNSNINKI-KIVPIIKCSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 PFYERNLNDKGIHLKELKRL---ERVDEPRLYNNVDKI----PWKKEIIYNNIKSNNIQ
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                                                                                                                                                    429;
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                                                                                                        DB 21;
                                                                                                      Query Match
4.3%; Score 362.5; DB 21;
Best Local Similarity 20.0%; Pred. No. 1.1e-07;
Matches 317; Conservative 262; Mismatches 574;
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MKNKSNNKSK------
                                                               1712 AA;
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                                                                  Seguence
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1132 YLGRLI--QIVEKLFKKYILKYSFHKLR-IFYEYKIEMEKLKKNYIHCIYDISDKLEFLI 1188
----DKKKTVGKYKMQIKKLTLLKEQLES-----KLNSLNNPKHV---- 1055
                                                                                                                                 963 NL------IKKENSYAAEMNVGLVFRKYIPILINLSCNYLLIKKNEKNVITCISYTNII 1015
                                                                                                                                                                     ELKEVIKNKNYTGN-----SPSENNTDVN-----NALESYKKFLPEGTDVATVV 1199
                                                                                                                                                                                                                                                KKKMQHYFNHIIINSYESSFINYQIKTNDML----YNLLLKEK----SAYQNHLG--- 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                     1465 TIQ--DKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQ 1522
                                                       ---LQNFSVF----FNKKKEAEIAETE-----NTLENTKILLKHYKGLVKYYNGESS 1100
                                                                                                               PLKTLSEESIQTEDNYASLENFKVLSKLECKLKDNLN----LEKKKLSYLSSGLHHLIA 1155
                                                                                                                                                                                                1016 DVKIVKKSKKNKERFLFKIVYVFKKKEQKTEKNVTLLFRANLMEIFEK-IKGRVDYCIIP 1074
                                                                                                                                                                                                                            SESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQV 1259
                                                                                                                                                                                                                                                                                    1260 VTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRF 1319
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                                                                        845 QDEELCSNNILVKDIEEKKMCGKLFFEEICVFRINEKNEHGHENLRKNNHNDDTHKMYSS 904
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CARUCCI D.
GARDNER M.
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of farugs to treat or prevent P. falciparum. Sequencing of the Plasmodium chromosome 2 and the csubsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite infecyle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many drugs. AaA70078 to AaA70287 and AAB18135 represent nucleotide and protein sequences given in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KLYQA-----QYDLSIYNKQLEEAHNLISVL- 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                             Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 KKRFDKFNDIYEIITNHKNKQPHIKENNIK---YITRN----VWYDRLSVDEKKKKNDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 KGNDNRLGVSSTSNDKKKNNKKRYNNNNNNDNNNDINNDCNNNKYNPCCSSCNGNVLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 YKERVIDINKEKDFVLLGISKTCVKKCNTCSGDNVTKDIDKCVEDEEKSKEGVILNYMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EKRIDTLKKNENIKELLDKINEIKNPPPANS--GNTPNT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 KTFNMCEGDKKI-SYGROITNLVSCYKYN-----NOLKSPYNIHTINQQVHDNNIYVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KESTEPNEYPNGVTYPLSYNDIN----NALNELNSFGDLIN--PFDYTKEPSKNIYTDNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 KEKHIHINKVYNNVYFVEGQEKLYSPSIKEETQFYIQNDYKHDDNVKMLSYNYYNDMVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NIDKYEKTKTCSYVLNNLHKKYNHHNNKMYDEYKFYDYYELINKIKKLKGFKNVIEERG
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4.3%; Score 360.5; DB 21;
Best Local Similarity 20.0%; Pred. No. 1.3e-07;
Matches 325; Conservative 251; Mismatches 592; I
  Venter JC;
                                                                                                                                                                 Disclosure; Page 312-316; 577pp; English.
  Gardner M,
Carucci D,
                                       WPI; 2000-365347/31
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Hoffman S,
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δy	632	KKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKN	691
op	544	REGORIGOEKHKKKDENKK	568
Qy	692	IKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQAQAQPPVPVPEA	751
QQ	569	KNKNNNNSNNINNKHGRVIQYTDEKIQNDYCKNKESSKRGNHKMMRK	615
οy	752	KAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYI-CHKYLLVS	795
Dp	616	-NKTRKPKNEGRKGEKYIY	674
δy	196	HSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIP	834
qq	675	HKRNNILNEENFIKEHQINGRNKEHVNEKNKEEDTFNISKENTKEGSYIITHKNKRNMDN	734
δ	835	VMYSMFDSLNNSLSQLFMEIYEKEMVON-LYK-LKDNDKIKNLLEB	878
QQ	735	IKIGRYDNINDKKEFSSNILYKCVKKNDKINKSQTSLFFEFMKGKGDQKH	784
ογ	879	KPEVSANDDTSHSTNLNNSL : :	936
a	785	NVIKKEDVFIKTFRTNK-SPTELTKKISDYKCNLLYTSLDRIHKNV	829
οy	937	NIYQELIGQKSSENFYEKILKDSDTFYNESFTNFYKSKADDINSLNDESK	986
g	830	SIYNERIERTKHVPQKKNDNIDIRGIYKSYNFFKSMMMNSLSKCYHT	877
Οÿ	987	RKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKE	1040
DP,	878	KTCDYSNYDFMKNKMSKKAQNKLVSKCISKYKKKAIKKKERKETTTTKKKYIYRKNEISI	937
ολ	1041	OLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESS	1100
QQ	938	SPDGNVFGHENRKRIKENNKSKESAYTSKSRKNNKIKGEEKKTKRSLCSYKLR	066
οy	1101	PLKTLSEESIQTEDNYASU-ENFKVLSKLEGKLKDNLN	1137
q	991	KMKHLCVENKMHIKKNVRQIIKKKKKNIYKTIKCLNSYKTLIDQVNVKGDEEHKLSNHVN	1050
δŷ	1138	LEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-NALESYKKFLPEGTDVA	1196
qq	1051	KKKKKNCINENNDDNNNDNYNDNNDDNNNDNYNDNNN	1092
δý	1197	IIVPI	1256
g	1093	NDNNNDNOREHSCEEI	1129
δλ	1257	GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVK	1312
QQ	1130		1177
δý	1313	DILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPY	1350
qa	1178		1237
οy	1351	KFLNKEKRGYKILS	1390
qq	1238	KCINMNNKRVYAMKVVLKECNEIFVDNFIKKYLFLKNNPHKNIISIYDIFCNNNYICIIM	1297
δý	1391	EKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNY	1446
QQ	1298	D-YCEGSTLLDYFMSLVPGSLDVYEIKKIMKNIFIALDFFHSNN	1351
ογ	1447	SNVEVKIKELNYLKTIQDKLADFKKNNNFVG	1505
QQ	1352	MFKNKKRKKKRFNYEKYGSFLFNNHEEISFSTSC	1398
φ	1506	#INLAKTVLSNLLDGNLQGMLNISQHQCVKRQCPQNSGCFRHLDBREBCKC	1555
QQ	1399	DTIGKKIMGGKKFIRNLYNEKHKN-LNIFQKNCSHI	1455

Oy 1556 LLNYKQEGD 1564 : | | | Db 1456 YIKYNNMD 1464 Search completed: March 31, 2003, 07:20:42 Job time : 161 secs

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Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
"Molecular cloning and sequence analysis of major merozoite
antigen(gp195)gene of Plasmodium falciparum isolate FCC1/HN.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF218248; AAF27526.1;
InterPro: IPR00063; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                               Plasmodium
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                                                           NTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYK'NLISKIENEIETLVENIKK
                                                                                                                                                  SENKILEKNFKGLTHSANAS----LEVSDIVKLQVQKVLLIKKIEDLRKIELFLKNAQLK
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                   KTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVE--TKESTEPN-EYPNGVTYPLSYND
                            INNAL---NELNSFGDLINPFDYTKEPSKNIYIDN-ERKKFINEIKEKIKIEKKKI----
                                                                                               ESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH
                                                                                                                                                                             DEEQLFEKK ---ITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELK
                                                                                                                                                                                                                                                                                                                                    ESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMETTYEKEMVCNLYKLKDNDKIK
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NDKQGENEKY
             KQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGS
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                                                                                         KNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 1694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117;
                                                                                                                                                                                                                                                                                                                                                                                                                Jiang G., Liu R., Daubenberger C.A., Pluschke G.; "Sequence analysis of the MSP 1 gene of Plasmodium falciparum Hainan, China.";
                                                                                                                                                                                                                                                                                                                                                         Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84CFC0E709F5673B CRC64;
                                                                                                                                                                                  NGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.3%; Score 5162.5; DB 5; Best Local Similarity 61.1%; Pred. No. 1.4e-153; Matches 1054; Conservative 226; Mismatches 328;
                                                                                                                                                                                                                                                                 AA
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 TDINFANDVLGYYKILSEKYKSDLDSIKKYI
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                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata;
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Q9TZT5;
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KTIKŖNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPN-EYPNGVTYPLSYND 	INNALNELNSFGDLINPFDYTKEPSKNIYTDN-ERKKFINEIKEKIKIEKKKI : : ::::	ESDKKSYEDRSKSLNDITKRYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHH :- :- :- :- :-	NTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKK	DEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELK : :	HNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPS : :	TEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPPPEAKAQVPTPPAPV	NNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEE : ::	ESKLSSCOPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMYCNLYKLKDNDKIK :::	NLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDD ::	TSHSTNLNNSLKLFENILSLCKNKNIYQEL-IGQKSSENFYEKILKDSDTEYNESF 	THFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK :	YKMQIKKLTLLKEQLESKLNSLNNPKHVLONFSVFFNKKKEAETAETENTLENTKILLKH 	YKGLVKYYNGESSPLKTLSEESIOTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLS 	SCLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE 	SGSDTLEQSQPKRPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDY	DDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKD :	ILNSREKKRENFRNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSID : : : :: : : : : LNSRLKKRKYFLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVE
359 355	416	468	528	588	645	705	763	814	874	913	968	1028	1088	1148	1202	1254	1314
g G	Qy Dp	Qy Db	Qy Db	Oy Op	Oy Dp	oy ob	oy O	Oy Dp	Oy Dp	Oy Dp	Oy Dp	Qy Dp	Qy Dp	oy op	Oy Dp	O.y	Oy Dp

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29;
                 1590 KQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGS 1649
                                                         1415 LPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFK 1474
                                                                                                                   1475 KNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVK 1534
                                                                                                                                                                            KQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGS 1594
-----NDKQGENEKY 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NF54;
MEDLINE-96123395; PubMed=8577332;
Pan W., Tolle R., Bujard H.;
"A direct and rapid sequencing strategy for the Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 RSNTSSGASPPADASDSDAKSYADLKHRVRNYLFTIKELKYPELFDLTNHMLTLCDNIHG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 60.6%; Score 5107.5; DB 5; Length 1720; Best Local Similarity 60.2%; Pred. No. 7.3e-152; Matches 1052; Conservative 216; Mismatches 343; Indels 137;
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precursor of the major merozoite surface antigens.
Plasmodium falciparum (isolate NF54).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=5843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 19 POTENTIAL.
SEQUENCE 1720 AA; 195725 MW; 717B2FD1E637A8A3 CRC64;
                                                                                                                                                                                                                                    Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              PRT; 1720 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen gene gp190/MSA1.";
Mol. Biochem. Parasitol. 73:241-244(1995).
EMBL, 235327; CAA84556.1;
Pfterpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Merozoite; Signal.
1374 TDINFANDVLGYYKILSEKYKSDLDSIKKYI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NF54;
Tolle R., Bujard H., Cooper J.A.;
Exp. Parasitol. 0:0-0(1995).
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STRAIN=NF54;
Tolle R.;
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ò	572	SKIENEIETLVENIKKDEBOLFEKKITKDENKPDEKILEVSDIVKVOVOKVLLMNKI	Qy	1572 PTCNENNGG
: A	593	TGLEADIKKLTEEIKSSENKILEKNFKGLTHSANGSLEVSDIVKLQVQKVLLIKKI	qa	1653 PTCNENNGC
è	629	DEL KKROL II KNUEL KHNIHUDNSVKORNKOBDVVI IVI KKRIINI KUBWKVETI INDE	Qγ	1632 MLILYSFI
g 8	649	EDLRKIELFLKNAQLKDSIHVPNIYKPONKPEPYYLIVLKĶEVDKKKEIPKVKDMLKKE	qα	1713 MLILYSFI
οy	689	KKNIKTEGOSDNS	RESULT	LT 5
q	709	QAVLSSITQPLVAASETTEDGGHSTHTLSQSGETEVTEETEETVGHTT 759	OI OI	AS QBT6A9 PF
δλ	743	743 PVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKY 791	TO TO	01-JUN-2002 (7
qq	760		DT	01-JUN-2002 (1 Merozoite surf
δ	792	! ILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLF 851	SO OS	MSP-1. Plasmodium fal
qq	817		0 00 0 0	Eukaryota; Alv NCBI_TaxID=583
οý	852	MEIYEKEMYCNLYKLKDNDKIKNLLEBAKKVSTSVKTLSSSS 893	RN	[1] SEQUENCE FROM
qq	877	FELYQKEMIYYLHKLKEENHIKKLLEEQKQITGTSSTSSPGNTTVNTAQSATHSNSQNQQ 936	RC RA	STRAIN=FCB-1; Li X.R., Liu S
٥y	894		RT	"83 kDa subfra FCB-1.";
QQ	937		RL DR	Submitted (FEE EMBL; AF480451
ΟŊ	946	KSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKLEEDINKLKKTLQLSF :: :: :	FT	NON_TER NON_TER 65
qq	997	TEMEKFYENILKNNDTYFNDDIKQFVKSNSKVITGLT-FTÖKNALNDEIKKLKDTLQLSF 1055	ŏs	SEQUENCE 656
0y 0b	1006	5 DLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLKEQLESKLNSLNNPKHVLQNFSVFFNK 1065 	Ou Be Ma	Ouery Match Best Local Simila Matches 656; Cc
δy	1066		Qy	20 VTHESYQEI
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٥y .	1126	SKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESY 118:	ογ	
g	1176	SKIDGKLNDNLHLGKKKLSFLSSGLHHLITELKEVIKNKNYTGNSPSENNKKVNEALKSY	qq	
οy	1186	KKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQ 1231	οy	140 KELKYPQLE

DKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYI----- 1404 HILLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLESIKKVIKEEKEKF 1473 LINYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKT 1511 SKRODMLNISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPN 1652 GCCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLIL 1631 ILENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYK 1351 ----NDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKS 1451 SNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPN 1571 VASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTI 139 FDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCAND 199 Gaps S.C., Chishti A.H., Oh S.S.; agment of MSP-1 gene of Plasmodium falciparum isolate WIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAG ; 0 39.9%; Score 3361; DB 5; Length 656; larity 100.0%; Pred. No. 7.6e-98; Conservative 0; Mismatches 0; Indels ılciparum. Lveolata; Apicomplexa; Haemosporida; Plasmodium. 833; 58-2002) to the EMBL/GenBank/DDBJ databases 51; AAL88455.1; -556 656 . 56 AA; 75698 MW; EIEF44CE341FD0C9 CRC64; TrEMBLrel. 21, Created)
TrEMBLrel. 21, Last sequence update)
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face protein 1 (Fragment). 656 AA PRT; RELIMINARY; 1639 1720 N.A.

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OY 61 AVTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120	181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED : :: : : : : : : 127 INFHYDLLRAKLHDMCAHDYCKIPEHLKISDKELDMLKKVVLGYRRPLDNIKDDIGKLET 241 YIKKNKKTIENINEL-IEESKK		Db 307 LQEAQKLIAVLEKRVKVLKEHKDIKVLLEQVAKEKERLPSDYPNTTNLTNVHKEAESKIA 366 Oy 349 EHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNI-DISAKVETKESTEPNE 402 1	456 IKEKTKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLMEIYDSKFNNNIDLTNFEKMAGK 51 1	QY 576 NEIETLVBNIKKDEBQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQ 635 : : : :	QY 691 NIKTEGQSDNSEPSTEG	QY 772 LDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLENI 829 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	QY 884 TSVKTLSSSSMQPLSLT-PQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL 942 1:
,121 KELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCAND ,121 KELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCAND 200 YCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEES 11111111111111111111111111111111111	OY 260 KKTIDKKNATKEEEKKKLYQAQYDLSIYNKOLEEAHNISVLEKRIDTLKKNRNIKELL 319 1111111111111111111111111111111111	Qy 380 REKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEP 439 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 500 FUNNIDLTNFERMAGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIV 559 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	50.		OX NCBI_TaxID=5855; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=SAL-1; RX MEDLINE-92158013; PubMed=1371329; RA Gibson H.L., Tucker J.E., Kaslow D.C., Krettli A., Collins W.E., RA Kiefer M.C., Bathurst I.C., Barr P.J.; RT "Structure and expression of the gene for Pv200, a major blood-stage	Yr Surface antigen of plasmodium vivax."; Nol. Blochem. Perasitol. 50:325-334(1992). Nol. Blochem. Perasitol. 50:325-334(1992). DR EMBL; M75674; AAA29735.1; DR InterPro; IPR000561; EGF-11ke. DR Pfami, PF00008; EGF; 1. KW Signal. 19 POTENTIAL. FT SIGNAL 1 19 POTENTIAL. FT CHAIN 20 1751 POTENTIAL. CONTENT 1751 NA. 105130 MAI ALCADOROUS CONTENTIAL. CONTENT 1751 NA. 105130 MAI ALCADOROUS CONTENT CONTEN	Ouery Match 36.7%; Best Local Similarity 38.2%; Matches 704; Conservative 316 1 MKIFFLCSFLFFINTQCVTHES 1 MKALLFLFSFIFFVTKCQCET-ES

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MEDLINE-91219506; PubMed-2023952;
Mel Portillo H.A., Longacre S., Khouri E., David P.H.;
Primary structure of the merozoite surface antigen 1 of Plasmo vivax reveals sequences conserved between different Plasmodium
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18 1726 MEROZOITE SURFACE ANTIGEN 1.
1726 AA; 194434 MW; BAODCD8333C6C727 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Merozoite surface antigen 1 precursor.
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EMBL; M60807; AA563427.1; -.
Interpro; IPR000561; EGF-like.
Pfam: PF00008; EGF; 1.
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                                                      YIKKNKKTIENINELI-EESKKTIDKNKNATK----
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Matches 678; Conserva
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NYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGN 1520
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KKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKEL 1460
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Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                           major merozoite surface proteins (MSP1) of Plasmor field isolates.";
Mol. Blochem. Parasitol. 59:95-100(1993).
InterPro; IPR000561; EGF-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00008; EGF.
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Jongwitiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00109; PROTEIN_KINASE_TYR; 1. EGF-like domain; Merozoite.
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Best Local Similarity 99.8
Matches 538; Conservative
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NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
MSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 2801; DB 5; 100.0%; Pred. No. 1.8e-80;
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Conservative 0; Mismatches
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EMBL, D13158; BAA02619.1; -.
InterPro: IPR001545; EGF-like.
Pram: PF00008; EGF: 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
EGF-like domain; Merozoite.
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MEDLINE-913295445; Pubwed-8515786;
MODULIWES S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 AA; 61075 MW;
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Jongwutiwes S., Tanabe K., Kanbara H.;
Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13361; BAA02622.1;
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001245; Tyr_pkinase.
Pfam: PF00008; EGF:
Prop. PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
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NYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLFKFLSTGMVFENLAKTVLSNLLDGN 420
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2795; DB 5;
Pred. No. 2.8e-80;
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99.8%;
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Matches 538; Conservative
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"Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates."

Mol. Biochem. Parasitol. 59:95-100(1993).

BenBL; D1337; BAA0261B.1;
InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00008; EGF: 1.
         KKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKEL
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Pred. No. 2.6e-80;
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99.8%;
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538; Conservative
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Matches 537; Conservative
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01-NOV-1996 (TrEMBLrel.
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Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
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EMBL, D13362; BAA02623.1; -.
InterPro; IPR001561; EGF-11ke.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00008; EGF: IPR0517F; PROSITE; PS00109; PROTEIN_KINASE_TYR; I.
EGF-11ke domain; Merozoite.
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Jongwutiwes S., Tanabe K. Kanbara H.;
Jongwutiwes S., Tanabe K. Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from filed isolates."; Sequence conservation in the C-terminal part of Plasmodium falciparum from filed isolates."; Parasitol. 59:95-100(1993).

EMBL; D13363: BAA02624.1; --
EMBL; D13363: BAA02624.1; --
InterPro; IPR001845; Tyr_pkinase.
PROSITE: PR00109; PROTEIN_KINASE_TYR; 1.
EGF-like domain; Merozoite.

SEQUENCE 539 AA; 61046 MW; 3EED87473EEB7B65 CRC64;
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"Sequence conservation in the C-terminal part of the precursor to analyn merozoite surface proteins (MSP1) of Plasmodium falciparum field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13356; BAA02617.1;
InterPro; IPR000561; EGF-like.
InterPro; IPR000245; Tyr_pkinase.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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protein (Fragment).
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Pred. No. 4.2e-80;
0; Mismatches 2;
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01-MAR-2002 (TrEMBLrel.
Major merozoite surface
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                               Last sequence update)
Last annotation update)
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                                                                              01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment)
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=9295445; PubMed=8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal
539
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EMBL; D13359; BAA02620.1; -.
InterPro; PR0000561; EGF-like.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000008; EGF; I.
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                                                     538 AKLFYESKFGNKLTSDIFEKFKTQRTEYMNKKTELEN--GLYGNTKQLISKLNKQLNYLQ
             P-DNTPITEDLATNEQARKNLIKAIKKKIEAEEKNLESLKTNYDNKLASFNQQKAPFKEA
                                   LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME
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                                                                                                                                                                                                                                                                                                                                                                                   Score 2532; DB |>; Lc...>-
Pred. No. 1.4e-71;
----hes 583; Indels 364;
                                                                                                                                                                                                                                       Jennings G.J., Toebe C.S., van Belkum A., Wiser M.F.;
"The complete sequence of Plasmodium berghei merozoite surface
protein-1 and its inter- and intra-species variability.";
Mol. Blochem. Parasitol. 93:43-55(1998).
                                                                  Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                1787 AA; 198156 MW; A585D64F5148E4EA CRC64;
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                               update)
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ
EMBL; U43521; AAC28871.1;
   01, Created)
05, Last sequence up
19, Last annotation
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                                                              Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                STRAIN-K173;
MEDLINE-98324404; PubMed-9662027;
                                                                                                                            MEDLINE=97235961; PubMed=9080880;
                                                                                                  SEQUENCE OF 219-373 FROM N.A.
01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19, Merozoite surface protein-1. Plasmodium berghei.
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32.0%;
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Matches 605; Conserv
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SEQUENCE FROM N.A.
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                                                                          NCBI_TaxID=5821;
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           VNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKN-NNFVGIADLS 1486
                                                                                      RHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECT 1604
                                                                                                                                                                                                                                                                                                                                                                 surface antigen 1 gene
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                                                       L----NNL-----NKSGLVGEGESKKILAKMLNMDSMDLLGIDPKHVCINTRDIPANAGCF
                                          TDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNIS-QHQCVK-KQCPQNSGCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score 2530; DB 5; Length 1791; 31.8%; Pred. No. 1.7e-71;
                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface antigen 1.
Plasmodium berghei (strain Anka).
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID-5823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Zhong H., Fan J.Y., Yang S., Davidson E.A.;
"Cloning and characterization of the merozoite of Plasmodium berghei.";
                                                                                                                               PRT; 1791 AA
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EMBL; AF187232; AAF13063.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=ANKA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            762 AGATSPTVTPVTERQSSQNAPPTTAATPATTPEAATTAATPEAATTSTTTSTTTS
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--TLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN
                                                      K---NIDISA--KVETKESTEP--NEYPNGVTYPLSYNDI-----NNALNELNSFGDLIN
                                                                                                                                                                                                                                                                                                                                                                                                               432 PFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME
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EDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVN 1310
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MTTGLNNKLQKRNDFLEVLNHELDLFKDLSTNKYVIRNŖYQLLDNDKKDKQIVNLKYAAK 1521
                                                                                                                                                                                                                                                                                                                         SIDTD-----INFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIET 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADLSTDYNHNNLLTKELSTGMVFENLAKTVLSNLLDGNIQGMLNIS-QHQCVK-KQCPQN 1540
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                                                  VKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDRYKFLNKEKRDKFLSSYNYIKD
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20 1785 MAJOR MEROZOITE SURFACE ANTIGEN.
1785 AA; 198887 MW; AC5307F90113F4F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               605; Indels
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Hamers-Casterman C., Hamers R.;
"Molecular cloning and sequence analysis of the gene
major merozoite surface antigen of Plasmodium chabaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1753 CTCKEPTPNAYDGVFCSSSFMGLSILLIITLIVEN 1789
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29.8%; Score 2509; DB 5
Best Local Similarity 31.6%; Pred. No. 7.5e-71
Matches 598; Conservative 324; Mismatches 60
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Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biochem. Parasitol. 43:231-244(1990).
EMBL: M34947; AAA29730.1;
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MEDLINE=91218805; PubMed=2090945;
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31.6%;
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                                                                                                                                          ELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTD----VATVVSESGSDTLEQS 1210
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein-1 precursor.
Plasmodium chabaudi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EMBL; L22982; AAA29499.1; -.
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                                                       991 EEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLN
                   SLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKL
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"Plasmodium falciparum: the repetitive MSA-1 surface protein
RO-71 isolate is recognized by mouse antibody against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotat
Merozoite surface antigen 1 (Fragment).
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                                                                    MEDLINE=95354793; PubMed=7628566;
repeat block of RO
1. 74:381-389(1992)
                                                                                                              merozoite surface antigen 1.";
Exp. Parasitol. 81:47-54(1995).
EMBL; Z35329; CAA84558.1; -.
InterPro; IPRO000561; EGF-like.
Pfam; PF00008; EGF, 1.
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Matches 422; Conservative
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"Wariation in the precursor to the major merozoite surface antigens plasmodium falciparum."
                                                                                                                                                                                                                                                                                                                                                                                                                            of
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                    Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                      Tolle R., Bujard H., Cooper J.A.; "Plasmodium falciparum: variations within the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                        Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 AA; 74292 MW; 2B6A87737B490A62 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.2%; Score 2119.5; DB 63.8%; Pred. No. 3.8e-59
                                                                                                                                                                                                          Biochem. Parasitol. 27:291-302(1988).
                                                                                                                MEDLINE-88142999; Pubmed-2449612;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95354793; PubMed=7628566;
                                                                                                                                                                                                                                                                                                                                                                                                                                          merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
EMBL: 235328; CAA84557.1;
InterPro: IPR000561; EGF-11ke.
Pfam; PF00008; EGF: 1.
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                                                                            SEQUENCE OF 1-298 FROM N.A.
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Matches 418; Conservative
Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                      NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                      STRAIN-FCH5/NF7;
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1360 KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLN 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1480 VGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ 1539
                                                                                                                                                                                                                                                                                                                                                                protein-1 produces a membrane-bound fragment containing two epidermal growth1 factor-like domains.";
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M64681; AAA29709.1; ...
InterPro; IPR000561; EGF-like.
InterPro; IPR001245; Tyr_Pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 VGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ 300
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                                                                                                                                                                                                                                                                                                                                             merozoite
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                                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
MEROZOITE SURFACE PROTEIN 1.
MEROZOITE SURFACE PROTEIN 1.
377F075058626AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                               Blackman M.J., Ling I.T., Nicholls S.C., Holder A.A.; "Proteolytic processing of the Plasmodium falciparum 1
                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1639
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Pred. No. 8.8e-59;
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100.0%; Pred. No. c...
0; Mismatches
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400
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PROSITE, PS00109; PROTEIN_KINASE_TYR;
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KILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKK 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-93295445; PubMed-8515786;
MEDLINE-93295445; PubMed-8515786;
MEDLINE-93295445; PubMed-8515786;
Medium Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.;
MOI. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13349; BAA02610_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                                                                                                                                                                                                                                                 962 FYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDK
                                                                                                                                                                                                                                                                                                                                                                      241 KLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE
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                                                                                                                                                                                                                                                                                                                                                  1022 KKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENT
     "38 kDa subfragment of MSP-1 gene of FCB-1 strain of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                            ;
0
                                                                                                                                            Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                   falciparum.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF286876; AAF87595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1161 IKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE-----
                                                                                                          9A5E9DE65E5A680B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               569 AA; 64459 MW; ED4284B2867C9703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
                                                                                                                                                                          0
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                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Score 1778; DB 5; 60.8%; Pred. No. 1.5e-48;
                                                                                                                                        21.6%; Score 1818; DB 5; 99.7%; Pred. No. 5.2e-50; iive 1; Mismatches 0
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Pfam; PF00008; EGF; 1.
EGF-11ke domain; Merozoite.
                                                                                                          360 AA; 40993 MW;
                                                                                                                                                                            Conservative
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                                                                                                                                                          Best Local Similarity
Matches 359; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li X.R., Goel V.K., Liu S.C., Chishti A.H., Oh S.S.;
"42 kDa subfragment of MSP-1 gene of Plasmodium falciparum FCB-1
isolate.";
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                                                                                                                                        Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Morozoite surface protein 1 (Fragment).
18asmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                        Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF325919; AAK07641.1; ...
InterPro; IPR001245; Tyr_pkinase. InterPro; IRR01245; Tyr_pkinase. Pfam; PF00008; EGF; I. PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 376 AA; 43218 MW; EB2A72EDF231A5AF CRC64;
                                                01-JUN-2001 (TrEMBLrel. 17, Last Sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update Merozoite surface protein 1 (Fragment).
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100.0%; Pred. No. 5.2e-55;
ive 0; Mismatches | 0;
376 AA
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Goel V.K., Liu S., Chisthi A.H., Oh S.S.
                                     Created)
 PRT;
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Matches 376; Conservative
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                                                                                                                    Plasmodium falciparum.
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                                                                                                                                      Eukaryota; Alveo
NCBI_TaxID=5833;
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PLKTLSEBSIQTEDNYASLENFKVLSKLBGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                                           PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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                                                                                                          180 VT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIITFNLNLNDILNSRLKKRKYFL 238
                                                                                                                                                                                                                                         359 LVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTNDFEAIKKLIN 418
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 61 IKNKNYTGNSPSENNKKVNEALKSYENFLPE-AKVTTVVTPPQPDVTPSPLSVRVSGSSG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93295445; PubMed=8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSPI) of Plasmodium falciparum field isolates.";
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Fukarvota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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20, Last annotation update)
protein (Fragment).
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EMBL; D13350; BAA02611.1; -.
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Pfam; PF00008; EGF; 1.
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01-NOV-1996 (TrEMBLrel. 01
01-MAR-2002 (TrEMBLrel. 20
Major merozoite surface pi
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                                               1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT 1266
                                                                                                            PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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180 VT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIITFNLNLNDILNSRLKKRKYFL 238
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of Plasmodium falciparum
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal
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Mol. Biochem. Parasitol. 59:95-100(1993).
BMBL; D1346; BAA02607.1; -.
InterPro; IPR000561; EGF-11ke.
Pfam; PF00008; EGF, 1.
EGF-11ke domain; Merozoite.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last sen
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Matches 347; Conservative
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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MEDLINE=93295445; PubMed=8515786;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Eukaryota; Alveolata;
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MEDLINE-93205445; PubMed=8515786;
Jongwutiwes S., Tanabara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSPI) of Plasmodium falciparum from field isolates.";
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                STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS
                                                     NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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     LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT
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01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment).
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EMBL; D13348; BAA02609.1; -
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF;
EGF-like domain; Merozoite.
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"Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL. D13352. BAA02613.1;
InterPro: IPR000561; EGF-11ke.
Pfam; PF000008; EGF-11ke.
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Best Local Similarity 60.5%; Pred. No. 3e-48;
Matches 346; Conservative 79; Mismatches 111;
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence u
01-NOV-1996 (TrEMBLrel. 01, Last sequence u
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Major merozoite surface protein (Fragment).
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EMBL; D13344; BAA02605.L; -.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF, II.
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EKVLAKYKDDLESIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNN 358
                                                                                                                                                                                                                                                                                                                                                   477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSP1) of Plasmodium falciparum ffield isolates.";
STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS
                                                                   NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
                                                                                                                                    KILSEKYKSDLDSIKKYI--------NDKQGENEKYLPFLNNIETLYKT
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.0%; Score 1767; DB 5; 60.5%; Pred. No. 3.2e-48;
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EMBL; D13355; BAA02616.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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Pfam; PF00008; EGF; 1.
EGF-11ke domain; Merozoite.
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SEQUENCE FROM N.A.
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MEDLINE=93295445; PubMed=8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSPl) of Plasmodium falciparum from field isolates.";
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                            359 LVNKIGDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTDDFEAIKKLIN
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
NCBL_TaxID-5833;
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EMBL: D13345; BAA02606.1; -.
Interpro: IPR000561; EGF-like.
Pfam: PF00008; EGF: I.
EGF-like domain; Merozoite.
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Major merozoite surface
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PSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFK 1326
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Plasmodium falciparum f
                 NVLESDLIPYKOLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
                                                                          Length 569;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Major merozoite surface protein (Fragment).
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part
major merozoite surface proteins (MSP1) of Pla
field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13354; BAA02615.1;
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Pfam; PF00008; EGF; 1.
EGF-like domain; Merozoite.
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NCBI_TaxID=5833;
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Matches 344;
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NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY 1386
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EKVLAKYKDDLESIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNN 358
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                                                  SEQUENCE FROM N.A.
MEDLINE=93295445; PubMed=8515786;
Jongwutiwes S., Tanabe K., Kanbara H.;
Sequence conservation in the C-terminal part of the precursor to major merozoite surface proteins (MSPI) of Plasmodium falciparum field isolates.";
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NCBI_TaxID=5833;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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EBBL; D1343; BAA02604.1; -
InterPro: IPR000561; EGF-11ke.
Pfam; PF000008; EGF;
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J. Mol. Biol. 195:273-287(1987).
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Jongwitiwes S., Tandbe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 59:95-100(1993).
EMBL; D13347; BAAQ2608.1; -.
Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF, 1.
EGF-like domain; Merozoite.
                                                                                                                                                                                              STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
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180 VT. MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIITFNLNLNDILNSRLKKRKYFL
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                                                  NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment)
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Matches 343; Conservative
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Eukaryota; Alveolata;
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STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                   DDTKKDMLGKLLSTGLV-QNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHL 477
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update).
Major merozoite surface protein (Fragment).
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59.8%; Pred. No. 1.6e-47;
iive 80; Mismatches 114;
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EMBL; D13353; BAA02614.1; -.
InterPro; IPR000561; EGF-like.
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EGF-like domain; Merozoite.
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Matches 342; Conserv
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  1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVT 1266
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Jongwutiwes S., Tanabe K., Kanbara H.;
"Sequence conservation in the C-terminal part of the precursor to the major merczotte surface proteins (MSP1) of Plasmodium falciparum from field isolates.";
                          STREETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                         TVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLS
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                                                                                                                                                                       NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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Last annotation updat
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence u
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Major merozoite surface protein (Fragment).
MSP1.
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EMBL: D13351; BAA02612.1; -.
Interpro. IPR000561; EGF-like.
Pfam: PF00008; EGF: I.
EGF-like domain; Merozoite.
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Matches 343; Conservative
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NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence diversity of the merozoite surface protein 1 of Pl falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL; AF061143; AAC69742.1;
NON_TER
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                                                                                                                                                                                      KINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSL 368
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Last sequence update)
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MEDLINE=20106724; Pubmed=10643908;
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Matches 329; Conservative
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Q9TZU5
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STKEETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAIS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 SVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIK 140
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                                                                                          NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
                                                                                                                                                      KILSEKYKSDLDSIKKYI--------NDKQGENEKYLPFLNNIETLYKT
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Last annotation update)
(Fragment).
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Kerr P.J., Ranford-Cartwright L.C., Walliker D.;
"Proof of intragenic recombination in Plasmodium
Mol. Blochem. Parasitol. 46:185-187(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-39107347, Pubmed-7808474;

KEAT P.J., Ranford-Cartwright L.C., Walliker D.;

"Proof of intragenic recombination in Plasmodium Mol. Biochem. Parasitol. 66:241-248(1994).

EMBL: X52962; CAA37135.1; -..
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Matches 334; Conserv
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SEQUENCE
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                                                                                                                                                              Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                  Jiang G., Daubenberger C., Huber W., Matile H., Tanner M., Pluschke G.;
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Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
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Pred. No. 9.4e-45;
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2011 (TrEMBLrel.), Last annotai
Merozoite surface protein 1 (Fragment).
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  PRT;
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MEDLINE=20106724; PubMed=10643908;
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91.0%;
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  PRELIMINARY;
                                      (TrEMBLrel.
                                                                                                                                         Plasmodium falciparum
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01-MAY-2000 (
01-DEC-2001 (
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118 SDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINEL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AVTTSTPG---SKGSVASGGSVASGGSVASGGSVASGGSVASGGSCNSRRTNPSDNS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence diversity of the merozoite surface protein 1 of Pl falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
NON_TER 357 357
SEQUENCE 357 AA; 39850 MW; 498FCDF8E2DF1AID CRC64;
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                                                                                                                Length
                                                                  39850 MW; AE9513F521FA9ED5 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                DB 5;
                                                                                                                                                           16;
                                                                                                           Query Match 19.4%; Score 1636.5; DB Best Local Similarity 90.6%; Pred. No. 2.4e-44 Matches 326; Conservative 11; Mismatches 1
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01-MAY-2000 (TrEMBLrel. 13, Last sequer
01-DEC-2001 (TrEMBLrel. 19, Last annot:
Merozoite surface protein 1 (Fragment).
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Acta Trop. 74:51-61(2000).
EMBL; AF061141; AAC69740.1; -.
NON_TER 357 357
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Eukaryota; Alveolata;
                                                                  SEQUENCE 357 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LISVLEKRIDTLKKNENIKELLDKINEIK-NPPPANSGNTPNTLLDKNKKIEEHEKEIKE 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                              118 SDSDAKSYADLKHRVRNYLFTIKELKYPELFDLTNHMLTLCDNIHGFKYLLDGYEEINEL
                                                 LYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGK
                                                                                                   MEDY IKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHN
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360 AA; 40170 MW; 224E3CD345BD2F7A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
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Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL, AF061136; AAC69735.1; -..
TRR 360 360
A0170 MW;
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Matches 325; Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveo
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-IFA9.
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61 AVTISTPGSK---GSVASGGSGGSVA---SGGSVASGGSVASGGSVASGGSGNSRRINPS 114
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                                                                                                                                                                                                                                        "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
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                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 363;
                                                                                                                   Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                             MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
Pluschke G.;
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s 18; Indels
                                                                                                                                                                                                                                                                                                                        363 AA; 40398 MW; C25F38CB636941B7 CRC64;
                                                                  Last sequence update)
Last annotation update)
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89.0%; Pred. No. 5.3e
iive 15; Mismatches
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                                                                                        Merozoite surface protein 1 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annota
Merozoite surface protein 1 (Fragment).
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Tanzania.";
Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL; AF061139; AAC69738.1; -..
... mpR 363 363
                                                   (TrEMBLrel. 13,
                                                                  (TrEMBLrel. 13, (TrEMBLrel. 19,
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Matches 323; Conservative
                          PRELIMINARY;
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Plasmodium falciparum.
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01-MAY-2000 (
01-DEC-2001 (
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01-MAY-2000 (
01-MAY-2000 (
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Q9TZU1
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

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301 VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKT 360
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Acta Trop. 74:51-61(2000).
BEMBL: AF061137; AAC69736.1; -.
NON_TER 365 365
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                                                                                                                                                                                                                                                                                                                                   232 YIKKNKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLFIYNKQLEEAHNLIS
               181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED
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Best Local Similarity 86.8%; Pred. No. 4.7e-43;
Matches 317; Conservative 16; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Last annotation update)
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MEDLINE=20106724; Pubmed=10643908;
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01-MAY 2000 (TrEMBLrel. 13, 0
01-MAY -2000 (TrEMBLrel. 13, 1
01-DEC 2001 (TrEMBLrel. 19, 1
Merozoite surface protein 1
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SEQUENCE
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                                                                                                                             protein 1 of Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKE 356
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                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                         Sequence diversity of the merozoite surface protein 1 of Pl falciparum in clinical isolates from the Kilombero District, Aranzania...;
Acta Trop. 74:51-61(2000).
EMBL. AF061147; AAC69746.1; -.
MON_TER SEQUENCE 344 AA: 38767 MW; 1225C0E1683007DF CRC64;
                                                                                                                                                                                                                                                                               Length 344;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                  14; Indels
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Last annotation update)
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                                                                                        Jiang G., Daubenberger C., Huber W., Matile H
Pluschke G.;
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                                                    STRAIN-HN6.27;
MEDLINE-20106724; PubMed-10643908;
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STRAIN-IFA9.16;
MEDLINE-20106724; PubMed-10643908;
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EMBL, AF061135; AAC69734.1; -.
WON_TER & 362 362
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es 322; Conserv
NCBI_TaxID-5833;
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Pluschke G.;
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Q9T2V3
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SEQUENCE
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294
                                     241 VGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEE 300
                                                                  295 AHNLISVLEKRIDTLKKNENIKELLDKINEIK-NPPPANSGNTPNTLLD-KNKKIEEHEK 352
                                                                              AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGGSGNSRRTNPSDNSSDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AVTTSTPGSKGSGGSGGSGGSVA---SVASGGSVA---SVASGGSGNSRTMPSDNSSDS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 1585.5; DB 5; Length 351; 88.2%; Pred. No. 9e-43; Live 16; Mismatches 19; Indels 7;
                                                                                                                                                                                                                                         Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                    "Sequence diversity of the merozoite surface protein 1 of Pl falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
BEMBL: AF061144; AAC69743.1; -.
NON_TER 351
                                                                                                                                                                                                                                                                                                             Jiang G., Daubenberger C., Huber W., Matile H., Tanner M., Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                   351 AA; 39465 MW; 06481719E004278D CRC64;
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 88.2
Matches 315; Conservative
                                                                                                                                                                                PRELIMINARY;
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361 KIKEI 365
                                                                                                           353 EIKEI 357
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Q9T2U4
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RESULT 50 Q9TZU3

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LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
BEMBL: AF061145; AAC69744.1; -.
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                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                    STRAIN-HN5;
MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner
Pluschke G.;
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MEDLINE-20106724; PubMed=10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner
Pluschke G.;
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                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 9e-43;
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 351
                                                                                        Merozoite surface protein 1 (Fragment).
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88.2%;
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                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
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PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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SSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
BEBBL: AF061131; AAC69730.1; -.
NON_TER 347 347 347
SEQUENCE 347 AA; 39603 MW; 5E155E74DB6CD0CB CRC64;
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                181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED
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                                                        LLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 347;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID⇒5833;
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Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=IFAA.26;
MEDILINE=20106724; PubMed=10643908;
Jiang G., Daubenberger C., Huber W., Matile Bluschke G.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annotai
Merozoite surface protein 1 (Fragment).
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                                                                                                                                                                                                                                                         DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEI 174
                                                                                                                                                                                                                                                                                                               NELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDN 234
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                                                                                                                                          1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
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                                                                                  Length 360;
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                                                                                                              22; Indels
                                                      498DE127997E8B9B CRC64;
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Last annotation update)
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MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H.,
                                                                                  18.7%; Score 1576; DB 5; 87.5%; Pred. No. 1.8e-42;
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EMBL; AF061133; AAC69732.1; -.
NON TER 353
SEQUENCE 353 AA; 40089 MW;
                                                      39814 MW;
          Acta Trop. 74:51-01,000.

EMBL; AF061138; AAC69737.1;

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                                                                                                              Matches 315; Conservative
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Plasmodium falciparum.
Eukaryota; Alveolata;
                                                      SEQUENCE 360 AA;
                                                                                                 Similarity
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                                                                                    Query Match
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PRT;
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Best Local :
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Q9TZV4
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Acta Trop. 74:51-61(2000).
BMB. AF061132; AAC69731.1: -
NON_TER 347 A54; 39603 MW; 5E155E74DB6CDDCB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 347;
                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                    Jiang G., Daubenberger C., Huber W., Matile H., Tanner M., Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HN1;
MEDILNE-20106724; PubMed=10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%; Score 1544.5; DB 5; Length
86.2%; Pred. No. 1.7e-41;
Live 11; Mismatches 29; Indels
                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
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Last annotation update)
                     347 AA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annota
Merczoite surface protein 1 (Fragment).
MSP1.
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Matches 307; Conservative
                     PRELIMINARY;
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Eukaryota; Alveolata:
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NCBI_TaxID=5833;
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                   O9TZV5
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61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
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falciparum in clinical isolates from the Kilombero District, Tanzania.";
Acta Trop. 74:51-61(2000).
EMBL; AF061142; AAC69741.1; -.
NON_TER 352 352
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EMBL: AF061134; AAC69733.1; -. NON_TER 347 347
                                                                                                                                                                           Length 352;
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MEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M.,
                                                                                                                            352 AA; 39477 MW; 1C62B4ED3025175B CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
                                                                                                                                                                           18.3%; Score 1544; DB 5; 86.0%; Pred. No. 1.8e-41; tive 19; Mismatches 23;
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MEDLINE-20106724; PubMed-10643908;
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EMBL; AF061149; AAC69748.1; -.
NON_TER 344 344
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                            PRELIMINARY;
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                                                                                                                                         Eukaryota; Alveo.
NCBI_TaxID=5833;
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                                                                     LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED
                                                                                                                                         132 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLFIYNKQLEEAHNLIS
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                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-IFA17.29;
BEDLINE-20106724; PubMed-10643908;
Jiang G., Daubenberger C., Huber W., Matile H., Tanner M., Pluschke G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1489; DB 5; Length 34
Pred. No. 9e-40; 1
5; Mismatches 35; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Merozoite surface protein 1 (Fragment).
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Acta Trop. 74:51-61(2000).
EMBL. AF061150; AAG69749.1; -.
NON_TER 344 AA; 39143 MW; A9DB2D
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82.68;
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01-DEC-2001
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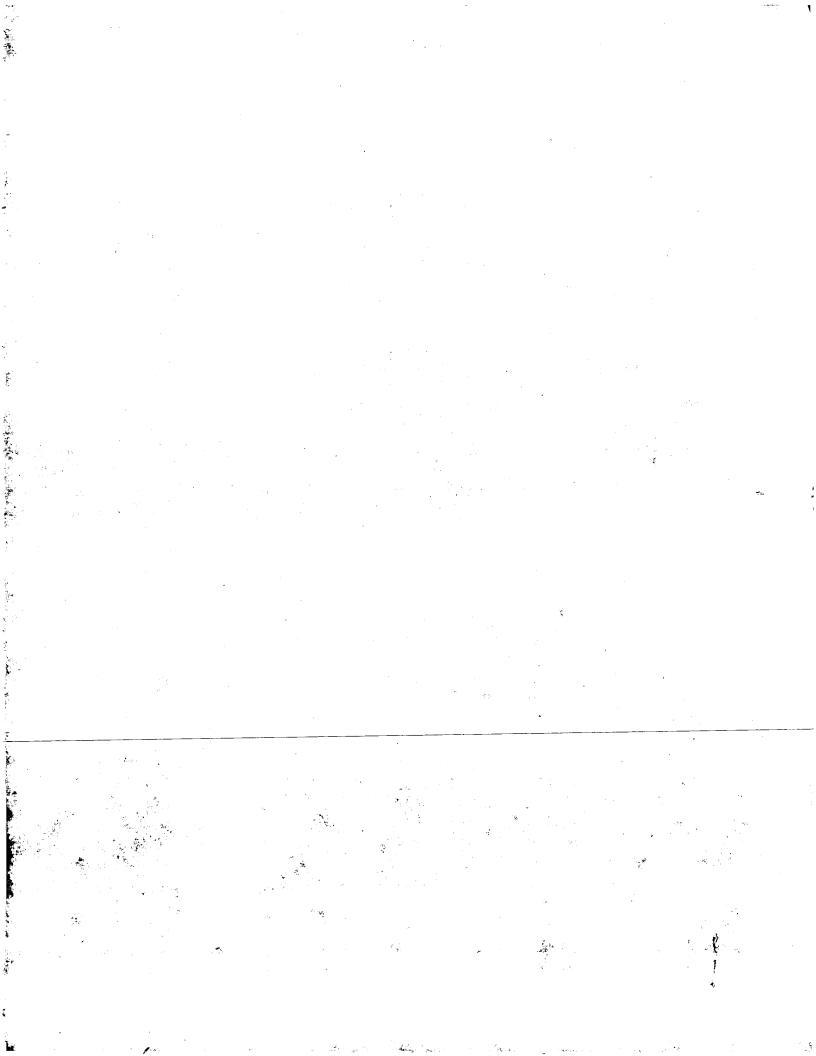
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"Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District, Tanzania.",
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporiĝa; Plasmodium.
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Merozoite surface protein 1 (Fragment)
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[2]
*SEQUENCE FROM N.A.
MEDLINE-95107347; PubMed-7808474;
Kerr P.J., Ranford-Cartwright L.C., Walliker D.;
*Proof of intragenic recombination in Plasmodium falciparum.";
*Mol. Blochem. Parasitol. 66:241-248(1994).
                                                                                                                                                                                        Query Match
17.4%; Score 1467.5; DB 5; Length 363;
Best Local Similarity 81.6%; Pred. No. 4.4e-39;
Matches 298; Conservative 10; Mismatches 38; Indels 19;
                                                                                               Ranford-Cartwright L.C.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X52963; CAA37136.1; -
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SEQUENCE 363 AA; 40336 MW; A86C08A93DE5AF9B CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Eukaryota; Alveolata;
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Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ database
-!- SUBCELLULAR LOCATION: Attached to the membrane by
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Merozoite surface protein 1 precursor (Merozoite
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MEDLINE-86136024; PubMed=3004972;
Mackay M., Goman M., Bone N., Hyde J.E.,
Stunnenberg H., Bujard H.;
"Polymorphism of the precursor for the ma
Plasmodium falciparum merozoites: studies
EMBO J. 4:3823-3829(1995).
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532 EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKII (601 ENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTV	661 PYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKT 	721 AGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQº	772 FLNTSYICHKYILVSHSTWNEKILKQYKITKEEE:	841	901 PQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKI 	951 TFYNESFTNEVKSKADDINSLNDESKRKKLEEDLI 	1021	7 1081 TKILLKHYKGLVKYYNGESSPLKTLSEESIQTED 	1141 KKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENI 	1201 ESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDI 	1261	1321 KRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNI 	1381 DVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYI 	1441 AKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKI	1501 TGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKI	1561 QEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSI	/ 1621 NFLGISFLLILMLILYSFI 1639
90 AQ	da qa	Qy	Qy	Qy Db	Oy Dp	QY Db	40 	QQ QD	Qy Db	Qy Db	Qy Db	Q7 Dp	Qy	Qy Db	QY	QY	Qy Db
cs Institute. Ther itutions as long as nt is not removed. se agreement (See h'se@isb-sib.ch).	EMBL; X03371; CAA27070.1; PIR; A25120; SAZOKI.	Pram; Prudud8; EGF; 1. Malaria; Merozoite; Polyprotein; Repeat; Signà Transmembrane; GP1-anchor. SIGNAL	CHAIN 20 1630 MEROZOITE SURRACE PROTI- DOMAIN 67 84 TRIPEPTIDE SG(TP) REPER TRANSMEM 1614 1630 MEMBRANE ANCHOR. CARBOHYD 97 97 N-LINKED (GLCNAC)	CARBOHYD 259 259 N-LINKED GLCNAC) CARBOHYD 755 755 N-LINKED GLCNAC) CARBOHYD 759 N-LINKED GLCNAC) CARBOHYD 774 774 N-LINKED GLCNAC)	CARBOHYD 835 835 N-LINKED (GLCNAC:) CARBOHYD 955 955 N-LINKED (GLCNAC:) CARBOHYD 1049 N-LINKED (GLCNAC:) CARBOHYD 1164 1164 N-LINKED (GLCNAC:)	CARBOHYD 1165 N-LINKED (GLCNAC:) CARBOHYD 1165 1165 N-LINKED (GLCNAC:) CARBOHYD 11436 11436 N-LINKED (GLCNAC:) CARBOHYD 11517 1117 N-LINKED (GLCNAC:) CARBOHYD 1517 1117 N-LINKED (GLCNAC:) SEQUENCE 1630 AA: 1187289 WW. ADRIFFCTCHOALG:)	Query Match 96.7%; Score 8144.5; DB 1; Le Best Local Similarity 97.1%; Pred: No. 3.6e-258; Attches 1591; Conservative 11; Mismatches 28; Ind	Qy	61 KGSAAOSGTSGT-SGPSGTSGPSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTS	121 DAKSVADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLJDGYEEINELLYK	181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGTRKPLDNIKDNVGKMED 111111111111111111111111111111111111	QY 241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYÖAQYDLSIYNKQLEEAHNLIS 300 11111111111111111111111111111111111	301 VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKKT 	361 IKFNIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGYTYPLSYNDINNAL 11111111111111111111111111111111111	421 NELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKİKIEKKKIESDKKSYEDRSKS	481 LNDITKEYEKLLNEIYDSKFNNNIDLTNFKKMGKRYSYKVEKLTHHNTFASYENSKHNI [541 EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKOEEQLFEKKITKD

1020 1080 1140 1200 1380 1440 1011 1071 1131 1191 1431 DDEVDDVIIVPIFGESEEDYDDLGQVV 1260 780 840 900 960 720 951 711 771 831 891 591 TQLILKNVELKHNIHVPNSYKQENKQE QVPTPPAPVNNKTENVSKLDYLEKLYE NKEKRDKFLSSYNYIKDSIDTDINFAN YLPFLNNIETLYKTVNDKIDLFVIHLE KKKNNNEVGIADLSTDYNHNNLLTKFLS SNGKKITCECTKPDSYPLFDGIFCSSS I ENEIETLVENIKKDEEQLFEKKITKD QVPTPPAPVNNKTENVSKLDYLEKLYE KNKNIYQELIGQKSSENFYEKILKDSD DDEVDDVIIVPIFGESEEDYDDLGQVV KKQCPQNSGCFRHLDEREECKCLLNYK ESKLSSCDPLDLLFNIQNNIPVMYSMF NNTDVNNALESYKKFLPEGTDVATVVS YLPFLNNIETLYKTVNDKIDLFVIHLE DNYASLENFKVLSKLEGKLKDNLNLEK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                           SEQUENCE OF 1104-1726 FROM N.A.
MEDLINE=88143999; PubMed=3278296;
Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
Werozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 16:1206-1206(1988).
-:- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                            surface antigens)
                                                                                                                                                                                                  Weber J.L., Leininger W.M., Lyon J.A.; "Variation in the gene encoding a major merozoite surface antigen
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                               Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5835;
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                                                                                                                                                                                                                           the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD8AD45FA352BCF3
                                                                           01-0CT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P195).
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llarity 60.1%; Pred. No. 2.5e-160;
Conservative 221; Mismatches 342;
                                                                  Last sequence update)
Last annotation update)
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                                 STANDARD;
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                                                                   01-MAR-1989
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Matches 1052;
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QSNASSTUTQNGVAVSSGPAVVEESHDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTI 1000 GOKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQL 1003 SFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFF 1063 418 649 331 NSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAK 391 477 737 KQAQPPV-----PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICH 789 NHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRA SQDPTKSVQIPKVPYPUGIVYPLPLTDIHUSLAADNDKNSYGDLMNP-DTKEKINEKIIT DN-ERKKFINEIKEKIKIEKKKI----ESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKF EKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK - - - ITKDENKPDEKILEVSDIVKV MPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQ KY ILVSHSTMNEK ILKQYK ITKEEESKLSSCDPLDLLFNIQNNI PVMY SMFDSLNNSLSO -- MQPLSLTPQDKPEVSAND---DTSHS----TNLNNSLKLFENILSLGKNKNIYQEL-I KGASAQSGTSGTSGTSGTSGTSGTSAQSGTSGTSAQSGT--SGTSAQSGTSGTSGTS GN--SRRTN------PSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLT NELDVLKKLVFGYRKPLDNIKDNVGKMEDY IKKNKKT I ENINEL I EESKKT I DKNKNATK EEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPA VE--TKESTEPN-EYPNGVTYPLSYNDINNAL---NELNSFGDLINPFDYTKEPSKNIYT NNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVV QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVF 710 IPKVKDMLKKEQAVLSS-----ITQPLVAASETTEDGGHSTHTLSQSGETEVTEET **EETEETVGHTTTVTITLPPKEVKVVENSIEHKSNDNSQALTKTVYLKKLDEFLTKSYICH** LFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKV------STSVKTLSSSS----

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the Swiss Institute of Bioinformatics and the EMBL outstation the Swiss Institute of Bioinformatics and the EMBL outstation-pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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PSSRSNTLPRSNTSSGASPPADASDSDAKSYADLKHRVRNYLFTIKELKYPELFDLT
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700008; EGF, 1.
8 Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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MEROZOITE SURFACE PROTEIN 1.

N-LINKED (GLCNAC...) (POTEN LINKED (GLCNAC...) (POTEN MW; SES9CEEFAZF9A026 CRC64;
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llarity 60.1%; Pred. No. 4.9e-160;
Conservative 221; Mismatches 343;
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                           1657 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLL 1716
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Merozoite surface protein precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLL
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MEDILINE-88011243; PubMed-3079521;
Tanabe K., Mackay M., Goman M.; Scaffe J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scaife J., Certa U.,
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Plasmodium.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat;
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Stunnenberg H., Bujard H.;
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J. Mol. Biol. 195:273-287(1987).
[2]
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PIR; B25120; B25120
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Eukaryota; Alveolata;
NCBI_TaxID=5837;
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P13819;
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                                                                        MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
        . .) (POTENTIAL).
. .) (POTENTIAL).
.) (POTENTIAL)
                                                 Best Local Similarity 60.1%; Pred. No. 3.8e-158;
Matches 1042; Conservative 226; Mismatches 339; Indels 126;
                                          Length 1701;
N-LINKED (GLCNAC ...)
N-LINKED (GLCNAC ...)
N-LINKED (GLCNAC ...)
N-LINKED (GLCNAC ...)
MW, 3FCZECS9AF96EA98 C
                                           Score 5069; DB 1;
Pred. No. 3.8e-158;
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                                                                                                  antigens)
                                                                                                                                                                                      -----SGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIF
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AND---DTSHS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSD
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OTT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozo
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                          tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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KDa AND 19 KDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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N-LINKED (GLCNAC...)
                      Mol. Biochem. Parasitol. 27:291-302(1988).
                                                                                                                                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 60.1%; Score 5065; DB 1; Best Local Similarity 60.1%; Pred. No. 5.2e-158; Matches 1042; Conservative 227; Mismatches 338;
Plasmodium falciparum.";
Biochem. Parasitol. 27:291-302(1988)
                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat;
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1291 GESEDNDEYLDQVVTGEAISVT-MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1061 FROM N.A.
MEDLINE-8816657; PubMed=3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen precursor pl90 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
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                                            C-terminal region of
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                                                                                                                                                                                                          CTEEDSGSSRKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI 1701
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EMBL; V00087; CAA68280.1; -.
EMBL; 235326; CAA84555.1; -.
PIR; S06286; S06286.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P190).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate ro-33 / Ghana).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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MEDLINE-99354793; PubMed-7628566;
MOLILE R., Bujard H., Cooper J.A.

"Plasmodium falciparum: variations within the
                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: Attached to the
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MW; C82A1E15948CAD6 CRC64;
                                                                                                                             DB 1; Length 1682;
                                                                                                                         Ouery Match 57.6%; Score 4854.5; DB 1; Length Best Local Similarity 58.4%; Pred. No. 3.6e-151; Matches 1007; Conservative 223; Mismatches 368; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis A.P.; "Sequence analysis upstream of the gene encoding the precursor to the major merozoite surface antigens of Plasmodium yoelii.";
                              924 HDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKIMIPIFNDDIKQ
                                                                                                                                  1103 GLVKYYNGESSPLKTLSEVSIQTEDNYANLEKFRYLSKIDGKLNDNLHLGKKKLSFLSSG
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HS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSDTFYNESFTN
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                                                                                                      FVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYK
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VCBI_TaxID=5862;
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Last annotation update)
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                                                                                      merozoite surface
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                                                                 Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.; The 3' portion of the gene for a Plasmodium yoeili merozoite suri antigen encodes the epitope recognized by a protective monoclonal antibody.";
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                                                                                                                                                                     -! - PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROZOITE SURFACE PROTEIN
N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
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N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
N-LINKED (GLCNAC. ) (F
                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 85:602-606(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2548.5; DB Pred. No. 3.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REF.
Parasitol. 39:285-288(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NI) A <-
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                       MEDLINE=88124889; PubMed=2448778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197230 MW;
Mol. Biochem. Parasitol. 39:285
[2]
SEQUENCE OF 1093-1772 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           EMBL; J03612; AAA29762.1; -. EMBL; J04668; AAA29702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%;
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1680
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PIR; A45532; A45532.
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406
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1018
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1521
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N	KKIEBHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTE	PLTIRYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKF	INEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLL 	MGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS :	KIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELK) KTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNI :: : : : : : : : : : : : :	KEG 	DSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTËNVSKLDYLEKLYEFLNTSYI	CHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPL : : :	SLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEA	- KKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHS	SNAATPAGTSASGSAASNASTTSDVTPPAAAAAVPSTSTPAPAQPPAANSQSGNPDSGIR	GQKSSENPYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEE	DINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNP:	KHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIGT 	EDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLH LIAELKEVIKNKNYTGNSPS 	ENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEGSQPKKPASTHVGAESNTI : : : : : :
335	345	400	453	513	573 598	633	693	728	788	846	941	917	944	993	1053	1113	1173
95 Pp	Oy Dp	Qy Dp	çy Pa	Qy Dp	Oy Dp	Qy Dp	yo. da	oy Ob	çy q	Oy Op	Oy Dp	Qy Dp	g 6	Oy Dp	Qy Dp	oy Pp	oy op

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                                                                                       1406 FTNESLYVYTKRLGSTYKSLKKHMLREFSTIKEDMTNGLNNKSQKRNDFLEVLSHELDLF 1465
                                                                                                                                                       1693 KGEGNTCVENNNPTCDINNGCDPTASCQNAESTENSKKIICTCKEPTPNAYYEGVFCSS 1752
                                 1358 GAVPGAVPGSGTDTRVAGSSVDD-----NED-DDIYQIASGQSEDAPEKD-ILSE 1405
                                                                   1277 IENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPY 1336
                                                                                                                                                                                                       LDSIKKYI-----ND-KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTY 1448
                                                                                                                                                                                                                                                                                                                                               1505 FENLAKTVLSNLLDGNLQGM--LNIS-QHQCV-KKQCPQNSGCFRHLDEREECKCLLNYK 1560
-----TISQNVDDEVDDVIIVPIFGESEEDYDDLGQVVIGEAVIPSVIDNILSK 1276
                                                                                                                                     KDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSD 1396
                                                                                                                                                                                                                                                                           EKSNVEVKIKELNYLKTIQDKLADF ----KKNNNFVGIADLSTDYNHNNLLTKFLSTGMV 1504
                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDINE-81106855; PubMed-3542719; HOWARD R.F., Ardeshir F., Reese R.T.; Conservation and antigenicity of N-terminal sequences of GP185 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07N-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (Glycoprotein 185) (GP185) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                 1561 Q-EGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate CDC / Honduras).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
MEROZOITE SURFACE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                different Plasmodium falciparum isolates.";
Gene 46:197-205(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1753 SSFMGLSILLIITLIVFN 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1620 SNFLGISFLLILMLILYS 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M14632; AAB59227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; GPI-anchor.
SIGNAL 1 19
CHAIN 20 >233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A25814; A25814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSP1_PLAFD
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 1228
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6150B76E0F21B299 CRC64;

31226 MW;

281 AA;

SEQUENCE

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                                                                                                  ij
                                                                                                                                                                                                61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120
                                                                                                                                                                                                                 61 AVTSTPGSKGSVASGG-----SGGSVASGGSVASGGSGNSRRTNPSDNSSDS 108
                                                                                                                                                                                                                                                              121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180
                                                                                                                                                                                                                                                                                 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240
                                                                                                                                                                                                                                                                                                                                               (Potential).
MISCELLANEOUS: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83K, 42K & 19K ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                  Gaps
                                                                                                                                                1 MXIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.;
"Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Biochem. Parasitol. 27:291-302(1988). SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                  MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
MEROZOTTE SURFACE PROTEIN 1.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                 Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                  0; Indels
                                26050 MW; 1DE4D31ACAEEE965 CRC64;
                                                               Score 1187; DB 1;
Pred. No. 7.4e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Ghana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (isolate NF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88142999; PubMed=2449612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
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                                                                 14.1%;
95.1%;
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                                                                                                Conservative
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109
248
281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B54498; B54498.
                             ,233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PMMSA) (Fragment).
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5842;
                                                                                                                                                                                                                                                                                                                                                                                                                              229 YIKK 232
                                                                                                                                                                                                                                                                                                                                                                                               241 YIKK 244
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CARBOHYD
NON_TER
SEQUENCE
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Matches
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Modol V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Modol V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

R. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

An Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

An Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

R. Annoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

R. Annoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

R. Skelton J., Simmonds M., Squares R., Squares S., Stewens K.,

Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

R. Andoward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Meeller-Auer S.,

R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Borzym K., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Cerrutti L., Lowe T., Morcondie W.R., Paulsen I., Potashkin J.,

R. Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;

R. The genome sequence of Schizosaccharomyces pombe.";
                                     5
                                                                                                                                                                                                                            61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGN--SRRTN----- 112
                                                                                                                                                                                      57 EITT-----KG--ASAQSGASAQSGASAQSGASAQSGTSGPSGPSGTSPSSRSNTLPRSN 109
                                     Gaps
                                                                         1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT '60
                                                                                             LIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRK
                                   25;
DB 1; Length 281;
                                                                                                                                                                                                                                                                                                                                                                              227 PLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKL 278
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                   Pred. No. 8e-30;
8; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ol-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein CIF3.06c in chromosome I SPACIF3.06c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1957 AA
Score 1096.5;
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(Rel. 34, Last sequ
13.08;
                                       Conservative
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01-0CT-1996
                                     Matches 227;
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1221 GAESNTITTSQNVDDEVDDV----1IVPIFGESEEDYDDLGQVVTG------1262
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                                                                                                                                                                                                                            984 KSSKLEADIEHLKNKVSEVEVERNALLASNERLMDDLKNNGENIASLQTEIEKKRAENDD 1043
                                                                                                                                                                                                                                                                                                                                                                                             1102 LKTLSEESIQTEDNYASL-ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
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880 NDQILTQLAELSKNYDSLEQESAQLNSGLKSLEAEKQLLHTENEELHIRLDKLTGKLKIE 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1263 EAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN-VNVKDI-LNSRFN
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                                                                                     1042 LESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSP
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01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                            DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL. SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNIHGFKYLIDG--YEEINEL------195
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                                                                                                                                                                                                                                             SUBCELLUIAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH INTRACELLULAR MEMBRANES, PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Golgi stack; Cytoskeleton; Coiled coil. GLOBULAR HEAD.
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CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FUNCTION.
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                                                                                                         SEQUENCE OF 1-8 FROM N.A.

SEQUENCE OF 1-8 FROM N.A.

Bal Y., Symington L.S.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: REQUIRED FOR PROTEIN TRANSFORT FROM THE ER'

-i- FUNCTION: REQUIRED FOR PROTEIN TRANSFORT FROM THE IN
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6CE2B216E9FD4818 CRC64;
                                          Hostetter M.K., Herman D.J., Bendel C.M., McClellan M.,
                                                                                         Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
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17 847 G -> E (IN REF. 2).
24 123 1253 V -> I (IN REF. 2).
25 1319 I -> V (IN REF. 2).
26 1319 I -> V (IN REF. 2).
27 1461 I -> V (IN REF. 2).
28 1319 I -> V (IN REF. 2).
29 1310 I -> V (IN REF. 2).
31 1581 G -> S (IN REF. 2).
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31 1561 I -> V (IN REF. 2).
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NTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREK-----NKNIDISAKV 392
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:: : :	312 NENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK-IEBHEKEIKEI- 357 	358AKTIKFNIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNG 406	407 VTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKK 466 1 1 1 1 1 1 1 1 1	467 IESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNIDLTNFEKMMGKRYSYK-VEKLT 525 1297 AGKVVEEMNSLKTKIEKLIQETSDDS-QNELVTTSITKHLENAKGYEDVIKRN 1348	526 HHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS-KIENE 577 1349 EEDSIOLREKAK-SLETLDEMKKLVQQVNMNLQSAIQGNAGISKELNELKGVIELLISTN 1407	578 IETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKID 629 13.1 1 1 1 1 1 1 1 1 1	630 E-KKTOLILKNY-ELKHNI	665MRVESLINE 1526 KANITDSQMEEVGNYVSKAEHAPHTVEAQVDKTKAFCESIVAYVTKMDNLFNESLMKEVK	688EKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV 744 : : : : : : : :	745 PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL 804 :: :: :	805 KQYKITKEEESKLSSCDPLDLLENIQNNIPVMYSMFDSLNNSLSQLFWEIYEKEMVCNLY 864 :	865 KLKDNDKIKNLLEEAKKVSTSVKTLSSS	922 SLKLFENILSLGKNKNI-YQELIGQ-KSSENFYEKILKDSDTFYNESFTNFVKSKADDIN 979 	980 SLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQ 1031	1032 IKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHY 1088 : : :: :: ::	1089 KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSY 1145 : : : : : :	1146 LSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSES 1202	1203 GSDTL
Qy 1330 ESDLIPYRDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKÖSIDTDINFANDVLGY 1385 Db 1645OELDSTOOKAAKSEEPRRAEVRKFOVEKSOLDFRAMILETKVNIJVV- 1691	1386 YKILSEKYKSDLDSIKKYINDKQGENEKYLPFLANIETLYKTVNDKIDLFV 1.	1437 IHLEAKVLNYTYEKSNVEVKI 1457	Sur	7. 1		OS Piasmooium vivax (strain Belem). OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. OX NCBI_TaxID=31273; RN fill RN fill	SEQUENCE FROM N.A. MEDILINE-S2315338, Pubmed-1617731; Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax	<pre>merozoltes.; Cell 69:1213-1226(1992)!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS!- SUBUNIT: HOMODIMER (POTENTIAL).</pre>	-i- SUBCELLULAR LOCATION: Membrane-bound. This SWISS-PROT entry is copyright. It is produced throug	CC the Buropean the Swiss Institute of Bioinformatics and the EMBL outstation - CC the Buropean Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as lists content is in no way CC modified and this statement is not removed. Usage by and for commercial Db		Malaria; Receptor; Signal; Tr SIGNA 1 17 CHAIN 18 2869 DOMAIN 18 2807	1 KANSMEM 2008 DOMAIN 2827 SITE 1030 SITE 2599 SEQUENCE 2869 AA	5.7%; Score 477; DB 1; Le Lty 20.9%; Pred. No. 1.4e-08; servative 300; Mismatches 617;	DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLF-DLTNHMLTLCDNIHGFKYLIDGYEE 173	174 INELLYKLNFYFDLLRAKLNDVCANDYCQIPFN 1	207 LKIRANELDVIKK-LVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENIN-	254 ELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKK

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EMBL; X73541; CAA51948.1; -.
EMBL; 228320; CAA82174.1; -.
PIR; S38173; S38173.
SGD; S0001803; MLP1.
Coiled coil; DNA repair.
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                                                                                                                                                                                                  1416
                                                                                                                                                          | | ::::|: :|: | 1 :| | :| | 2331 GSKL----TFSSASEIVQNADTYS-VNFAKHEK--ESLNAIRDIKKELYLFHQNSDISIV 2283
                                                                                                                                                                                                                                                                                   2402
                                                                                                                                                                                                                                                                                                             1491
                                                                                                                                                                                                                                                                                                                                                                                     1462 LVQAKTEYEQILENIKQNDDMLQNIFLKKVSILEYFENVKKKKESILNDLYE--QERLLK 2519
2052 VREALKRLSQVEGIRCHFENFHRLLDNTEELENLKKMVTIYRDKKSERESGLQEMENEMN 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94205265; PubMed-8154186; Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantalejo J.G., Remacha M., Jimenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPLI genes and three new open reading frames."; Fusc J. 1349-1354 (1993).
                                           2112 TYSNSITQLEGIVVSAGESKEDIEKLERSNEEMRNISEKISTIDSKVIEMNSTIDELYKL
                                                                                                                                                                                                                                                                        DVI---;----IVPIFGESEEDYDDL---GQVVTGEAVTPSVIDNILSKIENEYEVLY--
                                                                                 -----LKPLAGVYRSLK-----KQLENNVMTFNVNVKDILNSRFNKRENFKNVL
                                                                                                           GKNCQAHWISLISYTANMKTSKKLIMINKEKENTEKCVDY-IKDNSSSTDGYVETLKGFY
                                                                                                                                                                                                  -----KQGENEKYLP
                                                                                                                                                                                                                         EGGVQNMLALYDKLNEE-KREMDELYRNISETKLKQMEHSTDVFKPMIELHKGMNETNNK
                                                                                                                                                                                                                                                                                                                              ESDLIPYKDLTSSNYVVK - DPYKFLNKEKRDKFLSSYNYIKD - - - - - SIDTDINF -
                                                                                                                                                                                                                                                      FLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEK-----SNVEVKIKEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDITINE-92247549; PubMed-8483450;
MEDLINE-92247549; PubMed-8483450;
Koelling R., Nguyen T., Chen E.Y., Botstein D.;
"A new Yeast gene with a myosin-like heptad repeat structure.";
Mol. Gen. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                            1461 -NY------LKTIQDKLADFKKNNNFVGIADLSTDYNH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: SOME, TO THE TPR ONCOGENE.
-i- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
                                                                                                                                                                                                                                                                                                                                                                                                                         1527 ISQH-QCVKKQCPQNSGCFRHLDEREE--CKCLLNYKQE 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2520 IGEHLDEIKRNVTETLSSY-EIDQKMEMMSKNLLEKKSK 2557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLP1_YEAST

MLP1_YEAST

AC 002455;

DT 01-007-1993 (Rel. 27, Created)

DT 01-007-1993 (Rel. 29, Last sequence update)

DT 16-007-2001 (Rel. 40, Last annotation update)

DF 16-007-2001 (Rel. 40, Last annotation update)

DF 16-007-2001 (Rel. 40, Last annotation update)

Myosin-like protein MLP1.

GN MLP1 OR YKR095W OR YKR415.
                                                                                                                                                                                                ---ANDVLGYYKILSEKYKSDLDSIKKYIND-----
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78;
   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 TNPSDNSSDS-DAKSYADL------KHRVRNYLLT-IKELKYPQLFDLTNHML 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLIN 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; Score 474.5; DB 1; Length 1875; 20.7%; Pred. No. 1.1e-08;
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78 COILED COIL (POTENTIAL).
66 COILED COIL (POTENTIAL).
01 R -> A (IN REF. 1).
218455 MW; 683A0D34C9066867 CRC64;
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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the Swiss Institute of Bioinformatics and the EMBL outstation -
bean Bioinformatics and the EMBL outstation -
bean Bioinformatics Institute. There are no restrictions on its
non-profit institutions as long as its content is in no way
and this statement is not removed. Usage by and for commercial
requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                        213 1226(1992).
ION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO RETICULOCYTE CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1251;
                                                 M.R., Medina C.C., Ingravallo P., Barnwell J.W.; locyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1251 1251
1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                                                                                                                                                                                       LLULAR LOCATION: Membrane-bound (Probable).
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imilarity 21.1%; Pred. No. 2.5e-08;
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FROM N.A.
2315338; PubMed=1617731;
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is a putative kinetochore motor that accumulates just before
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Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                      CHARACTERIZATION.
MEDLINE-98437347; Pubmed-9763420;
                                                      MEDLINE-95196755; PubMed-7889940;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 215005; CAA78727.1; -. PIR; S28261; S28261.
HSSP; P17119; 3KAR.
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                                                                                                 EMBO J. 14:918-926(1995).
                     Nature 359:536-539(1992).
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MIM; 117143; -.
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                                                                                       microtubule motor.
                                          CHARACTERIZATION.
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                                                                          988 ----KKLEEDINKLKKTLQLSFDL---YNKYK-LKLE------RLFDKKKTVGKYKMQIK 1033
                                                                                                                      1034 KLTL-----LKEQLESKLNSL------NNPKHVLQNFSVFFNKKKEAEIAE-- 1073
                                                                                                                                                                -----TENTLEN-TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENF 1122
                                                                                                                                                                                                           1123 KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-NA 1181
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987
                                                    521 NYEIGFLEKLEEIGKNRKLKVDITKKSINSTVGNFSSLFNNFDLNQYDFNKNINDYENKM 580
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MEDLINE-93024922; PubMed=1406971;
Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
                                                                                                                                                                                     700 TGKNEEIQKITHSTLKNKAKTILGHVDTSAKYVGIKITPELALTE----
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Catarrhini; Hominidae;
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Last annotation update)
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01-JUL-1993 (Rel. 26, Last seq
30-MAY-2000 (Rel. 39, Last ann
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Mammalia; Eutheria; Primates;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 82; PHASE Chan G.K.T., Schar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";

Gell Biol. 143:49-63(1998).

-I- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION. IS 534 LDEFEALERKTKKDQEMQLIHEISNLKNLVKHREVYNODLENELSSKVELLREKEDQIKK 593 278 651 Gaps 126 ADLKHRVRNYLLTIKELK---YPQLFDLTNHMLT------------LCDNIHGFKY 166 ----LKKLVFG---YRKPLDN-----IKDNVGK 237 AND Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.; "Mitotic HeLa cells contain a CENP-E-associated minus end-directed :::|| ::|| ::|| 594 LQEYIDSOK --LENIKMDLSYSLESIEDPKQMKQTLFDAETVALDAKRESAFLRSENLEL 167 LIDGYEEI-----NELLYKLNFYFDL.--LRAKLNDVCANDYCQI-----PFNLKIR-ANE MEDYIKKNKKTIENIN------ELIEESKK------TID-KNKNATKEEEKKKL SMART; SW00129; KISC; 1. PROSITE; PS00411; KINESINHEAVY. PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1. PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1. Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis; Cell gycle; Centromere: 1 335. 559; SUBUNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
QUANTITATYVELY DISCARDED AT THE END OF THE CELL DIVISION.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. Length 2663; Indels 71. COILED COIL (POTENTIAL).
53 GLOBULAR (POTENTIAL).
53 ATP (8x SIMILARITY).
312087 MW; CEFC13880C8C8CB CRC64; -07; 617; DB 1; 1.6e-07 Local Similarity 18.4%; Pred. No. 1.6e es 345; Conservative 349; Mismatches Score 443.5;

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						:											
SGNT 336 - 	362 OKSE 768	YPLS 412 : CHMD 828	RKKF 452 RLNE 888	YEKL 491 :: RDQL 948	-YEN 535 MEEN 1000	IETL 581 :: : LQQM 1058	KTQL 636 KEGE 1114	K 689 KNKE 1171	AQAQ 735 ATGL 1231	ILVS 795 S 1274	846 EMER 1330	LSSS 892 DESQ 1383	QELI 943	KK 989 : CLKE 1488	MQIK 1033 : ENVN 1548	ETEN 1076 : ERDQ 1608	LKDN 1135 : NLEN 1662
LDKINEIKNPPPAN QSAFNEITKLTSLI	KEIKEIAKTIK ::: : SLPSEVERLRKEIQ	KESTEPNEYPNGVT:	-TKEPSKNIYTDNE : : KTQELQEKTREVQE	IESDKKSYEDRSKSLNDITKEYEKL 	EVSRNLH	VVEKELKYYKNLISKIENEIETL :: :: :: :: :: NEILEQORKIF-SLIQE-KNELQOM	VQKVLLMNKIDELK ::: : -QEIVAQEKNHAIK	. : :: . : ::	ALEGDSVQ 	(LYEFLNTSYICHKY	SMFDSLNNS : :: PEQSTTKDSTTLARI	ILLEEAKKVSTSVKT : :HIRETLAKI	NILSLGKNKNIYQELI : : LRIEIEMLGLSKRL	LKVAHC)KKKTVGKYK : : :: KEEQLNIKQISEVQ	KKEAEIAETEN :	ASLENFKVLSKLEGK : : : : :EIEHLKEQFETQKL
YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPANSGNT : : : : : ::: KEKMKELATTYKQMENDIQLYQSQLEAKKKMQVDLEKELQSAFNEITKLTSLIDGKV	PNTLL	FNIDSLFTDPLELEYYLREKNKNIDISAKÜTKESTEPNEYPNGVTYPLS 	YNDINNALNELNSFGDLINPF ^D Y-TKEPSKNIYIDNERKFF:	INEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL ::: :: :: :: MEQLKEQLENRDSPLQTVEREKTLITEKLQQTLEEVKTLTGEKDDLKQLQESLQIERDQL	LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYEN :: : :	LTADVKD	VENIKKDEBOLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL : :: ::	ILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK : : : : : LSRTCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIENLKNELKNKE	KNIKTEGOSDNSEPSTEGEITGQATTKPGQQAĞSLEGDSVQAQAQ ::::	EQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS 	HSTMMEKILKQYKITKEEESKLSSCDPLDLLENIQNNIPVMYSMFDSLNNS : : : : : : : : : : : : : :	LSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSS		GQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKK : : : : : : : : : : :	LEEDINKLKKTVGKYFEDLYN-KYKLKLERLFDKKKTVGKYKMOIK	KLTLLKEGLESKLNSLNNPKHVLQNFSVFFNKKKBAEIABTEN :	TLENTKILLKHYKGLVKYYNGESSPLKTLSEESI-QTEDNYASLENFKVLSKLEGKLKDN
KQLEEAHNLISVLEKR : : : KQMENDIQLYQSQ	DKNKKIEEHE 	FTDPLELEYYL ::: FSEVVHKESRVQGLL	DINNALNEL : : : VLEENERMNQEIVNLSKEAQ	INEIKEKIKIEKKK	IDLTNFEKMMGKRYS EQLR	SKHNLEKLTKALKYMEDYSLRNI : : : GETKDEFQQKMVGIDKKQDLEAKNTQT	EKKITKDENK : KTDLKENIEMTIE	HNIHVPNSYKQENKÇ : : : EKLKEKSQQLQEKQC	-GQSDNSEPSTEGEI 	VPEAKAQVPTPPAPV : : LKEHQETIDELRRSV	KITKEEESKLSSCDE : : : PVLHEEQELLPNVKK	KEMVCNLYKLKDN : : : : QEEIKSLTKERDNLK	SMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFE 	LKDSDTFYNE : AKEKDDLQRLQEVLC	KTLQLSFC : SEKETEISTIQKQLE	QLESKLNSLN :1 : DSALQSIESKMLELT	KGLVKYYNGESSPLK : 1 :: VAKMKESQEKEYC
YQAQYDLSIYNK : : : KEKMKELATTYK	PNTLL PKDLLCNLELEG	FNIDSL ELHIITSEKDKL	YNDIN : : FEQKYKMVLEEN	INEIKEKIK : :: ::: MEQLKEQLENRD	LNEIYDSKFNNNIDLTN :: : : KSDIHDT-VNMNIDTQ-	SKHNLEKLT : :: TGETKDEFQQKM	VENIKKDEEQLF : :: :: LESVIAEKEQL-	ILKNVELK : : :: LSRTCDRLAEVE	KNIKTE :::: LTLEHMETERLE	EQKQAQPPVPVP : : QTKEELKIAHIH	HSTMNEKILKQY : : : HTKLQEEI	LSQLFMEIYE :: LRLNEKFQES	SMQPLSLTPQDKPEV	GQKSSENFYEKI : : : QESHDEMKSV			
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1886 SVMKERDNLRRVEET------LQETKARDL 1920
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1136 LNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDV 1195
                                                                     1196 ATVVSESGSDTLEQSQPKKPASTH------VGAESNTITTSQNVDDEVDDV- 1240
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MEDLINE=96026346; PubMed=756993;

MEDLINE=96026346; PubMed=756993;

Fraser C.M., Gocaype J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
The minimal gene complement of Mycoplasma genitalium.";
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Cytadherence high molecular weight protein 2 (Cytadherence accessory
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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SEQUENCE OF 557-659 FROM N.A.
SEQUENCE 057-659 FROM N.A.
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
A survey of the Mycoplasma genitalium genome by using random sequencing.";
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           RNYLLTI------GFKYL 167
                                                                                                                                                                                                                                                                                                                      Gaps
Bacteriol. 175:7918-7930(1993).
FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH STABLIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS CYTOSKELETON-LIKE NEWDRANG OF ACCESSORY PROTEINS CONTAINING HAW PROPELS I TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEIN THE MYCOPLASMAL MEMBRANE AT THE ATTACHMENT ORGANELLE (BY
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W; 11D093AF173284FD CRC64;
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COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
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1.4e-07;
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19.7%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed coil; Alternative splicing.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
TOXKGNLYHIDVSLEGEPPEFEXIRKVLFEY -> HLTKV
ALTIRMSHSLENLPNLSICERCELSI (IN ISOFORM
2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1 (shown here), 2, 3 and 4; are produced by alternative splicing.
-!- DISEASE: ANTIGEN IN THE AUTOIMMUNE DISEASE SJOEGREN'S SYNDROME AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> HLTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE GOLGI MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thesís (1994), Instituto municipal de investigacion medica, Spain.
-!- FUNCTION: MAY PLAY A ROLE IN VESICULAR TRANSPORT FROM THE TRANS-
                                        GGG4_HUMAN STANDARD, PRT; 2230 AA. 013435; 013270; 013654; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-0TN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 60191 autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa GOLGA4.
                                                                                                                                                                                                                                                      Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.;
"Molecular characterization of trans-Golgi p230: a human peripheral membrane protein encoded by a gene on chromosome 6p12-22 contains extensive coiled-coil alpha-helical domains and a granin motif.";

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
MEDLINE=96125112; PubMed=8537393;
Fritzler M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.;
"Molecular characterization of golgin-245, a novel Golgi complex protein containing a granin signature.";
J. Biol. Chem. 270:31262-31268(1995).
                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutherla, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                            Seelig H.P.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-96215236; PubMed-8626529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | InterPro; | IPR000237; GRIP_domain. | Pfam; PF01465; GRIP; 1. | Golds stack; Antigen; Coiled coll; | DOMSIN | 276 | 1011 | COILED DOMSIN | 276 | 1014 | COILED DOMSIN | 1033 | 1214 | COILED DOMSIN | 1259 | 2152 | COILED DOMSIN | 255 | 2154 | 2185 | TPYKGG
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 131-2230 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 524-672 FROM N.A. TISSUE-Gastric fundus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U41740; AAC50434.1; -. EMBL; X82834; CAA58041.1; -. EMBL; U31906; AAC51791.1; -. EMBL; X76942; CAA54261.1; -. Genew; HGNC:4427; GOLGA4.
                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN HEPATITIS B.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:4
MIM; 602509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Balague C.;
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81;
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-----QSQDKSLRRIAELREELQMD 199
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                                                                                                                                                                                                                                                                                                                             EQLIQRLRRMERSLSSYRGKYSELVTAYQMLQREKKKL-------QGILS- 179
                                                                                                                                                                                                                                                                                                                                                                   GGSGGSVASGGSVASGGSVASGGSGASRRTNPSDNSSDSDAKSYADLKHRVRNY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNTPNTLLDKNKK--IEEHEKEIKEIAKT-----IKFNIDSLF-----TDPLELE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGEELREQKEKSERAAFEELEKALSTAQKTEEARRKLKAEMDEQIKTIEKTSEEERISLQ 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 VPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKI 803
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                          QELVKKLEALE------DAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVAS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NK-----LRDLQQEAETYRTRILELE-----SSLEKSLQENKNQSKDLAVHLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 YYL-REKNKNIDISAK------VETKESTEPNEYPNGVTYPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KSQSEYLKISQEKEQQESLALEELELOKKAILTESE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILKNV--ELKHNIHVPNSYKQENKQEPYYLIVLKKEID-----KLKVFMPKVESLINEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 VLKDOTDKMKOELEAKMDEOKNHHQQQVDSIIKEHEVSIQRTEKALKDQINQLELLLKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKHLKEHQAHVENLEADIKRSEGEL------QQASAKLDVFQSYQSATHEQTKAY--
                                                                                                                                                                                                                                                                                                                                                                                                                                          136 LLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 LI--TOLRDAKNLIEOLEODKGMVIAETKROMHETLEMKEEEIAQLKSKIKOM----TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 YNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKI--ESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 KKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVE
                                    SWLRSSS (IN ISOFORM 4).
                                                                                                                                                                                                                   Length 2230;
                                                546; Indels
(IN ISOFORM 2).
(IN ISOFORM 3).
             MISSING (IN ISOFORM FTSPRSGIF -> SWLRSSS
                                                                                                                                                                                                                     Score 424; DB 1;
Pred. No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANDYCQIPFNLKIRANELDVLKKL------VFGYR---
                                                                                                                                                                                                                                        Best Local Similarity 19.4%; Pred. No. 5.8e
Matches 343; Conservative 303; Mismatches
                                                   ~ ^ ^ ^ ^ ^ ^ ^ ^
                                                                                                                                                                                                                       5.0%;
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ETHEIQLQ---EKEQEVAELKQKILLFGCEKEEMNKEITWLKEEGVKQDTTLNELQEQLK 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKIL----KDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTL-QLSFDLY 1008
                                                                                                                                                                                                                                                                                                                                      ESSPLKTLSEE--SIQT--EDNYASLEN---FKVLSK------LEGKLK 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                        ENNT----DVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTIT 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKYKLKLERLFDKKKTVGKYKMQI-------KKLTLLKEQLESKLNSLNNPKHVLQ 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1229 TSQNVDDEVDDVIIV-PIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLK 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KDILNSRFNKRE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KSKMEKKESNLETELKSQTARIMELEDHITQKTIEIESLNEVLKNYNQQKDIEHKEL 1562
                                                                                                 ----STNLNNSLKLFENILSLG------KNKNIYQELIGQKSSEN-----FY
                                                                                                                                                                                                                                                                                      NFSVFFN-------KKKEAEIAET--ENT-----LENTKILLKHYKGLVKYYNG
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                                   LKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQ---LFMEIYEKEMY
                                                          LLTKQVAEVEAQKKDVCTELD-AHKIQ--VQDLMQQLEKQNSEMEQKVKSLTQVYES---
                                                                                   CNLYKLKDNDK - - - - IKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 NDYCQIPFNLKIRANELDVLKKLVFGYRK--PLDNIKDNVGKME---DYIKKN-KKTIEN 251
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LKQLLDES----SEQKNTAKEELNGLKDQLNEERSRYRREID--ALKKQLHVSHEAMREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IYTDNE--RKKFINEIKEKIKIEKKK----IESDKK-----SYEDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 TMTTSAVSPTVGKLFSDIKVLKRQLIKERNQKFQLQNQLEDFILELEHKTPELISFKERT
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                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser J
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones J
Couis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------LNELNS----FGDLINPFDYTK---EPSKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 1679 AA; 195141 MW; 298950CC52202D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.0%; Score 423; DB 1; Best Local Similarity 19.7%; Pred. No. 4.6e-07; Matches 335; Conservative 296; Mismatches 583
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SGD; S0001411; MLP2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1352 FLINKEKRDKF-----LSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYIND 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1520 NLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQE-GDKCVENPNP-TCNEN 1577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1037 SSLYSAQDLLDKHER---KWMEEKADYERELISNIEQTES--LRVENSVLIEKVDDTAAN 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 NGDKDHLKLVSLFSNLRHERNSLETKLTTCKRELAFVKQKN----DSLEKTINDLQRTQTL 1148
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---ILKNVELKHNIHVPNS 652
                                                                                                                                                                                                                                                       747 PVPEAKAQVPTPPAPVNNKTENVSKLD-----YLEKLYĖFLNTSYICHKYILVSHSTM 799
                                                                                                        788 -ERLKSDLOSKIQEIESIRSCKDSQLKW-AQNTI------DDTEMKMKSLLTELSNKET
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                        653 YKQENKQEPYYLI-----VLKKEIDKLKVFMPK-----VELINEEKKNIKTE-GQS
                                                                                                                                                                                                                                                                                                  754 RLKESEI-----SHNENKMDFSSKEGQYKAKIKELENNL
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                                                                                                                                                                                                                                                                                                                                          800 NEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEM
---ELKKTQL
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                                                                                                                                                                                               710 RIKIKSLEYEISKLKKETASFIPTKESLTRDFEQC----
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                                                                                                                                                                                                                                                                                                                                                                 Sweeney F.P., Watts F.Z., Pocklington M.J., Orr E.; "The MYO1 gene from Saccharomyces cerevisiae: its complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Ribes L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watts F.Z., Shiels G., Orr E., "The yeast MYOl gene encoding a myosin-like protein required for
                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 6:3499-3505(1987).
-!- FUNCTION: REQUIRED FOR CELL DIVISION.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                    1928 AA
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EMBL; X06187; CAA29550.1; -.
EMBL; U10399; AAB68872.1; -.
EMBL; S05806; S05806.
PIR; S12323; S12323.
PIR; S46773; S46773.
HSSP; P08799; IMND.
SGD; S0001065; WYO1.
InterPro; IPR001069; Myosin, head.
                                                                                                    PRT;
                                                                                                                                                                                             Myosin-1 isoform (Type II myosin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
MEDLINE-94378003; PubMed-8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88111539; PubMed=3322809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam: PF00063; myosin_head; 1. PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1. SMART; SM00015; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91088308; PubMed=2263482;
1499 KGSGEDAEEELWNSPSKGNSER 1520
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SEQUENCE OF 1-760 FROM N.A.
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                          MYO1 OR YHR023W.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                    MYS1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaudin M.;
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                                                                                                                      P08964;
                                                                                     MYS1_YEAST
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983 NELIKQISDLNCDISKEQSSQS-----LIKESKLKLENEIKRLKDVINSKEEEIKS-FN 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINGLASELNDSKIKELEARLSQEISLNQYLNKRISGNSVETNISSTRRS------TS 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1324 VDYLKRQLDIETRAHYDAENAISALHS-----KFRKI--QGESSLSSSDIYKLKFEAS 1374
                                                                                                                                                                                 121 DAKSYADLKHRVRNYLLTIK----ELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NENIKELLDKINEIKNPPPANSGNTPNTLLDKNK-KIEEHEKEIKEIAKTIKFNIDSLFT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 DPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSF---- 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDLINPFDYTKEPSKNIYTDNERKKFINEIKEK----IKIEKKKIESDKKSYEDRSKSLN 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEK 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 LTKALKYMEDYSLRNIV--VEKELKYYKNLISKIE-NEIETLVENIKKDEEQLFEKKITK 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 DENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQ 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 EPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQ 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773 -DYLEKLYEF-LNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI- 829
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                                                                                                                                                                                                              | | | | :: | | | :: | | | | 1765 DTKVY-----KIGNTKLFFKAGVLADLEKQKDVKLNNIMIKKLTATIR------GYTVRK
                                                                                                                                                                                                                                                                                                                176 ELLYKLNFYFDLLRAKLNDVCANDY -----CQIP-FNLKIR-----ANELDVLKKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEKKKLYQAQYDLSIYNK------QLEEAHNLISVLEKRI----DTLKK----
                                                                          Query Match 5.0%; Score 421.5; DB 1; Length 1928; Best Local Similarity 20.8%; Pred. No. 6e-07; Matches 304; Conservative 246; Mismatches 487; Indels 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 YSDDP----LDKEDIIK---------KYYDLQLAFTEITRN-----
  1902 1904 FWK -> NSGKRLDADDL (IN REF. 1).
1928 AA; 223634 MW; 6F54C7611F43DC9F CRC64;
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                                                                                                                                                                                                                   K -> I (IN REF. 1).

I -> T (IN REF. 1 AND 3).

V -> S (IN REF. 1 AND 3).

L -> F (IN REF. 1 AND 3).

MISSING (IN REF. 1).

MISSING (IN REF. 1).

N -> S (IN REF. 1).

N -> S (IN REF. 1).

S (AR REF. 1).

N -> S (IN REF. 1).

S (AR PET. 2).

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T -> LM (IN REF. 1).

R -> A (IN REF. 1).

H -> D (IN REF. 1).

ETYUGGMLSKN -> NTLWKAGYPKT (IN REF. 1).

MISSING (IN REF. 1).

EXSSA -> GKNLLVC (IN REF. 1).

R -> S (IN REF. 1).

EXSSA -> GKNLLVC (IN REF. 1).

R -> S (IN REF. 1).

ENSTYTET -> RKFNHHD (IN REF. 3).

E -> R (IN REF. 1).

N -> NGITKINTSTETPQSTYIGERPKRVICCN (IN REF. 1).

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NELRLREHIHALKQAEEDVKNMASIIEKLKTQNKQKEKLIW
EREMERNDSDMQLQETLLE -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D -> V (IN REF. 1).
DLLKQLDHYTKVVEMLN -> SEAARSLYKSGGNVD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQN -> KKI (IN REF. 1).

EBAH -> KKLD (IN REF. 1).

S -> C (IN REF. 1).

L -> D (IN REF. 1).

C -> S (IN REF. 1).

M -> I (IN REF. 1).

A -> E (IN REF. 1).

A -> C (IN REF. 1).

A -> C (IN REF. 1).

KSN -> MI (IN REF. 1).

KSN -> MI (IN REF. 1).

KSN -> MI (IN REF. 1).

KSN -> MI (IN REF. 1).
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LE -> WK (IN REF. 1).
LSQEISLNQYLNKRISG -> CHRKYLKSILKQKNIR
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MISSING (IN REF. 1).
TLOLOMBONSRNG -> NTTANGTKFKEW (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF. 1).
P -> S (IN REF. 1).
E -> Q (IN REF. 1).
E -> Q (IN REF. 1).
PDKESDINKLMLE -> LTKSLILTHGNAS (IN
                                       Myosin; Actin-Diding; ATP-binding; Coiled coil; Alkylation.
DOMAIN 794 823 IQ.
DOMAIN 866 1911 COILED COIL (POTENTIAL).
NP_BIND 180 187 ATP (BY SIMILARITY).
NP_BIND 460 529 ACTIN-BINDING (BY SIMILARITY).
MOD RES 703 ALKYLATION (BY SIMILARITY).
CONFLICT 36 36 K -> I (IN REF. 1).
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DDLVSE -> MTLFL (IN REF. 1).
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D -> E (IN REF. 1).
S -> D (IN REF. 1).
S -> D (IN REF. 1).
S -> W (IN REF. 1).
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D -> H (IN REF. 1).
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4.8%; Score 405; DB 1; L
Best Local Similarity 18.0%; Pred. No. 2.2e-06;
Matches 281; Conservative 308; Mismatches 553;
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EMBL; U12681; AAA80009.1; -. EMBL; J03995; AAA29412.1; -.
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417 187
2022 AA;
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Antigen; Coiled coil
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                                                                                          SLNNPKHVLQNFSVFFNKK-----KEAEIAETENTLENTKILLKHYKGLVKY-YN 1096
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                                                                                                                       1234 ALRSEVEKLOHEVOFMREOLLRKTDEYQAALSDLVNAHRTAEDGRVNAVQALEARKYEIN 1293
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16-OCT-2001 (Rel. 40, Last annotation update)
                              1013 LKLERL -- FDKKKTVGKYKM-QIKKLTLLKEQLESKL-
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Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
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Lueck-Vielmeter D., Schleicher M.,
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1130 IKGDIDSLFGE-
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SWISS-PROT entry is copyright. It is produced through a collaboration veen the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOMING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA HELICAL COILED COILS.

THE ACTIN-ACTIVATED ATPASE ACTIVITY.
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                                                                                                                                                                                                                              Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostellum discoldeum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-!- SUBGUNT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBGUNITS (MHC), 2 ALKAL)
LIGHT CHAIN SUBGUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBGUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "X-ray structure of the magnesium(II) ADP.vanadate complex of the Dictyostellum discoideum myosin motor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization
phosphorylatable heavy chain fragment of Dictyostelium myosin II."; FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.
MEDLINE-95345067; PubMed-7619796;
Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated head of Dictyostellum discoideum myosin to 2.7-A
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                                                                                             Wagle G., Noegel A., Scheel J., Gerisch G.;
Phosphorylation of threonine residues on cloned fragments
Dictyostelium myosin heavy chain.";
FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
"X-ray crystal structure and solution fluorescence chara
of Mg.2'(3')-O-(N-methylanthraniloyl) nucleotides bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
"X-ray structures of the MgADP, MgATPgammaS, and MgAD
of the Dictyostelium discoideum myosin motor domain."
Blochemistry 36:11619-11628 (1997)
                                                                                                                                                                                                                                                                    "X'ray structures of the myosin motor domain of Dicty discoideum complexed with MgADP.BeFx and MgADP.AlF4-Blochemistry 34:8960-8972(1995).
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MEDLINE=98070605; PubMed=9405148;
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MEDLINE-97452580; PubMed-9305951;
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MEDLINE-96206189; Pubmed-8611530;
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5; PubMed=2828113;
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966 QSDTISRLEKIKDE-LQKEVEELTESFSEESKDKGVLEKTRVRLQSELDDLTVRL 561 EKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKI : : : : : : : : : :	1020 DSETKDKSELLROKKKLEBEELKOVORALAAETAAKLAQEAANKKLQGEYTELNEKFNSEV 609 LEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPN :: :: :: :: :: 1: 1:	OY 652SYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGGSDNSEPSTE 706	OY 707 GEITGGATT-KPGQQAGSALEGDSVQ-AQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNN 764	QY 765 KTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEE 814	OY 815 SKLSSCDPLDLLFNIQNNIPVWYSMFDSLNNSLSQLFMEIYEKEWVCNLYKLKDNDKIKN 874 1303 KKQKESNEKRKVDLEKEVSELKDQIEEEVASKRAVTEAKNKKESE 1347	QY 875 LLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLF 926	QY 927 ENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDES- 985 1 1 1 1 1 1 1 1 1	QY 986 -KRKKLEEDINKLKKTLQLSFDLYNK-YKLKLERLFDKKKTVGKYK 1029 : : : : :	QY 1030 MQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYK 1089 1511 ELEVRVAELEESLEDKSGTVNVEFIRKKDAEIDDLRARLDRE 1552	OY 1090 GLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLS 1147	QY 1148 SGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTL 1207	QY 1208 EQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTP 1267	QY 1268 SVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKR 1322 : : : : :	QY 1323 ENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDV 1382	QY 1383 LGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAK 1442	QY 1443 VLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNH 1491	QY 1492NULLTKFLSTGMVFENLAKTVLSNLLDCNLQGMLNIS 1528 :
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RA Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,

RA Boroks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Collins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Honsby T., Howarth S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S.,

RA Money P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Allorer K., O'Nell S., Pearson D., Quali M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Sauders R., Squares S., Stevens K.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daniguez A., Revuelta J.L., Moreno S., Amarstrong J., Forsburg S.L.,

RA Daniguez A., Revuelta J.L., Moreno S., Amarstrong J., Forsburg S.L.,

RA Phakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Rhypakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Rhypakovski G.V., Barrell B.G., Nurse P.;

Rhypakovski G.V., Barrell B.G., Nurse P.;

Rhypakovski G.V., Barrell B.G., Nurse P.;
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-!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                         1529 QHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCT 1588
                                                                                 1908 -RETVEEAEDSKS-----EAEQSKRLVELELEDAR------RNLQKEIDAKEI 1948
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"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
Mol. Gen. Genet. 262:921-930(2000).
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16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Abnormal long morphology protein 1 (Sp8).
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MEDLINE-20223868; PubMed-10759889;
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MEDLINE-21848401; PubMed-11859360;
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Q9UTK5; 013313; Q9UTT8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 HKENVLTKKINFLEQQLQSSNNQAEESRNLISVLRNENESLKTNLENQNKRFDAL---- 117
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463 COILED COIL (POTENTIAL).
740 COILED COIL (POTENTIAL).
1106 COILED COIL (POTENTIAL).
1427 COILED COIL (POTENTIAL).
1555 COILED COIL (POTENTIAL).
1654 COILED COIL (POTENTIAL).
1664 COILED COIL (POTENTIAL).
1664 COILED COIL (POTENTIAL).
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SUBCELLULAR LOCATION: Cytoplasmic.
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EMBL; AF010473; AAB65416.1; ALT_INIT.
EMBL; AB028012; BAA87316.1; -.
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                                                                                                                                                                                                                                     967 FTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQ-LSFÖLYNKYKLKLERLFDKKKTV 1025
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RSSILSHNSSAGNI----
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                                                                       -----DDKMKSID--ESTRELEKNYEVYRNEMTAIQESLSKRNQDLLSEMEAIRKELENS
                                                                                                                                         688 KYQQQLSTDRLTNANNDVEAFKKEAKELRSINQNLQDI-ISRQDQRASKFAEELLHVNSL
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                                                                                                           863 LYKLK-DNDKIKNLLEEAKKVSTSVKTLSS--SSMQPLSLTPQDKPEVSANDDTSHSTNL
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                                               ITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQ
                                                                                                                                                                          920 NNSLKLFENILSLGK---NKNIYQELIGQKSSENFYEKIL
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P12753;
01-OCT-1989 (Rel. 12, Created)
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                                                                                                                                                                                                                                        containing a
                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the 33 kb long region between ORC5 and SUII from the left arm of chromosome XIV from Saccharomyces cerevisiae."; Yeast 13:649-6860(1997).

-i- FUNCTION: INVOLVED IN DNA DOUBLE-STRAND BREAK REPAIR (DSBR). THE RAD50/ARE11 COMPLEX POSSESSES SINGLE-STRAND ENDONUCLEASE ACTIVITY AND ATP-DEPENDENT DOUBLE-STRAND-SPECIFIC EXONUCLEASE ACTIVITY. RAD50 PROVIDES AN ATP-DEPENDENT COUTROL OF MRE11 BY UNWINDING AND/OR REPOSITIONING DNA BUDS INTO THE MRE11 ACTIVE SITE.
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01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA repair protein RAD50 (153 kDa protein).
RAD50 OR YNL250W OR N0872.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376;
                                                                                                                                                                                                    MEDLINE-89276917; PubMed-2659437;
Alani E., Subbiah S., Kleckner N.;
"The yeast RAD50 gene encodes a predicted 153-kD protein cont
purine nucleotide-binding domain and two large heptad-repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1312;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97377992; Pubmed-9234673;
Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 251; Mismatches 443; Indels
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COLLED COIL (POTENTIAL).
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                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomyces NCBI_TaxID=4932;
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Pred. No. 3.3e-06;
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EMBL; Z71256; CAA96157.1; --
PIR; S05808; BWBYDL.
SGD; S0005194; RAD50.
INCEPTO: IPR0004349; ABC_transportr.
InterPro: IPR004584; Rad50.
TIGRPAMS; TIGR00606; rad50; 1.
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STRAIN-S288c / FY1679;
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                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               Hegemann J.H.;
                                                                                                                                                                                       STRAIN-RE821
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Dp 0.007450 (Rel. 24, Least Sequence update)

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KLKKTLQLSFDLYNKYKLKL 1015 || |: | : | : | | |- | | : | | : | | ISLNNPK--HVLQNFSVFFNK 1065 : | | : : . KEKSAKLGHTVVSNEAYSEL 1112 SPLKTLSEESIQTEDNYASL 1119 | :: | |:| : | NDVEFLKEKSAKLGHTVVSN 1170 :: ::::| | SDSAYEDLVKCK----- 1212 EDYDDL------1256 THAVSON EYSELEK KLEOPSL 1377 QUVSNDEYIALKNTMEKPDV 1437 GYRLIEPNEYLDLNRIATTP 1497 | : :| | : :| IE----ENAALLDLVLVDKT 1549 ----SNVEVKIKELNY 1462 EQPSLEYLVEHAKATNHHLL 1008 E--LKEVIKNKNYTGNSPSE 1173 SQPK-----KPASTHVG 1221 EOPSLAYLVEHAKATDHHLL 1264 | | :| |RAYSELEKKLEQPSLEYLVE 1318 ---FLSSYNYI----- 1368 INDKQGENEKYLPFLNNIET 1423 GOKSSENFYE-----KIL 956 (Cytadherence accessory caceae; Mycoplasma.

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RAIYGKMAQFVSELRQEKKQLLSAQKQVDDKSRLLEQNQRHLQNLSSETKKKRQSLEHDI 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032 IKKLTLLKEQLESKLNSLNNPKHVLQNFSV---FFNKKKEAEIAETENTLENTKILLKHY 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |: | | :| | :| | :| | :| ELELLAÇKQAE------LKQELEÇKATALASQDQDTVQAKLDLARQQHELELRQNAFNQA 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005 SLSLNKQREQLTNOVKVLH---GELKKRHEKLTLKDRLLAEKEKDQHKKDAEIN---QRF 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ATVVSESGSDTLEQSQPKKPASTHVGAE 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KEKRDKFLSSYNYIKD-----SIDTDI 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDESKRKKLEEDINK--LKKTĻQLSFDLYNKYKLKLER----LFDKKKT----VGKYKMQ 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |: : | | | : || HLEQQQYEFERKQQESLLIKLETEHKQLQKRIGEFKIESEAKSEALLIQE--RELLEKRRE 424
                                                                                                                                                                                                                                                                                                                                                                      PPAPVNNKTENV----SKLDYLEKLYEFLNTSYICHKYILVSHSTMN--EKILKQYKIT 810
                                                                                                                                                                                                                                                                                                                                                                                              RRIADYESDLQARLAEVKTLE------KNQQETAAKSERELKVALEKLNQAKKAF 800
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                                                                                              125 IDDLLTQASLEYEQQRRTNQVLKEKHRQVQQHFQNLVHAKKKLDQKRHYLAEQKRIDEEQ 484
                                                                                                                                    LFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPN 651
                                                                                                                                                                                                                                                                                          710 TGQATTKPGQQAGSALEGDSVQAQAQ------EQKQAQPPVPVPVPVPEAKAQVPT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 KFKEKELEAAQKQLSLDN--NNNAGLKLQLDKLSESLKTERLELEASKERILDFYD-ESS 751
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                                                                                                                                                                                                                 SYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQ--SDNSEPSTEGEI
                                                                                                                                                                                                                                                     DFENEIEEKQNELFASOKSLOKSFTQLKNKEAELNQKAQKIAEDWAHLKQNKHHHADLEI
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                                                          ----LTKA-LKYMEDYSLRNIVVEKE----LKYYKNLI----SKIENEIETLVENIKKDEEQ
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                                                                                                                                                                                                                                                                                                          STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS
STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS
STOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HAW
PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS
IN THE MYCOPLASMAL MOMBRANE AT THE ATTACHMENT ORGANELLE (BY
                                                                                                                                                                                                                                   "Transposon mutagenesis reinforces the correlation between Mycoplasma pneumoniae cytoskeletal protein HWM2 and cytadherence."; Ju. Bacteriol. 179:2668-2677(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHGFK----YLIDGYEEINELLYKLNFYFDLLR-----AKLNDVCANDYCQIPFNLKI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLDQFQAL-------IDQQNQTIKQLNEQIAANQGLIDQNVQR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 IDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKI 322
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                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-AUCC 29342 / M129;
MEDLINE-97252497; PubMed-9098066;
Krause D.C., Proft T., Hedreyda C.T., Hilbert H., Plagens H.,
Herrmann R.;
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MEDLINE-97105885; Pubmed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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66DF4B08F0FCFBC0 CRC64;
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COILED COIL (POTENTIAL)
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                                                                                                  Nucleic Acids Res. 24:4420-4449(1996)
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1818 AA;
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 N-----KFDQRRKEAVSSILNSHKK-LKQKEGELQGILQKLSLKKTQIEQEFSKLYQQ- 1392
                                                                                            ---FVGIADLSTDYNHNNLLTKFLSTGMVFENLAK---TVLSNLLDGNLQGMLNISQHQC 1532
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SEQUENCE FROM N.A.

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

MELON G.G. J. Malke O., Olsen G.J., Zhou L., Fleischmann R.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jannaschii.";
Science 273:1058-1073(1996).
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
rad50/mre11 complex possesses single-strand endonuclease activity
and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of mre11 by unwinding
and/or repositioning DNA ends into the mre11 active site (By
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DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP_BIND 32 39 ATP (BY SIMILARITY).
DOMAIN 158 849 COILED COIL (POTENTAL).
SEQUENCE 1005 AA: 119387 MW; 9BBB48173E788F3 CRC64;
                                                NDKID-----DKLAHLEAKVLNYTYEKSNVEVKIKELNYLKTIQ---DKLADFKKNNN--
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                                                                                                                                                                                                                                                                                                                                                               RAD50 OR MJ1322.
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 ATPase.
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InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
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Pfam; PF02483; SMC_C; 1
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      Length 1005;
4.4%; Score 372; DB 1;
Similarity 20.9%; Pred. No. 1.2e-05;
'2; Conservative, 204; Mismatches 364
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EMBL; AF083037; AAD22767.1; -.
EMBL; AC004013; AAB96867.1; ALT_FRAME.
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Jahnsen T., Oerstavik S.;
"Cloning and characterization of a cDNA encoding an A-kinase anchoring
protein located in the centrosome, AKAP450.";
                                                                                 SIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND 1430
                                                                                                                                                                                                     1431 KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQ----DKLADFKKNNNFVGIADLS 1486
                                                                                                                                                                                                                                                                                                                         1487 TDYN-----HNNLLT-KFLSTGMVFENLA----KTVLSNLLDGNL------QGMLNIS 1528
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609996; 09U004; Q9U0H3; Q9Y6Y2; 014869; 043355; 094895; Q9Y6B8;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
MEDIATE-99151389; PubMed-9482789;
MEDIATE-99151389; PubMed-9482789;
Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M.;
"Yotiao, a novel protein of neuromuscular junction and brain that
"Yotiao, a novel protein of neuromuscular junction and brain that
interacts with specific splice variants of NMDA receptor subunit
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                                                                                                                                             812 EIETGI-----MSNLE----KEKE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-99115654; PubMed-9915845;
Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS. MEDLINE-99219864; Pubmed-10202149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             QHQCVK------KQCPQNSGCFRHLDEREECKCLLNYKQEGD 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2)
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Kemmner W.A., Deiss S., Schwarz U.;
"Cloning of Hyperion.";
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SEQUENCE OF 17-1800 FROM N.A.

RM UA., Graves T., Eradshaw H.;

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RM UA., Graves T., Eradshaw H.;

RM UA., Graves T., Eradshaw H.;

RM UA. SCAFFOLDING PROTEIN THAT ASSENBLES SEVERAL PROPEIN KINASE

- A SCAFFOLDING PROTEIN THAT ASSENBLES SEVERAL PROPEIN KINASE AND PHOSPHATASES ON CENTROSOME AND GOLGI APPARATUS WHERE PHYSIOLOGICAL EVENTS CAN BE REGULATED BY PHOSPHORYLATION STATE OF PROTEIN CONSTRUCT ON THE NETHYLL-D-ASPARTATE RECEPTOR AND IS ASSOCIATED WITH THE NETHYLL-D-ASPARTATE RECEPTOR AND IS ASSOCIALLY FOUND IN THE NETHYLL-D-ASPARTATE RECEPTOR AND IS SPECIFICALLY FOUND IN THE NETHYLLOST CONSTRUCT ON CORGANIZE POSTSYNAPPIC SPECIALLY FOUND IN THE NETHYLLOST CONSTRUCT ON THE NETHYLLOST CONSTRUCT ON THE NETHYLLOST CONSTRUCT ON THE NETHYLLOST CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE CONSTRUCT ON THE PRODUCT ON THE CONSTRUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE CONSTRUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODUCT ON THE PRODU
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the Buropean Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
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-!- DOMAIN: RII BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURRACE ON THE R-SUBBURT DIMER.

-!- CAUTION: REF. 6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.

-!- CAUTION: REF. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - TISSUE SPECIFICITY: WIDELY EXPRESSED. ISOFORM 4/YOTIAO IS HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milgram S.i., Goldenring J.R., Schmidt P.H.;
"AKAP350: A multiply spliced family of proteins with centrosomal
association.";
Trotter K.W., Milgram S.L., Goldenring J.R.;
"AKAP350, a multiply spliced protein kinase A-anchoring protein
associated with centrosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                              Hinds K., Sutterer C., Becker M., Hawkins M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3)
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                                                                                                                                                                                                                                                                                       SEQUENCE OF 1802-3876 FROM N.A. (ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM
                                                                                                                                                                           Biol. Chem. 274:3055-3066(1999).
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MEDLINE=99087487; PubMed=9872452;
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AB018346; BAA34523.1; -. AC000066; AAC60380.1; ALT_FRAME.

AAD39719.1; BAA34523.1;

AF091711;

AAB86384.1;

AF026245;

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VKSKADDINSLNDESKRKKL-------EEDINKLKKTLQLSFDLYNKYKLKLERLF 1019 : | : | | | : | | | : | | | :| : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | EAEIA----ETENTLENTKILL----KHYKGLV-----KYYNGESSPLK-TLSEESIQ 1111 TED-----NYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKN 1163 1112

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InterPro;
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SNTITT-----SQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSK 1276
                                                                                             |: | :| :| :| :| SDAQRTMY.PGSCVKKNIDGTIE---FSGEFGVKEE-------TNIVKL 1443
                                                                                                                                                                                           -----TEQNYEAE--IHCLOKRL-----QAVSES-----TVPPSLPVDSVVITE 1405
                                                                                                                               IENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPY 1336
                                                                                                                                                     SDLDSIKKYINDKQGENEKYLPFLNN------IETLYKTVNDKIDLFVIHLEAKV 1443
                                                                                                                                                                              KDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGY--YKILSEKYK 1394
                                                                                                                                                                                                                                                   1524 EEFKPLSKEL----GEHGKEILLSNSDPHDIPESKDCVLTISEEMFSKDKTFIVR---- 1574
                                                                                                                                                                                                                                                                             1444 LNYTYEKSNVEVKIKELNYLKTI---QDKLADFKKNNNFVGIADLSTDYNHNNLLTKFL 1499
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                                                                                                                                                                                                                                                                                                   ----QSIHDEISVSSMDASRQLMLNEEQLEDMRQ-----ELVRQYQEHQQATELL 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASMA MEMBRANE.

-!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING DOMAIN, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).

-!- SIMILARITY: CONTAINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).

-!- SIMILARITY: CONTAINS 2 CALPONIN-HOWOLOGY (CH) DOMAINS.

-!- SIMILARITY: CONTAINS 1 WM DOMAIN.

-!- SIMILARITY: CONTAINS 1 WM DOMAIN.

-!- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
                                1164 KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lemaire C., Heilig R., Mandel J.L.;
"Nucleotide sequence of chicken dystrophin cDNA.";
Nucleic Acids Res. 16:11815-11815(1988).
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01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                3660 AA
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MEDLINE-89210800; PubMed=3072195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89098331; PubMed=3062582;
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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PROSITE; PS50135; ZF_ZZ_2; 1.
Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 4.3%; Score 361; DB 1; Length 3660; Best Local Similarity 18.8%; Pred. No. 0.00011; Matches 343; Conservative 297; Mismatches 592; Indels 588;
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SPECTRIN 7.
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SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 7
SPECTRIN 8
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                                           InterPro; IPR001589; Actbind_actnin
InterPro; IPR001715; Calponin-like.
                                                             Calponin-like.
Spectrin.
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                                                                           IPR002017; Spectrin.
IPR002349; WW.
IPR001202; WW_Rsp5_WWP.
IPR000433; Znf_ZZ.
                                                                                                                                                                                                                        SMART; SM00033; CH; 2.
SMART; SM00150; SPEC; 21.
SMART; SM00456; WW; 1.
SMART; SM00291; ZnF_ZZ; 1.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
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Pfam; PF00569; 22; 1.
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Pfam; PF00397;
EMBL; X13369;
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InterPro;
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66; PubMed-7798308;

et D.J., Pante N., Cooper C.S., Abbi U., Gerace L.;

v Mitchell P.J., Cooper C.S., Abbi U., Gerace L.;

coiled coil protein whose amino terminus is involved in
oncogenic kinases, is localized to the cytoplasmic
inclear pore complex."; gene encodes a protein of 2094 amino acids that has ed-coil regions and an acidic C-terminal domain."; 9-2333(1992). : :: | | | : |: LDREIKAQRVIVGDLDDINDMIIKQKANMQDLEQRRPQL------DEL LSKIENEYEVLY------LKPLAGVYRSLKKQLEN-----azoa; Chordata; Craniata; Vertebrata; Euteleostomi; eria; Primates; Catarrhini; Hominidae; Homo. el. 12, Created) el. 34, Last sequence update) el. 40, Last annotation update) PRT; 2349 AA. N.A. 11; PubMed=1437155; | | ::|: LFLADQPVEGL 2878 SNLLDGNLQGM 1524 Cooper C.S.; STANDARD; Human).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                -!- FUNCTION: COMPONENT OF THE CYTOPLASMIC FIBRILS OF THE NUCLEAR PORE COMPLEX INFLICATED IN NUCLEAR PROTEIN IMPORT. ITS AMINO TERMINUS IS INVOLVED IN ACTIVATION OF ONCOCRONIC KINASES.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURRACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STEPWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER
                                                                                                                                                                                                                                                                                                  COMPONENTS, INCLUDING P62.

TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.

DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
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SEQUENCE OF 1-142 FROM N.A.
MEDLINE-88262257; PubMed=3387099;
King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.;
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Genew; HGNC:12017; TPR.
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99 TNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKINDVCANDYCQIPFNLKIR 210 242 IKKNKKTIENINELIEE--SKKTIDKNKNATKEEEKKKLYQAQYDLS-IYNKQLEEAHNL 298 MNGLKTSNEHLQKHVEDLLTKLKEAKEQQASMEEKFHNELNAHIKLSNLYKSAADDSEAK 299 SNELTRAVEELHK-----LLKEAGE------ANKAIQDHLLEVEQ-- 333 211 ANELDVLKKLV--------FGYRK------PLDNIKDNVGKMEDY 241 ----SKDQMEKEMLEKIGRLEKELENAN---DLLSATKRKGAILSEEELAAMSPTAAA- 384 Gaps 299 ISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIA KTIKFNIDSLFTDPLE----LEYYLREKNKNIDISAKVETKESTEPNE-----YPNGVTY 365; Length 2349; Indels 4.3%; Score 358.5; DB 1; ilarity 18.5%; Pred. No. 8.3e-05; Conservative 317; Mismatches 659; Similarity Best Local Sim Matches 305; Query Match Local 151 130 334 ò g ŏ g ò g δy g οy g

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SFINFVK---SKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYK---LKLERLF 1019
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                                                                                                                                                                    THHNTFASYE----NSKHNL--EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEI 578
                                                                                                                                                                                                                SQQIRVLLMELEEARGNHVIRDEEVSSA-----DISSSSEVISQHLVSYRN-IEELQQQN 550
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                                     ----VAKIVKPGMKLTELYNAYVETQDQLLLEKLENKRINKYLDEIVKEVEAKAPILK
                                                                                                            :: | | :: : : : : : : | :: | | SQREEYERAQKAVASLSVKLEQAMKEI--QRLQEDTDKANKQSSVLERDNRRMEIQVKDL
                                                                                                                                                                                                                                                                                 : |: ::|:: ::|: :::|551 QRLLVALRELGETREREEQETTSSKIT-------ELQIKLESALTELEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     797 STMNEKIL----KQYKITKEEESKLSSCDPLDLLFNIQ-NNIPVMYSMFDSLNNSLSQLF
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                                                                                  SDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMM----GKRYSYKVEKL
                                                                                                                                                                                                                                                        ETLV-----ENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDEL
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"Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";
J. Cell Biol. 143:49-63(1998).
-I- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.; "The C terminus of mitosin is essential for its nuclear localization, centromere/Kinetochore targeting, and dimerization."; J. Biol. Chem. 270:1954-19550(1995).
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SEQUENCE OF 2194-3210 FROM N.A.

MEDLINE-95336446; PubMed-7612011;

Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;

Li Q., Ke Y., Kapp J.A., Fertig Solving Model of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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TISSUE=Breast carcinoma;
MEDILNE-55348175; Pubbed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
"CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late 62 and is rapidly degraded after mitosis.";
J. Cell Biol. 130:507-518(1995).
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Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shar Jones D., Yang-Feng T.L., Lee W.-H.;
"Characterization of a noveley-kilodalton nuclear phosphoprothat is specifically involved in mitotic-phase progression.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENF_HUMAN STANDARD; PRT; 3210 AA. P49454; Q13246; Q13171; Cleated) 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 34, Last sequence update) 01-CCT-2001 (Rel. 40, Last annotation update) CENP-F kinetochore protein (Centromere protein)
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MEDLINE-98437347; Pubmed-9763420;
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                              -:- SUBCELLUIAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS), REORGANIZATION TO THE KINETOCHORE/CENTROMENE (CORONAL SURFACE OF THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.
-:- DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE CELL CYCLE.
-:- PIM: "HYPERPHOSPHORYLATED DURING MITOSIS.
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CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI. SUBUNIT: HOMO- OR HETERODIMER.
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Chromosomal protein; Nuclear protein; Centromere; Coiled
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        COLLED COLL (POTENTIAL).

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D -> N (IN REF. 3).
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18.8%; Pred. No. 0.00015;
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FitzGerald L.M., Clayton R.A., Gocayne J.D.,
ty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
F., Weinstock K.G., Merrick J.M., Glodek A.,
S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
M., Hurst M.A., Kaine B.P., Borodovsky M.,
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F. Weinstock K.G., Merrick J.M., Glodek A.,
S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
M., Hurst M.A., Kaine B.P., Borodovsky M.,
F., Smith H.O., Woese C.R., Venter J.C.;
the EMBL/Genbank/DDBJ databases.
IMPORTANT ROLE IN CHROMOSOME STRUCTURE AND
TIAL FOR CHROMOSOME PARTITION (BY SIMILARITY).
TO THE SMC FAMILY.
                                                        EDYDDLGQVVT-----GEAVTPS----VIDNILSKIE 1278
                                                                                                                                                                      VYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLE 1330
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C This SWISS-PROT entry is copyright. It is produced through a collaboration cC between the Swiss Institute of Bioinformatics and the EMBL outstation cC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial cC entities requires a license agreement (See http://www.isb-sib.ch/announce/cor send an email to license@isb-sib.ch).	·	4.2%; 20.1%; 20.1%; ative 226 EKMVLNEGTE: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	Db 143	Qy 413 YNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKK 465

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KP----GQQAGSALEGDSVQAQAQEQKQAQ 741
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TISSUE-Heart;
MEDLINE=90016823; PubMed=2798112;
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing Dacterium Clostridium accetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing Dacterium Clostridium accetobutylicum.";

"Bacteriol. 183:4823-4838(2001).

"I Bacteriol. 183:4823-4838(2001).

"I PUNCTION: SDCCD cleaves DNA hairpin structures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3->5 double strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity (By similarity).

"SUBUNIT: Heterodimer of sbcc and sbcD (By similarity).

"STMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMEKKDEIDLKEKRARLGESSSKVKPY------IDNYENTLKQIDILKE
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InterPro: IPR013439; ABC_Lransportr.
Hydrolase; Nuclease; Exonuclease; Endonuclease; DNA replication;
Hydrolase; Nuclease; Exonuclease; Endonuclease; DNA replication;
Nuclease; Exonuclease; Exonuclease;
Nuclease; ATP-binding; Coiled coil; Complete proteome.
NP RIND 35 42 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 1003 COILED COIL (POTENTIAL).
1163 AA; 135507 MW; CE5F0BD2215D7A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (PÓTENTIAL). COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 20.1%; Pred. No. 6e-05;
Matches 274; Conservative 212; Mismatches 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.2%; Score 352.5;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE007771; AAK80682.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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DINKLK-KTLQLSFDL--YNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSL 1049
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                           PVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSC
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                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-007-1989 (Rel. 12, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
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 Myosin; Muscle
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                                                                                                                                                                                                                                                                                                                                                                                          EUR. Heart J. 5:181-191(1984).

-1- SUBGUIT. WUSCLE CONTRACTION.
-1- SUBGUIT: WUSCLE CONTRACTION.
-1- SUBGUIT: WUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBGUITS (MHC), 2 ALKALI LIGHT CHAIN SUBGUITS (MLC).
-1- SUBGLIATORY LIGHT CHAIN SUBGUITS (MLC-2).
-1- SUBGLIALULAR LOCATION: Thick filaments of the myofibrils.
-1- DOMAIN: THE RODILKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALHA-HELICAL COILED COTLS.
-1- FTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPÀSE ACTIVITY.
-1- MISCELLANBOUS: EACH WYOSIN HEROMY CAN IN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LAFER BE SPLIT PUTTHER INTO 2 GLOBULAR SUBFRAGMENTŞ (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                 SEQUENCE OF 1524-1935 FROM N.A.
MEDILINE-82220036; Publed-7045682;
Mahdavi V., Periasamy M., Medladi-Ginard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                        MEDLINE-90133919; PubMed-2614840; MCN31ly E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.; "Full-length rat alpha and beta cardiac myosin heavy chain sequences. "Comparisons suggest a molecular basis for functional differences."; J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                      Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.; "Cardiac myosin heavy chain isozymic transitions during development and under pathological conditions are regulated at the level of mRNI availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2).
MISCELLANGOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
craft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
Complete nucleotide sequence of full length cDNA for rat beta
                                             Nucleic Acids Res. 17:7529-7530(1989).
                                                                                                                                                                                                                                                                                                      STRAIN-Wistar; TISSUE-Heart;
MEDLINE-85179510; PubMed-6241892;
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PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000035; Myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
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InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                           SEQUENCE OF 1871-1935 FROM N.A.
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Pfam; PF00612; IQ; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X15939; CAA34065.1; -. EMBL; J00752; AAA41654.1; -. EMBL; M32698; AAA41659.1; -. PIR; S06006; S06006. PIR; A02989; A02989; A02989.
                                 cardiac myosin heavy chain.
                                                                                                                                                                                                                                                             Nature 297:659-664(1982).
                                                                            DISCUSSION OF SEQUENCE.
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protein; Coiled coil; Thick filament; Actin-binding;
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                                                                                                                                                                                                     ACTIN BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
IRK -> VRR (IN REF. 3).
D -> H (IN REF. 3).
N -> K (IN REF. 3).
T -> N (IN REF. 3).
R -> K (IN REF. 3).
R -> K (IN REF. 3).
MW; C8376C32AA7BDB2B CRC64;
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                           Methylation; Alkylation; Multigene family;
                                                                                                                               COILED COIL (POTENTIAL).
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Matches 286; Conservative 265; Mismatches 589;
                                                                                 MYOSIN HEAD-LIKE
                                                                                                                                                            ATP.
ACTIN-BINDING.
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                                                                                                                    EETEAKAELORVLSKANSEVAOWRTKYETDAIORTEELEEAKKKLAORLODAEEAVEAVN 1408
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1191 ALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKAN 1244
                                       LEXMCRTLEDQMNEHRSKAEETQRSVNDLTRQRAKLQTENGELSRQLDEKEALISQLTR- 1303
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                                                                                                                                                      A-KCSSLEKTKHRLQNEIEDLMVDVERSNAAAAALDKKQRNFDKILVEWKQK--YEESQS
                                                                                                                                                                                                                        -----QLSFDLYNKYKLKLER-LF
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                   ----TKPGQQAGSALEGDSVQAQAQEQKQAQPVPVPVPEAKAQVPTPPAPVNNKTEN
                                                                                                  IQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEAKKVSTSVK
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                                                          VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFN
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P12883; Q14904; Q16579;
O1-OCT-1989 (Rel. 12, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
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Catarrhini; Hominidae;
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MEDLINE-91065634; PubMed=2249844;
Medlicke T. Diederich K.W., Haas W.,
Pfordt M., Bach A., Vosberg H.P.;
                                                                                                                                                                                                                       -----ESKRKKLEEDINKLKKTL-----
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Mammalia; Eutheria; Primates;
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                                                                              1304 -GKLTYTQQLEDL-----
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myosin heavy chain expressed in
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                                                                                                                                                     MEDLINE=90301496; PubMed=2362820;
Liew C.-C., Sole M.J., Yamauchi-Takihara K., Kellam B.,
Anderson D.H., Lin L., Liew J.;
"Complete sequence and organization of the human cardiac beta-myosin
heavy chain gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
human beta-myosin heavy chain gene product.";
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                                                                                                                                                                                                                                                                                                                                                                                                          K., Sole M.J., Llew J., Ing D., Llew C.-C.; of human cardiac myosin heavy chain genes."; Sci. U.S.A. 86:3504-3508(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction of a human ventricular cDNA library and characterization of a beta myosin heavy chain cDNA clone. Hum. Genet. 76:47-53(1987).
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MEDLINE-89264452;
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myosin heavy chain gene in hypertrophic cardiomyopathy.";
Hum. Mutat. 6:197-198(1995).
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                                                                                                                                                                                                                                                   VARIANTS CMH1 CYS-513; ARG-716 AND TRP-719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
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                                                                                                                                                                                                                                                                                    MEDLINE=94110336; PubMed=8282798;
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1024 KVKLEQQVDD--LEGSLEQEKKVRMDLERAKRKLEGDLKLT-QESIMDLENDKQLDERL 1080
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                                                                                                                                                                                                                                                                                                           LSRELEEISERLEEAGGATSVQIE----MNKKREAEFQKMRRDLEEATLQHEA----TAA 1190
                                                                                                                                                                                                                                                                                                                                                                                    1191 ALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKAN 1244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKKKTVGKYKM-QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTL 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1245 LEKMCRTLEDOMNEHRSKAEETORSVNDLTSORAKLOTENGELSROLDEKEALISOLTR- 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GKLTYTQQLEDL-------KRQLEEEVKAKNALAHALQSARHDCDLLREQYE 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1674 VERRNNLLQAELEELRAVVEQTERSRKLAEQELIETSERVQLLHSQNTSLINQKKKMDAD 1733
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                                                                      EIIAKL--TKE------KKALQEAHQQ-ALDDLQAEDK-----VNTLTKA 1023
-- NKVKNLTEEMAGLD 986
                                                                                                                                                                                                                                                                                                                                                  655 QENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQAT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTEN 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            769 VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFN 828
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                                    DLIMPPDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKE 487
                                                                                                                                                                                                                                                                     597 ITKDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKKTQLILKNVELKHNIHVPNSYK
                                                                                                               YEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASYENSKHNLEKLT
                                                                                                                                                                                          KALKY------MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK
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--AKVEKEKHATE-
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1888 QANTNLSKFRKVQHELD 1904
-----DLELTL--
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 SIYNKQLEEAHNLISVLEKRIDTLK-----KNENIKELLDKINEIKNPPPANSGNTPNT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 SDAKSYADLKHRVRNYLLTIKELKYPQL-----FDLTNHMLTLCDNIHGFKYLIDGYEE 173
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                                                                                                                                                                                                                                                                                                                Coulson A.,
                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Teliton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F
Sims M., Smaldon N., Smith A., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 IKDNVGKMEDYIKK-NKKTIENINELIEESKKTIDKNKNATK--EEEKKKLYQ--AQYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 IKESDESGKEIFDEIRK-----CSMVWN-EISATFQQMLDPTATDTSNYEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 VHETWSNFQEYIDSLHKKLSEN----ERFQKFVDNAEDLIKWMDDKEKEICEKYSKMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2198;
                                                     01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 256.3 kDa protein C50C3.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2198 AA; 256260 MW; CD1B2C1092C5EDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 349.5; DB 18.8%; Pred. No. 0.00015
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                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
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InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
Pfam; PF00036; efhand; 2.
Pfam; PF00435; spectrin; 10.
ProDom; PD000012; EF-hand; 1.
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                                    (Rel. 28, Created)
(Rel. 28, Last seq
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STANDARD;
                                                                                                                                  Caenorhabditis elegans.
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                                    01-FEB-1994
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Db 1110 NLVKARETIDTKQDDLCRFADILL Qy 1284 LYLKPLAGVYRSLKKQLENNVMT Qy 1284 LYLKPLAGVYRSLKKQLENNVMT :: :: Db 1159 CDAKTLVRRMNEVEKMMMSRIGE	1207	1236	1461	OY 1517 LDGNLQGMLNISQHQCVKKQCPQ DD 1319 IESSTTRQKSLAQEC-Q	SU H6	AC P1339; Q00202; DT 01-3AN-1990 (Rel. 13, Create DT 15-DEC-1998 (Rel. 37, Last s DT 16-OCT-2001 (Rel. 40, Last s DT Model)	MYH6. Meavy Chain, MYH6. Mesocricetus auratus Eukaryota; Metazoa;	Manumalia; Eulheria; Mesocricetus. NCBI_TaxID=10036; [1]	RC SEQUENCE FROM N.A. RC STRAIN=FIB; TISSUB-Liver; RX MEDLINE-95115033; PubMed=781 RA Wang R., SOLE M.J., Cukerman Professional Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control o	heavy chain gene far. 3. Mol. Cell. Carc	RP SEQUENCE OF 1030-1399 FROW N RDLINE=8650589; PubMed=345 RA Liew CC., Jandreski M.A.; RT "Construction and characteri	RT Myosin heavy chain character. RT Syrian hamster."; RL Proc. Natl. Acad. Sci. U.S.A CC -!- FUNCTION: MUSCLE COMPRAC		CYCLES OF A CHARACTERIST CHARACTERIST -!- PTM: TWO CYS	SINITATED AND AND SINITATION SINITATION -: -: - MISCELLANEOUS: EACH MEROMYOLIN (LMM) & MEROMYOLIN SINITATION PROPERTY SINITATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER	1	CC -:- SIMILARITY: CONTAINS I M
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: : : :	TEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEFSKNIYTDNERKFINEIK	EKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRY 	SYKVEKLTHHNTFASY-ENSKHNLEKLTKALKYMEDYSL QKAVILASFLQNHEESPEDMNAED	IENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVL : : :	IMMKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYL 	VESLINEEKKNIKTEGOSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQE : ::::: :	QKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKL : : : : : : NO	STMNEKILKQYKITKEEESKLSSC 	LEMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVST :: : :: :: : : :: : : :: : : :: : : :: : :	DKPEVSANDDTSHSTNLNNSLKLFEN	KILKDSDTFYNESFTNFVKSKADDINSLNDES	LQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLN :	SLNNPKHVLQNFSVFNĶKKEAETAETENTLENTKILLKHŸKGLVKYYNGESSPLKTLSE :	ESI	GKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNAL :	ESYKKELPEGTDVATVVSESGSDTLEQSOPKKPASTHVGAES:	NTITISQNVDDEVDDVI-IVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEV
Db 215 Qy 340 Db 260	Qy 398 Db 320	Oy 458 Db 349	Qy 518 Db 402	Qy 574 Db 443	Qy 624 Db 503	Qy 681 Db 545	Oy 737 Db 605	Qy 797 Db 633	Qy 850 Db 671	Qy 903 Db 723	Qy 954 Db 781	Oy 1001 Db 839	Qy 1048 Db 894	Oy 1108 Db 939	Qy 1130 Db 999	Qy 1183 Db 1051	Oy 1225

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IN ISA HEXAMERIC PROTEIN THAT CONSISTS OF 2 (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) 1 THICK FILDMENTS (MLC.) 2 THICK FILDMENTS OF THE MYOTHDE IS SEQUENCE IS HIGHLY REPETITIVE, SHOWING UR REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, LPHA-HELICAL COLLED COLLS.

SIDURE IN THE SI DOMAIN ARE SELECTIVELY OUTRED FOR MYOSIN ATPASE ACTIVITY (BY
                                                                           NYIKDSI---DIDINFANDVLGYYKILSEKYKSDLDSI 1400
                                                                                                                                                                       -ELASDINDYHTIYEDFLNNGQVEEEKVQVIRHLWSSL 1318
LG-AERDCERLYSWASGKR------HQLETEATM 1158
                                                                                                                                                                                                                                    TLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKEL 1460
                                                                                                                                                                                                                                                                                                                                ADLSTDYN-HNNLLTKFLSTGMVFENLAKTV---LSNL 1516
                                                ITENVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSN 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n hamster).
.a, Craniata; Vertebrata; Euteleostomi;
.a, Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJAC ALPHA ISOFORM IS A 'FAST' ATPASE ISOFORM IS A 'SLOW' ATPASE.
MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
annotation update)
: muscle alpha isoform (MyHC-alpha).
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58174;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASGGSVASGGSVASGGSG----NSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681
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Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Alkylation; Multigene family;
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ACTIN-BINDING.
ACTIN-BINDING.
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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178 185 ATP (POTENITAL).
179 143 POLIX-BLADING.
170 ACTIN-BINDING.
129 129 ACTIN-BINDING.
189 1697 ALKYLATION (TRI-) (FOTENITAL).
180 1697 ALKYLATION (SH-1) (POTENITAL).
181 1651 H -> O (IN REF. 2).
181 1651 H -> O (IN REF. 2).
182 1693 V -> G (IN REF. 2).
184 184 K -> R (IN REF. 2).
187 187  A -> T (IN REF. 2).
187 187  A -> T (IN REF. 2).
188 188  B -> O (IN REF. 2).
189 1879 A -> T (IN REF. 2).
189 1879 A -> T (IN REF. 2).
180 1879 A -> T (IN REF. 2).
181 1879 A -> T (IN REF. 2).
182 1885 B -> O (IN REF. 2).
183 1936 O -> N (IN REF. 2).
184 185 C -> O (IN REF. 2).
185 186 B -> O (IN REF. 2).
187 188 B -> O (IN REF. 2).
188 188 B -> O (IN REF. 2).
188 188 B -> O (IN REF. 2).
189 189 O -> N (IN REF. 2).
189 189 O -> N (IN REF. 2).
189 189 O -> N (IN REF. 2).
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COILED COIL (POTENTIAL).
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ATP (POTENTIAL).
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19.4%; Pred. No. 0
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InterPro; IPR004009; Myosin_N.
InterPro; IPR0042028; Myosin_Lail.
InterPro; IPR001509; myosin_head.
Pfam; PF00612; Myosin_head; 1.
Pfam; PF01576; Myosin_Lail; 1.
Pfam; PF01576; Myosin_Lail; 1.
Pran; PR00193; MYOSINHEAVY.
PRODOM; PR000193; MYOSINHEAVY.
PRODOM; PR000193; MYOSINHEAVY.
                                                                                                                                                                                                            EMBL; L15351; AAB59701.1; -.
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SMART; SM00242; MYSC; 1.
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----ESKRKKLEEDINKLKKTL------QLSFDLYNKYK 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLLREQYEEEMEAKAELORVLSKANSEVAQWRTKYETDAIORTEELEEAKKKLAORLODA 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1071 IAETENTLENTKILL----KHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLS 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV-----N 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEAVEAVNA-KCSSLEKTKHRLONEIEDLMVDVERSNAAAAALDKKORNFDKILAEWKOK 1461
                                                                                                                                                                                                                                                      NDITKEYEKL----LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKH 538
                                                                                                                                                                                                                                                                                                                      539 NLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKIT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTK 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 PGQQAGSALEGDSVQAQAQEQKQAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLE 776
                                                                                                                                                        --DDLELTL------AKVEKEKHATE------NKVKNLTEEMAGLD 988
                                                                                                                                                                                        DLINPFDYTKEPSKNIY-----TDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSL 481
256 IEESKKTIDKNKNATKEEEKK--KLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE 313
                                                                                                                          FTDPLELEYYLREKNKNIDISAKVE-TKESTEPNEYPNGVTYPLSYNDINNALNELNSFG 427
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                                                                             KLYEFLNTSYICHKYILVSHSTMNE----KILKQYKITKEEESKLSS------C
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                                                            ----NIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSL
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as lats content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
1288 PLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVK 1347
                                                            1830 -----AEQKRNAESVKGMRKSERRIKELTYQTEEDKKN-----LVRLQDLVDKLQLKV 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: WUSCLE MYOSIN IS A HEXAMERIC PROȚEIN THAT CONSISTS OF 2 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC), 2 SURALI LIGHT CHAIN SUBUNITS (MLC) SUBCELLULAR LOCATION: THICK filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEFILDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR WYOSIN ATPASE ACTIVITY.

MISCELLANGOUS: EACH WYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROWYOSIN (LMM) AND 1 HEAVY MEROWYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1502-1940 FROM N.A.
MEDLINE-83161144; PubMed-6833296;
Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
Jakovcic S., Rabinowitz M.;
"Cloned mRNA sequences for two types of embryonic myosin heavy chains
from chick skeletal muscle. I. DNA and derived amino acid sequence of
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Molina M.I., Kropp K.E., Gulick J., Robbins J.;
The sequence of an embryonic myosin heavy chain gene and isolation
of its corresconding about ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                                                                       1940 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to licensedisb-sib.ch).
                                                                                                                    1348 DPYKFLNKEKRDKF---LSSYNYIKDSID 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 258:5196-5205(1983).
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     its corresponding cDNA.";
Biol. Chem. 262:6478-6488(1987).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-87194881; PubMed-3571266;
                                                                                                                                                                                                                                (Rel. 01, Created)
(Rel. 33, Last sequ
(Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; V00430; CAA23712.1; -. EMBL; J02714; AAA48972.1; -.
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A02990; A02990.
PIR; A29320; A29320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meromyosin.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P13538;
                                                                                                                                                                                                                                  21-JUL-1986
                                                                                                                                                                                                    MYH3_CHICK
P02565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 GGSVASGGS------GNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQ 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 DAVLTGYSLFQKEKMVLNEGTSCTAVTTSTPGSKGSVASGGSGSVASGGSVASGGSVAS 96
                                                                                                                                                                                                                                                                                                        Myosin, Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; AFP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVFGYRKPLDNIKDNVG------KMEDYIK--KNKKTIENINELIEESKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 LF--DLTNHMLTLCDNIHGFKYLIDG------YEEINELLYKLNFYFDLLRA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        808 KMMERRESIFCIQYNVRAFMNVKHWPWMKLFFKIKPLLKSAESEKEMANMKEEFEKTKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 IDKNKNATKEEEKK--KLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNE----NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (TRI-) (POTENTIAL). ALKYLATION (SH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       682 ACTIN-BINDING.
776 ACTIN-BINDING.
130 METHYLATION (TRI-) (POTENTIAL)
700 ALKYLATION (SH-1).
710 ALKYLATION (SH-2).
379 G -> D.
1547 T -> A (IN REF. 2).
1915 ERA -> GRT (IN REF. 2).
AA; 222816 MW; C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1;
0.00015;
                                                                                                                                                                                                                                                                                                                                                                                            MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 19.1%; Pred. No. 0.000
Matches 299; Conservative 262; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 348;
                                                                                                                      Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N: 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD0000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSG; 1.
                        IPR002928; Myosin_tail
IPR001609; myosin_head
IPR004009; Myosin_N.
                                                                      PF00063; myosin_head;
                                                                                                                                                                                                                                                                                     PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1940 AA;
                                                                                                                                                                                                                                                                                                                                                              Multigene family.
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Last sequence update)

(Rel. 27, C

01-OCT-1993

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                                                                                                            1045 KLNSLNNPKHVLQNFSVFFNKKKEAEI-------AETENTLENTKILLKHYKG 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLEQS----QPKKPASTHVGAESNTITTSQ------NVDDEVDDVIIVPIFGES 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTIQEARNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLDQTVKDL----- 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1250 EEDYDDLGQV-VTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLE--NNVMT 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYN 1366
                                                                                                                                                                                                                                                                                                                                                                                                          1151 HHLIAELKEVIKNKNYTGNSPSENNTDV-----NNALESYKKFLPEGTDVATVVSESGS 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603
                                                                                                   745
                                                                                                                                                                     854
                                                                                                                                                                                                                                      ANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL----IGQKSS-----ENFYE 953
          SQIQSKIEDEQALGMQLQKKIKELQARIEELEEEIE--AERTSRAKAEKHRADLSRELEE
                                                                                                                                                    -----MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENK
                                                                                1207 DVGEQIDNLQRVKQKLEKEKSE-----LKMEIDDLASNMESVSKAKANLEKMCRSLEDQ
                                                                                                KKNIKTEGOSDNSEPSTEGEITGQAT --- TKPGQQAGSALEGDSVQAQAQAQEQKQAQPPVP
                                                                                                                                                                   QYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFD-----SLNNSLSQLFMEI----
                                                                                                                                                                                                     --YEKEMVCNLYKLKD-NDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPE---VS
                                                                                                                                                                                                                                                                       KILKDSDTFYNESFTNFVKSKADDINSLND-------ESKRKKLEEDINKLK---
                                                                                                                                                                                                                                                                                                       :: | :: | | | : | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | EIRS------RNEALRIKKKMEGDLNEIEIQLSHANRQAAEAQKNLRNTQGVLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHRLDEAEQLALKGGKKQ1QKLEARVRELEGEVDA-------EQKRSAEAVKGVRK
                                                                                                                                  746 VPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILK
                               PDEKILEVSDIVKVQVQKVLLMNK - - IDELKKTQLILKNVELKH - - -
                                                                 ----NIHVPNSYKQENKQEPYYLIVLKKEID---
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1225 AA.

PRT;

STANDARD;

SMC1_YEAST P32908;

SMC1_YEAST ID SMC1_YEACT SMC1_YEAC P32908;

RESULT 39

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                          MEDLINE-94103320; PubMed-8276886; Strunnikov A.V., Larionov V.L., Koshland D.; Strunnikov A.V., Larionov V.L., Koshland D.; SMC1: an essential yeast gene encoding a putative head-rod-tail protein is required for nuclear division and defines a new ubiquitous protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 IPFNLKIRANEL--DVLKKLVFGYRKPLDNIK----DNVGKMED----YIK----KNKK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COULD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.";
Nat. Genet. 10.261-268(1995).
Nat. Genet. 10.251-268(1995).
PURTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD PART OF A CHROMOSOME CONDERSATION MOTOR.
-!- SUBUNIT: HOMODIMER OR HETERODIMER WITH SMC2 OR OLIGOMERS.
-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
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                                                                                                    Saccharomycetes;
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Matches 284; Conservative 248; Mismatches 505; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1225;
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N->D: IN TS MUTANT SMC1-1.
W; B504017AA0ECCA8C CRC64;
                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                       Chromosome segregation protein SMC1 (DA-box protein SMC1 or CHL10 or YFL008W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coil; Nuclear protein.
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9.6e-05;
     update)
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Pred. No. 9
  (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 123:1635-1648(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
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PIR; A41804; S41804.
SGD; S0001886; SMC1.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PP02463; SMC_N.
Pfam; PP02483; SMC_C; 1.
Mitosis; ATP-binding; Coiled co DOMAIN 173 489 CO
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15-JUN-2002
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366 201 426 236 478 294	529 345 574 403	623 463 672 520	730 559 779 618	839 661 890 721	948 763 999 823	1059 870 1119 913	1178 959 1237 1005	1283 1062
DTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKETAKTIKFNID ::::	-KSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMGKRYSYKVEKLTHHNT E	ENEIETLVENIKKDEEQLFEKKITKDENKPDEKI-LEVSDI-VKVQVQKVL (: ::: ::: :: :: :: ::		FELNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSM [TLOLSFDLYNKYKLKLERLFDKKKTYGKYKMQIKKLTLLKEQLESKLNSLNNPKHYLONF 1 QILTVENI : : : : : :	ENEKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTG-NSPSENNTDV 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	-AVTPSVIDNILSKIENEYEV
DTLKKNEN : : : EQIAAQSP SLFTDPLE : : INRRIHGE GDLINPFD OALWQL	-KSLNDIT : KSKLDYIF FASYENSK : : YVERFE'	ENEIETLV : EEKIAVLN LMNKIDEL ::	KLKVEMPK MLKRFFPG QAQA IVENLTVA	EFLNTSYION 1: E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-KAMQYVI E-	SSSMQPLS: : SDIANLRT	TLQLSFDL: QILTV SVFFNKKK	ENFKVLSK: : : SNLQVLKR	DDVIIVPII : HEVEEI
307 1 155 1 367 3 202 1 427 0	479 295 1 530 1	575 404 624 464	673 1 521 1 731 (780 1 619 1 840 1 662 2		1000 3 824 (1060 3	914 8 914 8 1179 1	1238 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                              1120 LKRFKDM------EYLSGGEKTVAALALLFAINSYQPSPFFVLDEVDAALDITN- 1167
1284 LYLKP-----LAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIP- 1335
                                                                    ---YKDLTSSNYVVKDPYKFLNKEKR-------DKFLSSYNYIKDSIDTDINFAND 1381
                                                                                                                                          1382 VLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEA 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392.353-358(1998).

-I- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.1%; Score 344.5; DB 1; Length 978; Best Local Similarity 19.2%; Pred. No. 9e-05; Matches 228; Conservative 232; Mismatches 353; Indels 377; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
--- SUBUNIT: Forms a complex with mrell (By similarity).
--- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 978;
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COILED COIL (POTENTIAL).
A; 9B0F2BF51ADD1151 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable DNA double-strand break repair rad50 AFPase.
RAD50 OR AQ_1006.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                    1203 GVYRQQQENSSKIITLDLSNY 1223
                                                                                                                                                                                                              1442 KVLNYTYEKSNVEVKIKELNY 1462
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex aeolicus.
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RA50_AQUAE
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31 KLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVASGGSVAS

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Tue Apr

SVASGGSVASGGSGNSRRTNPSDN	
THIMLTICDNIHGFKYLIDG- GRRINIKANEVEKWLFKISGI IRANELDVLKKLVFGYRKPLI I	GGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLITKELKYPQ :
(IRANELDVLKKLVFGYRKPLI : : :: 	-LFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQI :::
	PFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINEL
KKTIDKNKNATKEEEKKKLYQ <i>F</i> : : : : KETEEKLRQELKKAEEKDSI	IEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLBEAHNLISVLEKRIDTLKKN
ENIKELLDKINEIKR : : : : SRKVAPYVPIAKRIEEIDKKLTELK-	ENIKELLDKINEIKNPPPANSGNTPNTLLDKNKIEEHEKEIKEIAKTI : : : : : : : : : :
KFNIDSLFTDPLELEYYLREKNKNIDISAKVETK 	KFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALN 421 SFAQEELNRIEAEKEKFEEKELEHRLKKLQEIKEILK 353
SFGDLINPFDYTKEPSKNIYTD- : : : : QLSSSLKEKEREYEQAKQEFEDI	ELNSFGDLINPFDYTKEPSKNIYTD-NERKKFINEIKEKI-KIEKKKIESDKKSYE 47' :
DRSKSLNDITKEYEKLLNEIYDSKFN 	DRSKSLNDITKEYEKLLNEIYDSKFNNNIDLINFEKMGKRYSYKVEKLTHHNTFASYEN : : :: ::
SKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIET 	SKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVEN
IKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKV :	KKDEBQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLANKIDELKKTQL 636
KNVELKHNIHVPNSYKQENKQEPY : : : EIPENLKER	ILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEG 696 : : : :
ONSEPSTEGEITGQATTKPGQQAC	QSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQAGGQKQAQPPVPVPVPEAKAQVP
PPAPVNNKTENVSKLDYLEKLYEFI : : HKAQTELEL	TPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESK : : :: :: :
LSSCDPLDLLFNIQNNIPVMYSMFDSLNNSL ::: LYRVER	LSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK
NLLEEAKKVSTSVKTLSSSSMQPI : 1: 1 : : : EIEEKEKKLRKHFEELSSRKSKL	IKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENI ::: : :
LSLGKM-KNIYQELIGQKSSENFYEKILKDSDTFYNESFINFVKSKA : : : : : : : : YEVAKSPREVVELYLGDKEAELERKIKEFEESFQSL	LSLGKN-KNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRK : : : : : : : : : : :
EEDINKLKKTLQLSFDLYNKYKLK : : : : : : EEKLKEYEGIRELS-DIKGEYESV	KLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNS 1048 :: ::
PKHVLQNFSVFFNKKKEAEIAET ::: : EELQKEISEI	LNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKG-LVKYYNGESSPLKTL 110 :: :

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                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=F1B; TISSUE=Liver;
MEDLINE=95115033; PubMed=7815459;
Wang R., Sole M.J., Cukerman E., Liew C.-C.;
"Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster.";
J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 962-1935 FROM N.A.
SEQUENCE OF 962-1935 FROM N.A.
JandIrNE-88247788 Pubmed=3380703;
JandIreski M.A., Sole M.J., Liew C.-C.;
"Sequence of cDNA encoding the Syrian hamster cardiac beta-myosin
                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
1106 -SEESIQTEDNYASLENFKVLSKLEGKLKDNLNLE-----KKKLSYLSSG 1149
                                                                                                       P13540; 060540;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
               PRT; 1934 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
Probom; PR00193; MyoSin_Heavy.
Probom; PD000355; myosin_head; 1.
SMART; SM00015; IQ; IQ; II.
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InterPro; IPR004009; Myosin_N.
InterPro; IPR0012928; Myosin_tail.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; IPR001612; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L12104; AAA62313.1; -. EMBL; X07273; CAA30256.1; -. PIR; A28298; A28298. HSSP; P08799; IMND.
                                                                                              STANDARD;
                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=10036;
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                                                                   RESULT 41
MYH7_MESAU
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559 VVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQ
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01-MAR-1989 (Rel. 10, Last sequence update)
02-CT-2001 (Rel. 40, Last annotation update)
Hypothetical 259 kba protein ycf2 (ORF 2136).
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Marchantia polymorpha (Liverwort).
Chloroplast.
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P09975;
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                  Coiled coil; Thick filament; Actin-binding;
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                                                                                                                                                                                                                                                                                                   Length 1934;
                                                                                              ACTIN BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
D -> E (IN REF. 2).
T -> TE (IN REF. 2).
E -> Q (IN REF. 2).
DLQAEED -> ALEARKT (IN REF. 2).
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K (IN REF. 2).
FDBAC58310B0B57D CRC64;
       PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Ac
ATP-binding; Methylation; Alkylation; Multigene family;
Calmodulin-binding.
                                                          IQ.
COILED COIL (POTENTIAL).
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19.4%; Pred. No. 0.00019;
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D -> V (IN REF. 2)
D -> N (IN REF. 2)
D -> N (IN REF. 2)
D -> N (IN REF. 2)
T -> A (IN REF. 2)
L -> V (IN REF. 2)
M -> L (IN REF. 2)
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AA; 222928 M
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TL-----QLSFDLYNKYKLKLER-LFDKKKTVGKYKM-QIKKLTLLKE 1040
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                                                                           VQKVLLMNK - - IDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKV
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Marchantiopsida; Marchantiidae; Marchantiales; Marchantiineae;
Marchant&aceae; Marchantia.
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                                                                                               Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
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                                                                                                                             Ozeki H.; "Chloroplast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA "; Nature 322:572-574(1986).
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Chloroplast; Hypothetical protein.
SEOUENCE 2136 AA; 259911 MW; 5
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--EEKKNIKTEGOS 698
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European Bioinformatics Institute.
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Best Local Similarity 19.7%; Pr¢
Matches 304; Conservative 267;
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                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-94140346; PubMed-8307559;
Epp T.A., Dixon I.M., Wang H.Y., Sole M.J., Liew C.-C.;
Structural organization of the human cardiac alpha-myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
                                                                                                                                                                                                                                        Matsuoka R., Beisel K.W., Furutani M., Arai S., Takao A.; "Complete sequence of human cardiac alpha-myosin heavy chain geamino acid comparison to other myosins based on structural and functional differences.";
                                                                                 P13533; Q13943; Q14907; C14307; D1-3AN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MYOSII heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89264452; PubMed-2726733; Yamuchi-Takihara K., Sole M.J., Liew J., Ing D., Liew C.-C.; Telbaracterization of human cardiac myosin heavy chain genes."; Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBFRAGMENT ($2).
MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATP MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: COUPAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamauchi-Takihara K., Sole M.J., Liew J., Ing|D., Liew C.-C.
Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).
                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                               PRT; 1939 AA
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SEQUENCE OF 1-177 AND 1551-1939 FROM N.A.
              1638 IVIYKVGKTIIQNILIKSSSMNLLNI 1663
MVFENLAKTVLSN-LLDGNLQGMLNI 1527
                                                                                                                                                                                                                                                                                       Am. J. Med. Genet. 41:537-547(1991).
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SEQUENCE FROM N.A.
MEDLINE-92133665; Pubmed-1776652;
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are no restrictions on its its content is in no way Usage by and for commercial
             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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Pfam; PF000613; myosin_head; 1.
Pfam; PF01612; 109; 2.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
                                                                                                                L; M25140; AAA60386.1; -.
L; M25162; AAA60386.1; -.
L; M25141; AAA60387.1; -.
L; M25141; AAA60387.1; -.
L; M21664; AAA36344.1; -.
R46762; A46762.
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1. Biol. Chem. 266:9180-9185(1991).
2. J. Biol. Chem. 266:9180-9185(1991).
2. IF PUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
2. AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
3. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
3. PRESULATOR TAILS FAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLED COLLES.
3. CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLES.
4. PTW.: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
5. MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO I LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (MMM). IT CAN LAFER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
1512 SDLTEQLGEGGKNVHELEKVRKQLEVEKLELQSALEEAEASLEHEEGKILRAQLEF---N 1568
                                                                                                                                                                                                                                                   1128 LEGKLKDNLNLEKKKLSYLSSGLHHLIAEL------KEVIKNKNYTGNSPSENNT 1176
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                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=BALB/C, A/J, C57BL/6J, and DBA/2J;
MEDLINE=92250040; Pubmed=1577481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91225025; PubMed-2026617;
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Genomics 13:176-188(1992).
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SEQUENCE OF 1-67 FROM N.A.
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                                                                                       1014 AEEDK------VNTLTKSKVKLEQQVDD--LEGSLEQEKKVRMDLERAKRKLEGDLK 1062
                                                                                                                                                                                            1122 BELE--AERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIE----MNKKREAEFQK 1175
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ATP-binding; Methylation; Alkylation; Multigene family;
Calmodulin-binding; Polymorphism.
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CALMODULIN-BINDING (BY SIMILARITY).
CALMODULIN-BINDING (BY SIMILARITY).
METHATATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
SUBFRAGMENT (S2).
MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 467; Indels 303;
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Pred. No. 0.00024;
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COILED COIL (POTENTIAL).
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ACTIN-BINDING.
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InterPro: IPR000048; IQ_region.
InterPro: IPR00409; Myosin_L
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223564 MW;
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SMART; SM00242; MYSC; 1.
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SWISS-2DPAGE; Q025(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: MUSCLE CONTRACTION.
-i- SUBUNT: MUSCLE WYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 1-818, AND REVISIONS 204-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dominguez R., Freyzon Y., Trybus K.M., Cohen C.; "Crystal structure of a vertebrate smooth muscle myosin motor domain and its complex with the essential light chain: visualization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY. MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO I LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                             Complete primary structure of vertebrate smooth muscle myosin heavy
                                                                                                                                                                                                                                         chain deduced from its complementary DNA sequence. Implications on topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-88118918; Pubmed-2892941;
Yanagisawa M., Hamada Y., Katsuragawa Y., Imamura M., Mikawa T.,
                                                                                                                                                                                                                                                                                                                                                                                          Maita T., Onishi H., Yajima E., Matsuda G.;
"Amino acid sequence of the amino-terminal 24 kDa fragment of heavy chain of chicken gizzard myosin.";
J. Biochem. 102:133-145(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBFRAGMENT (S2).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases
            01-JUL-1989 (Rel. 11, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                         Myosin heavy chain, gizzard smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88032919; PubMed-3312184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98412652; PubMed-9741621;
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Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1BR1; 09-SEP-98.
PDB; 1BR2; 09-SEP-98.
PDB; 1BR4; 09-SEP-98.
InterPro; 1PR000048; IQ_region.
InterPro; IPR004099; Myosin_N:
InterPro; IPR002928; Myosin_tail.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pre-power stroke state.";
Cell 94:559-571(1998).
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-203.
                                                                                                                                  NCBI_TaxID=9031;
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1079 LQAQIAELKAQLAKKEEELQAALARLEDETSQKNNALKKIRELESHISDLQEDLESEKAA 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1188 LEEETRTHEAQVQEMRQKHTQAVEELTEQLE---QFKRAKANLDKTKQT-LEKDNADLAN 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 KKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKH 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 EESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ITKEYEKL---LNEIYDSKFNNNIDLTNFEKMMGK----RYSYKVEKLT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         906 ELYAEAEEMRVRLAAKKOELEEILHEMEARIEEEEERSQOLQAEKK----KMQQQMLDLE 961
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                                                                                                                                                                                                                  Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELE
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                                                                                                                                                                                                                                                                                                                                         IQ.
RODLIKE TAIL (S2 AND LAM DOMAINS).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 ALKYLATION (SH-1).
716 ALKYLATION (SH-2).
1127 MISSING (IN REF. 3).
215 KDTSITOGPSFS -> RTPASLKVHLFP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 341.5; DB 1; Length 1978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHYLATION (TRI-) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 202; Mismatches 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.00024
                                                                                                                                                                                                                                                                                                                  MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN-BINDING. ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOCKED.
                                                                                                                       myosin_head; 1.
                                                                                                                                                                                                                                                                Multigene family; 3D-structure.
INIT_MET 0 0 0
DOMAIN 1 790 MY(
                      Pfam; PF00612; IQ; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRIWTS; PR0193; MYOSINIEAVY.
ProDom; PD000355; myosin_head;
myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.0%;
                                                                                                                                           SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 12
706 70
716 71
127 12
204 21
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CONFLICT
CONFLICT
SEQUENCE
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NP_BIND
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50;

ATI Physical Physical Query Mat. Best Loca. Matches 182 NI 182 NI 242 II	278 - 130 V 324 E 324 E 379 L 238 K 2238 K 2238 K 2286 N	346 N :: 346 N :: 5195 N :: 579 E: 639 K N E: 534 K N N :: 534 V V :: 534 V V :: 544 N :: 534 V V :: 534 V V :: 544 N :: 544 N :: 534 V V :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N :: 544 N	
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	1727 SGRTSLQDEKRRLEARIAQLEEELDEEHSNIETMSDRMRK 1107 EESIOTEDNYASLENFWULSKLEGKLKDNLNLEKKKLSY 1107 E.	SUL SB_	REQUENCE FROM N.A. RECOLINE-98065943: PubMed-9403685; RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., RA Lathigram R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., RA Dougherty B., Tomb JF., Fleischmann R.D., Richardson D., RA Peterson J., Kerlavage A.R., Quackenbush J., Salaberg S., Hanson M., RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., RA Garland S., Eujii C., Cotton M.D., Horst K., Roberts K., Hatch B., R. Genomic sequence of a Lyme disease spirochaete, Borrelia R. Lurgdorferi." R. Lathigram REQUIRE FOR EFFICIENT DNA REPAIR: IT CATALYZES THE CCI FUNTION: OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE- CC. STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION. ALL OF THESE ACTIVITES REQUIRE CONCOMITANT HYDROLYSIS OF ATP CCI CATALYTIC ACTIVITE: Exonucleolytic cleavage (in the presence of

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Pro; IPR000212; UvrD-helicase.
Pro; UvrD-helicase; 1.
PMS; TIGR00609; recB; 1.
AMS; TIGR06609; recB; Endonuclease; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYDFLRKSDSLIQALDIKDYELKVFKSDAKKTEEIVLKIKKAYE----RDTTQELGDWLK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLF-----TDPLELEYY 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KENDIFKIAETLLKNKFFSTLIEKETKKNSK------LSPKEL-KIKNDLICLGI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTP 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 4.0%; Score 338; DB 1; Length 1169;
11 Similarity 19.6%; Pred. No. 0.00018;
288; Conservative 237; Mismatches 455; Indels 490; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRE-----KNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINPFDYTKEPSKNIYTDNERK------KFI-NEIKEKIK----IEKKKIESDKK 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SY ---EDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKR-----YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKKNKKTIENINELIEESKK----TIDK-----NKNATKEEEKKK----
either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                     IMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                              hosphooligonucleotides.
UBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
BY SIMILARITY).
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W; B61D63C1C959B91F CRC64;
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ND 18 25 ATP
NCE 1169 AA; 137828 MW;
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us-09-269-874a-3.rsp

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TNYLGKNKEDYNITULENTIKKEYYD---LQYKIYALGIRKILFKNKKEY--NQKFGGII 1122
                                                                                                                                                                                                                                                                                                                                                                                968 ---TNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKK- 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1368 IKDSIDTDINFANDVLGYYK-ILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYK 1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1070 EIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLE 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1249 SEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFN 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1309 VNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE-KRDKFLSSYNY 1367
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                                                                                                                                                                                                                                                                                                                     --EIEEKINNINNDNESIE-LMTIHKSKGLGMIVV-----FLLNTTPIENSNFF 766
                                                                                                                                                                                                                                                                                                                                                                                                             1032 DKHFEDLHIKLSD---GYLKGIVDLIFKA---NNKIYILD--------YK 1067
                                                                                                                                                                                                                              663 WAKNKINYKGLLIKEGKLENLKTYETTLEIISKIYHKEQNIQSLISTLESLIINEEPE-- 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      807 FYVGATRAKFALFIIKINSITSKLLEIAKIFTIDDIKH---DFNIHEFIGQKRFNKKK-- 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887
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                                                                                                                                                  F------IENIIVLEEKNEITLINAINKI---TFEKNLWIKIANITKDQKIIE 662
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                                                                                                                                                                                                                                                                                         909 ANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESF- 967
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Sciurognathi; Muridae; Murinae; Rattus.
                                                             565 -----KTKEFSEIFYIIKCLDRKQSFKTLNYILSSKILNVPWNLQRILIKQDKICLIEE
                                                                                                                                                                                                 ------KNLLEEAKKVSTSVKTLS----SSSMQPL----SLTPQDKPEVS
                                                                                                          SKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKI--
                     PAPVNNKTENVSKLDY - - - - LEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEE
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).
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Mammalia; Eutheria; Rodentia;
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MEDLINE=82220035; PubMed=7045682;
Mahdavi V., Periasamy M., Nadal-dinard B.;
"Molecular characterization of two myosin heavy chain genes expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90133919; PubMed=2614840; MCDLINE=90133919; PubMed=2614840; MCNally E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.; "Full-length rat alpha and beta cardiac myosin heavy chain sequences." (Comparisons suggest a molecular basis for functional differences."; J. Mol. Biol. 210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.; "Carddiac myosin heavy chain isozymic transitions during development and under pathological conditions are regulated at the level of mRNA availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS ($1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-167 FROM N.A.
MEDLINE-84194059; Pubmed-6585819;
MADAINE-94194059; V. Chambers A.P., Nadal-Ginard B.;
"Cardiac alpha- and beta-myosin heavy chain genes are organized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS I TO DOMAIN.
                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 81:2626-2630(1984).
                                                                                                                                                                                                                                     cardiac myosin heavy chain.";
Nucleic Acids Res. 17:7527-7528(1989)
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MEDLINE-85179510; PubMed-6241892;
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InterPro; IPR002928; Myosin_tail.
                                                            PubMed=2798111;
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PIR; A02988; A02988.
HSSP; P08799; IMND.
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TISSUE=Heart;
MEDLINE=90016822;
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DISCUSSION OF
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DAEEAVEAVNA-KCSSLEKTKHRLQNEIEDLMVDVERSNAAAALDK 1445 YKLKLER-LEDKKKTVGKYKM-QIKKLTLLKEQLESKLNSLNNPKHV 1055 LSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSP 1171 ----NVDDEVDDVIIVPIFGESEEDYDDLGQV-VTGEAVTPSVIDN 1272 AEIAETENTLENTKILL----KHYKGLVKYYNGESSPLKTLSEESIQ 1111 LKPLAGVYRSLKKOLENNVMTFNVNVKDILNSRFNKRENFKNVLESD 1332 REBEISERLEEAGGATSVQIE----MNKKREAEFQKMRRDLEEATL 1184 NNALESYKKFL-PEGTDVATVVSESGSDTLEQSQPKKPASTHVGAES 1224 -----AEQKRNAESVKGMRKSERRIKELTYQTEEDKKN---- 1861 KDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKKTQLILKNVEL 643 KLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKL 817 -CDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYK 865 INPEDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYED 476 NKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEP 703 PGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV---PTPPA 760 EAKKVSTSVKTLSSSSMQPLSLTPQDKPE---VSANDDTSHSTNLNN 921 KLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASY LKY------MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENI ---ENFYEKILKDSDTFYNES AKL--TKE------KKALQEAHQQ-ALDDLQAEEDK---KVKAYKRQAEEAEEQANTNLSKFRKVQHELD 1905 VKDPYKFLNKEKRDKF---LSSYNYIKDSID 1373 NKNIYQELIGQKSS-----

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"Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanley J.R., Tanaka T., Mueller S., Klaus-Kovtun V., Roop D.; "Isolation of complementary DNA for bullous pemphigoid antigen by use of patients' autoantibodies."; J. Clin. Invest. 82:1864-1870(1988).
                                                                                                                                                                                                                                          Elgart G.W., Stanley J.R.; "Cloning of the 5' mRNA for the 230-kD bullous pemphigoid antigen by rapid amplification of 10NA ends."; "rapid amplification of 101:244-246(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The hemidesmosomal plague. I. Characterization of a major constituent protein as a differentiation marker for certain forms of anothers.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of the cytoplasmic bullous pemphigoid antigen (BPAGI). Empirical Jocalization of the N-terminal globular domain-rod boundary.";
J. Biol. Chem. 271:9716-9722(1996).
-!- FUNCTION: COMPONENT OF HEMIDESMOSOME PLAQUE. THE PROTEINS PROBABLY SELF-AGGREGATE TO FORM FILAMENTS OR A TWO-DIMENSIONAL MESHWORK. POTENTIAL INTERACTION WITH KERATIN INTERMEDIATE FILAMENTS.
                            03001; 013775; Q9UGDB; Q9UGD7; 01-071-1996 (Rel. 34, Created) (1-0CT-1996 (Rel. 34, Created) (1-0CT-2001 (Rel. 40, Last sequence update) (16-0CT-2001 (Rel. 40, Last annotation update) (Bullous pemphigoid antigen 1 (230 kDa bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein).
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             Hopkinson S.B., Jones J.C.; "Identification of a second protein product of the gene encoding human epidermal autoantigen."; Biochem. J. 300:851-857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1650-2257 FROM N.A.
MEDLINE-91216368; Pubmed-2090522;
Owaribe K., Kartenbeck J., Stumpp S., Magin T.M., Krieg T.,
                                                                                                                                                                                                                                                                                                                              Tanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M., Stanley J.R.;
                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1777-2704 FROM N.A. (ISOFORM 4).
                    2704 AA.
                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
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f. Biol. Chem. 266:12555-12559(1991),
                     PRT;
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MEDLINE=89067122; PubMed=2461961;
                                                                                                                                                                                                                      TISSUE=Keratinocytes;
MEDLINE=93346806; PubMed=8345227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelia."; Differentiation 45:207-220(1990).
                                                                                                                                                                                                                                                                                                                      PubMed=1712022;
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MEDLINE=94280413; PubMed=8010969;
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                     STANDARD;
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                                                                                                                                                                                                                                                                                                           TISSUE=Keratinocytes;
MEDLINE=91286285; Pub
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                    BPA1_HUMAN
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NSCISFGSESFDGH -> ISDIHVTGESEDMSAKERLLLWT
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VAVQSNLANLEHAFYVAEKIGVIRLLDPEDVDVSSPDEKSV
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VOWTRHUYTNSERTFFNDVPELKALYNNYLLGKFETETPPKE
TEKSKIRLYKLLKLEKVPCFKKIWIEFERKLLGGYFBNDIE
KEWGKLIIAMLBREKALRPEVE (IN ISOFORM 1).
ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE) AND 4; MAY
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                                                                                                        -!- SIMILARITY: CONTAINS 10 PLECTIN REPEATS.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
-!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
-!- CAUTION: ISOFORMS 2 AND 4 ARE FRAGMENTS AT THE N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 domain; Structural protein;
                        BE PRODUCED BY ALTERNATIVE SPLICING.
DISEASE: INVOLVED IN THE SUBEPIDERMAL BLISTERING DISEASE
BULLOUS PEMPHIGOID, AN AUTOIMMUNE DISEASE.
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Pfam: PF00018; SH3; 1.
Pfam: PF00018; SH3; 1.
Pfam: PF00681; Plectin; 6.
SWART: SM00150; PEEC; 1.
SWART: SM00150; SPEC; 3.
PROSITE: PS50002; SH3; FALSE_NEG.
Antigen; Colled coll; Repeat; SH3 domain; Structural progression; Colled coll; Repeat; SH3 domain; Structural browning coll adhesion; Alternative splicing.

DOMAIN
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SPECTRIN 2.
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PLECTIN 2.
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InterPro; IPR001452; SH3.
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EMBL, M8361B, AAA35606.1;
EMBL, U04450, AAA55184.1;
EMBL, X58677; CAA41528.1;
EMBL, M22442, AAA35588.1;
Genew, HGNC:1090; BPAGI.
MIM; 113810.
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1544 RITRAHAVAEKNIQHLNSQIHSFRDEKELERLQICQRKSDHLKEQFEKS----HEQLLQ 1598
                                                                    1717 EFKQKCDQQNIIIQNTKKEVRNLNAELNASKEEKRRGEQKVQLQQAQVQELNNR-LKKVQ 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LIAQKRE-----C 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLKKQLENNVMT----FNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPY 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1130 GKL-----KDNLNLEKKKLSYLSSGLHHLIAE-----LKEVIKNKNYTGNSPSENNTDVN 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                               LEKQTIQQRCEALKIQADGFKDQLRSTNEHLHKQTKTEQDFQRKIKCLEEDLAKSQNLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                        1835 VSLQQENSRAQENAKLCETNIKELERQLQQYREQMQQGQHM--EANHYQKCQKLEDE---
                                                                                                                                 KYKMOIKK----KEAEIAETENTLE
                                                                                                                                                                                                                          NTK-----ILLKHYKGLVKYYNGE---SSPLKTLSEESIQTEDNYASLENFKVLSKLE
                                                                                                                                                                                                                                                                                                                                                                                                        1180 NALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1240 VIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKI----ENEYEVLYLKPLAGVYR
                                            FVKSKA - - - DDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVG
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | : | | | 1981 QHRVVEQIPKEVQFQPPGAPLEKEKSQQCYSEY-FSQTSTELQITF 2025
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IW; D901314E981BF001 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypochetical protein KIAA0373.
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Hypothetical protein; Coiled coil.
DOMAIN 18 1514 COILE
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MEDLINE-97349984; PubMed-9205841;
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1539 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 RLEEEEEVIINSEHPVNIKELEIKRCKETSEHGAYSDLLQRQKATVLENSKLTGKISELER 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QIDNRLRDLEGIGKSLKYYRDTYHPLDDWIQQVE 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      875 KGYCLISFLRTKTVNLVLKNTQAAEALVKLYETKLCEEEAVIADKNNIENLISTLKQWRS 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSS EVDEKRQVFHALEDELQK-AKAIS---DEMFKTYKERDLDFDWHKEKADQLVERWQNVHV 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNEKILKOYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFWEIYEKE 858
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                                                                                                                                                                                                                                               211 AN------KMEDYIKKLVF-----GYRKPLDNİKDNVG----KMEDYIKKNK 246
                                                                                                                                                                                                                                                                                                                                                                                                                               EAHNLISVLE-KRIDTLKKNENIKELLDKINEIK----NPPPANSGNTPN---TLLDKNK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 KIEEH-----EKEIKEIAKTIKFNIDSLFTD----PLELEYY-----LREKNKNIDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 -----YTKEPSKNIYTD-NERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDI- 484
                                                                                                                                                        166 YLIDGYE-----EINELLYKLN----FYFDLL----RAKLNDVCANDYCQIPFNLKIR 210
                                                                                                                                                                                                                                                                                                                                        247 KT------IENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFG-+----DLINPFD----- 434
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                  485 --TKEYEKLLNEIYDS-----KFNNNIDLTNFEKM-MGKRYSYKVEKLTHHNTFAS---
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                                                                                                           Matches 292; Conservative 232; Mismatches 514; Indels 448;
                                                                 Length 2704;
313084 MW; A7219E687A634A77 CRC64;
                                                                    , DB 1;
0.00045;
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                                                               Score 338;
Pred. No. 0
                                                                    4.08;
    1998
                       2704 AA;
                                                                                         Similarity
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                       SEQUENCE
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  CONFLICT
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Db 1031 VDQVLGIRALESEKELEELKKRNLDLENDILYMRAHQALPRDSVVEDLHLQNRYLQEKLH 1090 1 1	RESTLUMAN LO ARE1993 (Rel. 25, Created) DT 01-ARF-1993 (Rel. 25, Last sequence update) DT 01-ARF-1993 (Rel. 25, Last sequence update) DT 01-ARF-1993 (Rel. 25, Last sequence update) DT 15-UUN-2002 (Rel. 41, Last annotation update) DE Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-Sternberg intermediate filament associated protein). DE RESTLUM-2002 (Rel. 41, Last annotation update) DE Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-Sternberg intermediate filament associated protein). OS Homo sapiens (Human). OC EUKaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; OX MELTAXID=9606; M.A. RN FERSIM. (NELTAXID=9606; M.A. RN FERSIMEE FROM N.A. RN FERSIMEE FROM N.A. RA CETIELTINE-92289675; Pubmed-1600942; RA Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M., RA CETIELTIN, Sorg C., Odink K., Tarcsay L., Wiesendanger W., de Wolf-Peeters C., Shipman R.; RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRESCONCE FROM N.A. RN FRE
dels 477; Gaps 81; "ILCDNIHGFKYLI 168 "EILNAQQOSR 236 ANELDVLKKLVFG 223 "I	DIVKUQVQKVLL 624 :::
Best Local Similarity 20.2%; Pred. No. 0.00025; Matches 319; Conservative 276; Mismatches 505; Indels 477; G 115 DNSSDSDARSYADL-KHRVRNYL-LITKELKYPQLFDLTNHMLTLCDNIHGFKYLI 1	
Mat. Mat. Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy Oy	

	767 722 813 778 841	QY 837 YSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLE : : : : : : : : : :	954 966 1014 1017	OY 1073 ETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTE :::	QY 1193 TDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNV I	OY 1297 - FKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPY	OY 1414 YLPFLNNIETLYKTVNDKIDLFVIH 1438	
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC -1- SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS. CC This SWISS-PROT entry is copyright. It is produced through a collaboration contented the Swiss Institute of Baloinformatics and the EMED outstation - CC the European Bioinformatics Institute. There are no restrictions on its cuse by non-profit institutions as long as its content is in no way conditied and this statement is not removed. Usage by and for commercial contents and commercial contents.		SMART; SMO343; ZnF_CZHC; 1. PROSITE; PS00845; CAP_GLY_1; 2. PROSITE; PS00845; CAP_GLY_2; 2. CYLOSKeleton; Microtubules; Colle DOMAIN 173 204 DOMAIN 322 274 CAP- DOMAIN 330 314 SER- DOMAIN 350 1342 CAP- CAP- CAP- CAP- CAP- CAP- CAP- CAP	DOMAIN 1408 1421 VARSDELC 457 491 COMFLICT 1069 1069 SEQUENCE 1427 AA; 160989 W VUEY MATCH 4.0%; Rest Local Similarity 19.3%; fatches 283; Conservative 249	OY 43 YSLFQKEKMVLNEGTSGTAVTTSTPG-SKGSVASGGSGSVASGGSVASGGSVASGGSVA 	153 HMLTLCDNIHGFKYLIDGYEE-INELLYKLNFYFDLLRAKLNDVCANDYCQIPF	QY 266 NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELL 319 266 NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELL 319 26 NKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELL 319 27 JARIELEDTRYATVSEKSRIMELEKDLALRYQEVAELRRRLESNKPAGDVDMSL 535 QY 320 DKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLEL 375 CHEKEIKEIAKTIKFNIDSLFTDFLEL 375 CHEKEIKEIAKTIKFNIDSLFTDFLEL 375	376 EYLLGELSS	QY 487 EYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKA 546

:: |:| :: | : KLSDLEKKMETSHNQCQELKA 1016 | | | :| ::| : -ELLTVENQKMEEFRKEIETL 1150 DINKLKKTLQLSFDLYNKYKL 1013 KH-VLONFSVFFNKKKEAEIA 1072 :|| :|| :|-|| :|-|| :|-|| :|-|| NSGLLQELE---ELRKQADKA 1071 TEDNYASLENFKVLSKLEGKL 1132 SENNTDVNNALESYKKFLPEG 1192 :::| ::: :: KLEEERSVLNNQLLEMKKRES 1207 YKSDLDSIKKYINDKQGENEK 1413 NVDDE---VDDVII-----V 1243 VL----YLKPLAGVYRSL-- 1296 || | | | ::| VLRGENASAKSLHSVVQTLES 1267 PYKDLTSSNYVVKDPYKFLNK 1355 ADEDERA------0 1308 LNGNGDDLNNYDSDDQEKQSK 1361 : | |:| IAEIMKMS-----926 SELOLKLTKANENASFLO 965 : | ; | † NQO---DSERAAHAKEMEALR 685 KKDEEQ-LFEKKITKDENKPD 605 PVNNKTENVSKL----DYLEK 777 : | ||:|:: : ||| -LTNLQENLSEVSQVKETLEK 840 KNIYQ-ELIGOKSSEN--FYE 953 VELKHNIHVPNSYKQENKQEP 661 SEPSTEGEITGQATTKPGQQA 721 KLSSCDPLDLLFNIQNNIPVM 836 : / / : / : / WILSSD----LEKLRENLADM 894 LEEAKKVSTSVKTLSSSSMQP 896

dystrophy gene.";

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Pearson P.L., van Ommen G.J.B.;
"High resolution deletion breakpoint mapping in the DMD gene by whole cosmid hybridization.";
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Roberts R.G., Gardner R.J., Bobrow M.;
"Searching for the 1 in 2,400,000: a review of dystrophin gene point mutations.";
                                                                                                                                                                                                                                                                                                                                                    "Two human cDNA molecules coding for the Duchenne muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and
                                                                                          Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 404-1137 FROM N.A.
MEDINE-88111212; Pubmed=3428261;
Cross G.S., Speer A., Rosenthal A., Forrest S.M., Smith T.J.,
Edwards Y., Flint T., Hill D., Davies K.E.;
"Deletions of fetal and adult muscle cDNA in Duchenne and Becker
muscular dystrophy patients.";
EMBO J. 6:3277-3283(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Deletion screening of the Duchenne muscular dystrophy locus via multiplex DNA amplification."; Nucleic Acids Res. 16:11141-11156(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVIEW ON VARIANTS.
MEDLINE-94320940; PubMed-8045556;
Rininsland F., Reiss J.;
"Microlesions and polymorphisms in the Duchenne/Becker muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                               Koenig M., Hoffman B.P., Bertelson C.J., Monaco A.P., Feener C. Kunkel L.M.;
                                                                                                                                                                                                                                                                                                                  Rosenthal A., Speer A., Billowitz H., Cross G.S., Forrest S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary genomic organization of the DMD gene in normal and affected individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89345155; Pubmed-2569720;
Blonden L.A.J., den Dunnen J.T., van Paassen H.M.B.,
Wapenaar M.C., Grootscholten P.M., Ginjaar H.B., Bakker E.,
                                                                                                                                                                                        Koenig M., Monaco A.P., Kunkel L.M.;
The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein.";
Cell 53:219-228(1988).
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huth A., Will K., Speer A., Bauer D.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 665-722; 2098-2204 AND 2305-2366 FROM N.A. MEDLINE-89083552; PubMed-3205741; Chamberlain J.S., Gibbs R.A., Ranier J.A., Nguyen P.N.,
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     (DMD) locus are highly homologous.";
Nucleic Acids Res. 17:5391-5391(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 17:5611-5621(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIEW ON DMD POINT MUTATION VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-497 FROM N.A.
MEDLINE-87273512; Pubmed-3607877;
                                                                                                                                                                            MEDLINE-88194521; PubMed-3282674;
                                                                                                                                                                                                                                                                                                  MEDLINE-89345106; PubMed-2668885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2305-2364 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2147-2204 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fum. Mutat. 4:1-11(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 50:509-517(1987).
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caskey C.T.;
                                                                                                                                                                                                                                                                                                                                 Davies K.E.;
                                       Dystrophin.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYSTROPHIN-1, -2 AND -3 DOUGHLAN WARRINGS AND CALLED DYSTROPHIN-1, -2 AND -3 DOUGHLAN WARRINGS AND CALLED DYSTROPHIN-1, -2 AND -3 DOUGHLAND DYSTROPHIN-1, -2 AND -3 DOUGHLAND DYSTROPHY (BMD). DWD IS THE MOST COMMON OF THE WASCLEAR OF STROPHY (BMD). DWD IS THE GISORDER. It typically presents in boys aged 3 to 7 year as proximal muscle weakness causing wadding agit, to e-walking, lordosis, frequent falls, and difficulty in standing up and climbing up stairs. The pelvic girdle is affected first, then the shoulder girdle. Progression is steady and most patients are confined to a wheelchair by age of 10 or 12. Flexion contractures and scoliosis ultimately occur. About 50% of patients have a lower 10 than their genetic expectations would suggest. There is no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment. BMD ressembles DMD in hereditary and clinical features but is later in onset and more benign.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89181947; Pubmed-2648158;
Feener C.A., Koenig M., Kunkel L.M.;
"Alternative splicing of human dystrophin mRNA generates isoforms at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiomyopathy (XLCM).
MISCELLANEOUS: THE DMD GENE IS THE LARGEST KNOWN GENE IN HUMANS.
IT IS 2.4 MILLION BASE-PAIRS IN SIZE AND COMPRISES 79 EXONS.
SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
                                                                                                       Prior T.W., Papp A.C., Snyder P.J., Burghes A.H.M., Bartolo C., Sadra M.S., Western L.M., Mendell J.R.;
"A missense mutation in the dystrophin gene in a Duchenne muscular dystrophy patient.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the carboxy terminus.";
Nature 338:509-511(1989).
-!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE
                                                                                                                                                                                                                                                                                                                    "Novel small mutations along the DMD/BMD gene associated with different phenotypes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Βĭ
                                                                                                                                                                                                                                VARIANTS DMD HIS-365; TRP-2191 AND ARG-2937.
MEDLINE-99152525; PubMed=7849724;
Nigro V., Nigro G., Esposito M.G., Comi L.I., Molinari A.M., Puca G.A., Politano L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED I ALTERNATIVE SPLICING; THE 3 SHORTER VARIANTS ARE CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: Defects in DMD are a cause of X-linked dilated
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SIMILARITY: CONTAINS 2 CALPONIN'HOMOLOGY (CH) DOMAINS.
SIMILARITY: CONTAINS 22 SPECTRIN REPEATS.
SIMILARITY: CONTAINS 1 WW DOMAIN.
SIMILARITY: CONTAINS 1 WW DOMAIN.
SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
DATABASE: NAME-DMD; NOTE-DYSTOPHIN Mutation Database;
WWW-"http://www.dmd.nl/database.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miles N. P., Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING (DYSTROPHIN-1 AND -2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING (DYSTROPHIN-3).
                                                                                                                                                                                                                                                                                                                                                              3:1907-1908(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X06179; CAA29545.1; ALT_SEQ.
EMBL; X06178; CAA29544.1; -.
                                                                                   MEDLINE=94004962; PubMed=8401582;
                 Hum. Genet. 94:111-116(1994).
                                                                                                                                                                                            Nat. Genet. 4:357-360(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASMA MEMBRANE.
                                                            VARÍANT DMD ARG-54.
                                                                                                                                                                                                                                                                                                                                                                   Hum. Mol. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Retina;
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1460 LFQKPANFELRLQESKMILDEVKM 387 DISAKVETKESTEPNEYPN 1: : : 1520 EMVIKGRQIQKKQTENPKELDE	Oy 418 -NALMELNSFGD	Qy 506LTNFEK	Qy 521 VEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEI :	Qy 579 ETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNK	Qy 628 IDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLI : : : : : : : : : :	Qy 686 NEEK-KNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQA :	Qy 741 Q	Qy 787 ICHKYILVSHSTMNEKILKQYKITKE-EESKLSSCDPLDLLENIQNNIPVMYSMF	QY 841 DSLNNSLSQLFMEIXEKEWVCNLYKLKDNDKIKNLLEBEAKKVSTSVKTLSSSSMQPLSLT 1	QY 901 PODKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILK	QY 958 DSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLER :::: ::	OY 1018 LEDKKKTYGKYKMOIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENT 1 1 1 1 1 1 1 1 1	QY 1078 LENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFRV	Qy 1125LSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSB : ::	Qy 1174TUEDSQPK	
EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;	027203; 027203; X15148; 27605; 27162; 05291;	Genew; HGNC:2928; DMD. MIM; 300377; MIM; 300376;	Mim; 302045; -: InterPro; IPR001589; InterPro; IPR001715; InterPro; IPR002017; InterPro; IPR002017;	InterPro InterPro InterPro Pfam; PF(Pfam; FF00397; w Pfam; PF00435; s Pfam; PF00569; Z PRINTS; PR00403;	SMART; SM00150; CH; Z. SMART; SM00150; SPEC; Z1. SMART; SM00456; WW; 1. SMART; SM00291; ZnF_ZZ; 1.	PROSITE; PROSITE; PROSITE;	PROSITE; PS30020; W PROSITE; PS01357; Z PROSITE; PS50135; Z Structural protein;	Nebat; Disease mutation; Alternation	FT REPEAT 448 SPECTRIN 1. FT REPEAT 448 SPECTRIN 2. FT REPEAT 559 667 SPECTRIN 3. FT REPEAT 719 828 SPECTRIN 4.	Query Match 4.0%; Score 335; DB 1; Length 3685; Sest Local Similarity 19.3%; Pred. No. 0.00079; Match Concerniation 19.3%; Pred. No. 0.00079;	OLFDLTNHMLTLCDNIHG-FKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIP 204 FIRST	205 FNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKK	DD 128/ FKLKTTENIPGGAEEISEVLDSLENLMRHSEDNPNQIRILAGTLTDG-GVMDELINE 1342 OY 245 NKKTIEN-INELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKOL 292 OH 1343 FFFFFNSOEDEFLEPENVOONT FOSTOSTENSE KETHIOTOSTANDAN 1401	293EEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSG	1402 DAAQMPQEAQKIQSDLTSHEISLEEMKKHNQGKEAAQRVLSQIDVAQKKLQDVSMKFR 1459

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LAPGLTTIGASPTQTVTLVTQPVVTKETAISKLEMPSSLMLEVPALADFNRAWTELTDWL 2486
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                                                                                                                                                                                                              1432 IDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNH 1491
                                                                                                                                                                1388 --ILSEKYKSDLDSIKKYINDKQG-------ENEKYLPFLNNIETLYKTVNDK 1431
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J. Biol. Chem. 265:2603-2612(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green K.J., Parry D.A.D., Steinert P.M., Virata M.L.A., Wagner R.M.,
Angst B.D., Nilles L.A.;
                                                                                                                                                                                                                                                            1492 NNLLTKFLSTGMVFENLAKTVLS-----NLLDGNLQGM------LNISQH 1530
                                                                                                                                                                                                                                                                                   2754 N-----LDENSQKILRSLEGSDDAVLLQRRLDNMNFKWSLLRKKSLNIRSH 2799
                                                                                                                                 2599 ARAKLESWKEGPYTVDAIQKKITETKQLAKDLRQWQTNVDVANDLALKLLRDYSADDTRK
                                                                                                                                                                               2659 VHMITENINASWRSIHKRVSEREAALEETHRLLQOFPLDLEKFLAWLTEAETTANVLOD-
                       -- LGQVVTGEAVTPSVIDNILSKIENEYEVL-----YLKPLAGVYRSLKKQLENNVM
                                                                     1306 TFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLN-KEKRDKFLSS
                                             2487 SLLDQVIKSQRVMVGDLEDINEMIIKQKATMQDLEQRRPQLEELITAAQNLKNK----
                                                                                                                  1365 YN-----YIKDSI-----DTDINFAND----VLGYYK----
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Keane F.M., Eady R.A.J., McGrath J.A.;
                                                                                                                                                                                                                                                                                                                                           DESP_HUMAN STANDARD; PRT; 2871 AA.
P15924; 014189; 075993; 09UHN4;
01-APR-1990 (Rel. 14, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virata M.L.A., Wagner R.M., Parry D.A.D., Green K.J.;
"Molecular structure of the human desmoplakin I and II amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips S.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 265:11406-11407(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20062965; PubMed=10594734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Foreskin;
MEDLINE=92115697; PubMed=1731325;
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MEDLINE-90153880; PubMed=1689290;
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SEQUENCE FROM N.A. (ISOFORM DPI).
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THARACTERIZATION.

RA MEDLINE-98012209; Pubmed-9348293;

RA MEDLINE-98012209; Bornslaeger E.A., Borgwardt J.E., Palka H.L.,

RA Kowalczyk A.P., Bornslaeger E.A., Borgwardt J.E., Palka H.L.,

RA Daliwal A.S., Corcoran C.M., Denning M.F., Green K.J.;

RA Daliwal A.S., Corcoran C.M., Denning M.F., Green K.J.;

RT "The amino-terminal domain of desmoplakin binds to plakoglobin and clasters desmosomal cadherin-plakoglobin complexes.";

RT "The amino-terminal domain of desmoplakin binds to plakoglobin and class and complexes.";

R. "Cell Biol. 139:773-784(1997).

C. "INVOLVED IN THE ORGANIZATION OF THE DESMOSOMES.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRATIFIED ORIGIN.

DOMAIN: THE N-TERMINAL REGION IS REQUIRED FOR LOCALIZATION TO THE DESMOSOMAL PLAQUE AND INTERACTS WITH THE N-TERMINAL REGION OF PLAKOPHILIN 1. THE C-TERMINAL REGION INTERACTS WITH INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERATODERMA II (PPKS2, KPPS2 OR SPPK2), CHARACTERIZED BY SKIN THICKENING IN THE PALMS (LINEAR PATTERN) AND THE SOLES (ISLAND-LIKE PATTERN) AND THE SOLES (ISLAND-LIKE PATTERN) AND THE SOLES (ISLAND-LIKE PATTERN) AND FLEXOR ASPECT OF THE FINGERS; AND RARELY BY ABNORMALITIES OF THE NAILS, THE TEETH AND THE HAIR.

-!- SIMILARITY: CONTAINS 17 PLECTIN REPEATS.
-!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
palmoplantar keratoderma resulting from desmoplakin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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56 GLOBULAR 1.
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PLECTIN 2.
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                                                                  Invest. Dermatol. 113:940-946(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN
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InterPro; IPR002017; Spectrin.
Pfam; PF00681; Plectin; 10.
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J05211; AAA35766.1; -.
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SMART; SM00150; SPEC; 1.
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Genew; HGNC:3052; DSP.
MIM; 125647;
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OY 800 NEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVWYSNFDSLNNSLSQLFWEIYEKEM 859	QY 1018 LFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVL-ONFSVFFNKKREAEIAETEN 1076	OY 1186 KKFLPEGTDVATVVSESGSDTLEOSOPKKPASTHVGAESNTITTSONVDDEVDD 1239 :	OY 1331 SDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILS 1390 2075 RDLIDPDD	QY 1483 ADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNL 1521 : : : Db 2214 RQPVTVTELVDSGILRPSTVNELESGQI 2241 RESULT 53 MYSA, DROME	DD MYSA_DRONE STANDARD; PRT; 1962 AA. AC POSSGI, DT 10-NOV-1988 (Rel. 09, Created) DT 15-JUN-2002 (Rel. 41, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DT 15-JUN-2002 (Rel. 41, Last annotation update) C
PLECTIN 11. PLECTIN 12. PLECTIN 13. PLECTIN 14. PLECTIN 14. PLECTIN 16. PLECTIN 16. PLECTIN 16. PLECTIN 16. PLECTIN 17. INTERACTS WITH PLAKOPHILIN 1 AND JUNCTION PLAKOGLOBIN. PHOSPHORYLATION (BY PKA) (POTENTIAL). PHOSPHORYLATION (BY PKA) (POTENTIAL). PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. PLAKOGLOBIN. P	34.5; DB 1; Length 2871; o. 0.00062; atches 552; Indels 477; GaLLTIKELKYPQLFDLTNHMLTLC TSGLETLINI-PIKRTMIQSPSGVILQEA AKLNDVCANDYCQIPFNLKIRANELDVLK	ADVHA-RYIELLTRSGDYYRPLSEMLKSLEDLKLKNTKIEVLE 1038 KLVFGYRKPLDNIKDNVGKMEDYIKKNKTIENINELIEESKKTIDKNKNATKEEEKKKL 278 SELRLARDANSENCNKNKFLDQNLQKYQAECSOFKAKLASLEELKR 1084 YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANS 333 SQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANS 333 SQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELDKINEIKNPPANS 333 GABELDGKSAKQNLDKCYGQIKELNEKTTRLTVEIEDEKRRKSVEDRFDQQKND 1138 GNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVE 393 STATEL TILL TILL TILL TILL TILL TILL TILL T	SKNI : SKNI : SKNIENQ	MQQRSEDNARHKOSLEERAKTIQDKNKEIERLKAEFQEEAKRRWEYENELSKVRNNYD 1356 NFEKMMGKRYSYKVEKLT-HHNTFASYENSKHNLEKLTKALKYMEDYSLRNIV 559 III	/PEDIQQQRATGSEVSQRRQQLEV IVPNSYKQENKQEPYYLIVLKKEIDKLKVF
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InterPro; IPR002928; Myosin_tail

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             Isoforms containing exon 9a are expressed in indirect flight muscles, exons 9a and 9b are expressed in indirect flight and 9c are expressed in other larval and adult muscles, exons 9b and 9c are expressed in other larval and adult muscles.

DOMAIN: Alternative splicing exons contribute to the specialized contractile activities of different muscle types. Exon 3 encodes the hydrophobic pocket adjacent to the ATP-binding site, exon 9 is adjacent to the actin-binding domain, exon 11 is involved in actin-binding, exon 15 hide S2 hinge and exons 18 and 19 the noncolled tail region.
                                                                                                              Wassenberg D.R. II, Kronert W.A., O'Donnell P.T., Bernstein S.I.; "Analysis of the 5' end of the Drosophila muscle myosin heavy chain gene. Alternatively spliced transcripts initiate at a single site and intron locations are conserved compared to myosin genes of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                             Kronert W.A., Edwards K.A., Roche E.S., Wells L., Bernstein S.I.;
"Muscle-specific accumulation of Drosophila myosin heavy chains: a
splicing mutation in an alternative exon results in an isoform
            MEDLINE-89384556; PubMed-2506434;
George B.L., Ober M.B., Emerson C.P. Jr.;
"Functional domains of the Drosophila melanogaster muscle myosin
heavy-chain gene are encoded by alternatively spliced exons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Expressed in larval and adult muscles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                                                                                                                     STRAIN-Canton-S; TISSUE-Embryonic muscle; MEDLINE-91330870; PubMed-1907912;
                                                                                                                                                                               Biol. Chem. 262:10741-10747(1987)
                                                            Mol. Cell. Biol. 9:2957-2974(1989)
                                                                                                 MEDLINE-87280141; Pubmed=3038896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_N.
STRAIN-Canton-S; TISSUE-Pupae;
                                                                                                                                                                                                         SEQUENCE OF 333-614 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M61229; AAA28686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA28687.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A28492; A28492.
PIR; A32491; A32491.
PIR; B32491; B32491.
HSSP; P08799; IMND.
Flybase; Fbgn0002741; Mhc.
                                                                                     SEQUENCE OF 1-264 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60196; CAA42752.1;
EMBL; X60196; CAA42753.1;
EMBL; X60196; CAA42754.1;
                                                                                                                                                                                                                                                                                     substitution.",
                                                                                                                                                                    organisms
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74;
                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
VRDIKSEKVEKVNPPKFEKIEDMADMTVLNTPCVLHNLRQR
YYAKLIY -> TRDLKKDLLQQVNPPKYEKAEDMSNLTYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELSDNIYDYNVSQCKVTVPNMDDGEEFQLAD (IN ISOFORM 7D AND ISOFORM BDBBA).
YNGFBQLCINFTNEKLQOFFNHIWFWBQEBEYKKEGINWDF IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQOFFN HHMFVLEQEEYKREGIDWAFIDFGMDLLACIDLIEK (IN ISOFORM BDBBA AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> YKIMCPKLLQGVEKDKKATEIIIKFIDLPEDQYRLGNT
K (IN ISOPORM ID AND ISOPORM BABDB).
Y YOUNDEGIKELDCPKKASKVLIESTELNEDLYRLGHTK
-> YMILAPAIMAAEKVAKNAAGKCLEAVGLDPDMYRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD -> EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K (IN ISOFORM 11B AND ISOFORM BDBBA).
YQLINPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK
X (IN ISOFORM 11C).
K (IN ISOFORM 11C).
YQLINPRGIKDLOCPKKASKVLIESTELNEDLYRLGHTK
YQLINPRGIKDLOCPKKASKVLIESTELNEDLYRLGHTK
                                                                                                                                                                                                                                                                                                                                                                                                                     -> EY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNGFEQLCINFTNEKLQQFFNHIMFVMEQEEYKKEGINWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> YNGFEQLCINFTNEKLQOFFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> YQILNPAGIVGVDDPKKCGSIILESTALDPDMYRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQQFF?
HHMFVLEQEEYQREGIEWTFIDFGMDLQLCIDLIEK (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQILNPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 CVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٨
                                                                                                                                 SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
PM90Sin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; ATP-binding; ATP-binding; Calmodulin-binding; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLLSNNIYDYRIVSQGKTTIPSVNDGEEWVAVD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFLGQHIGDYPGICQGKTRIPGVNDGEEFELTD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 CVSYNITGWLEKNKDPLNDTVVDQFKKSQNKLLI------EIFADHAGQSG-----
                                                                                                                                                                                                                                                                                                                                                                          DASVLHNLRQRYYNKLIY (ÎN ISOFORM 3B,
ISOFORM BDBBA AND ISOFORM BABDB).
DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD
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                                                                                                                                                                                                                                                                             IQ.
COILED COIL (POTENTIAL).
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MISSING (IN ISOFORM 18).
EK -> RE (IN REF. 2).
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-> M (IN REF. 2)
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                                                   pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
Probom; PD000355; myosin_head; 4.
IPR001609; myosin_head.
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                Pfam; PF00063; myosin_head; 7.
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68
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1962 AA;
                                                                                                                                                                                                                                    Multigene family.
DOMAIN
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                                     PF00612;
InterPro;
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IKELKYPQLEDLTNHMLTLCDNIHGFKYLIDGYEEINELLY-KLNFYFDLLRAK-LND			EKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETL 	ELKHNIHUPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKN ::	KOYKITKEEESKLSSCDPLDLLFNIONNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLX	NAEAQVWRSKYESDGVARSEELEEAKRKLQARLAEAEFIESLNKKLKKT
139 676 195 734 246 790	306 825 358 870	408 912 462 958	522 1000 582 1034	642 1069 692 1127 751 1180	805 1238 865 1280 925 1324	982 1364 1001 1424 1055
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its 1542 ALEEAEAALEQEENKVLRAQLELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLE 1601 ---NALESYKKFLPEGTDVAT 1197 1198 VVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLG 1257 QVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSL-------KKQLENNV 1304 QADRGR-----RQAEQE-----RQAEQE-----LADAHEQLNEVSAQNASISAAKRKLESEL 1733 MTFNVNVKDILNSRFNKRENFKNV-----LESDLIPYKDLTSSNYVVKDPYKFLNKEKR 1358 DKFLSSYNYIKD-SIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPF 1417 1418 LNNIETLYKTV------NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLK 1464 HEAVY CHAIN SUBBRITISMENT CHAIN SUBUNITS (MLC).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC).

-! SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-! DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COILES.

-! PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLAPED AND ARE REQUIRED FOR MYOSIN APPASE ACTIVITY.

-! MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENTS (S1) AND 1 ROD-SHAPED 1105 LSEE---SIQTEDN---YASLENFKVLSKLEGKLKDN----LNLEKKKLSYLSSGLHHLI 1154 Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: MUSCLE CONTRACTION. -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF Euteleostomi; Sus. MISCELLANBOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
SIMILARITY: CONTAINS I MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS I 10 DOMAIN. 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutherla; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823; 1465 TIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTG 1502 PRT; 1935 AA AELK --- EVIKNKNYTGNSPSENNTDVN------STANDARD; SEQUENCE FROM N.A. STRAIN-Domestica; Sus scrofa (Pig). MYH7_PIG 1155 1258 1305 1892 1693 1359 qq q ŏ q δ q à g ŏ P ò g δ qq δλ

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SCP1_HUMAN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                            InterPro; IPR000048; IQ_region.

R InterPro; IPR000048; IQ_region.

R InterPro; IPR00102928; Myosin_N.

R InterPro; IPR0015029; Myosin_N.

R InterPro; IPR001509; Myosin_head.

R InterPro; IPR00150; Myosin_head.

R Pfam; PF00151; IQ; I.

R Pfam; PF00151; IQ; I.

R Pfam; PF00155; Myosin_tail; I.

R Pfam; PF00155; Myosin_head; I.

R Promom; P000155; Myosin_head; I.

R Promom; P000155; Myosin_head; I.

R MART; SM00015; IQ; I.

R MART; SM0015; IQ; I.

R PROSITE; P550096; IQ; I.

W Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosin; Myosi
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MAKYLATION (SH-1) (POTENTIAL).
MAKYLATION (SH-2) (POTENTIAL).
223110 MW: 149CDBFD910DB08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.9%; Score 332.5; DB 1; Length: Best Local Similarity 18.7%; Pred. No. 0.00047; Matches 286; Conservative 266; Mismatches 576; Indels
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COILED COIL (POTENTIAL).
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ACTIN-BINDING.
ACTIN-BINDING.
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695
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DOMAIN 1 78

DOMAIN 781 81

NP_BIND 178 19

DOMAIN 655 67
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488 YEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVE---KLTHHNTFASYENSKHNLEKLT 544
                                          1024 KVKLEQHVDD--LAGSLEQEKKVRMDLERAKRKLEGDLKLT-QESIMDLENDKQQLDERL
                                                                                                                                                             KALKY-------MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK
                                                                                                                                                                                                                                               597 ITKDENKPDEKILEVSDIVKVQVQKVLLMNK--IDELKKTQLILKNVELKHNIHVPNSYK
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976 AA

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STANDARD;

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976 AA;
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CYTOGENET. CELI GENEL. 78:103-104(1997).

SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN HOMOLOGOUS
CHROMOSOMES DURING METOTIC PROPHASE.

CHROMOSOMES DURING METOTIC PROPHASE.

SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS OF SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEMENTS IN THE NUCLEUS.

FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS N-TERMINUS
CHRONION DONLY WHERE THE CENTRE OF THE SYNAPTONEMAL COMPLEX WHILE THE CTERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE SYNAPTONEMAL COMPLEX (BY SINILARITY).

CHOMAIN CONSISTS OF AN ALPHA-HELICAL STRETCH OF 700 AA RESIDUES, FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS. THE C-TERMINAL COMPLEX (BY SINILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

ARG/LYS-RICH (BAŞIC).
                                                                                                                                                                                                                                                                                                                    Tanaka H., Uchida K.,
Matsumiya K., Namiki
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              Okuyama A., Nishimune Y.;
"Assignment of synaptonemal complex protein 1((SCP1) to human chromosome 1p13 by fluorescence in situ hybridization and its expression in the testis.";
                                                                                                                                                                                                              "Human synaptonemal complex protein 1 (SCP1): isolation and characterization of the cDNA and chromosomal localization of
                                                                                                                                                                                     Leschot N.J.,
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F -> Y (IN REF. 2)
F -> C (IN REF. 2)
E -> D (IN REF. 2)
B -> D (IN REF. 2)
N -> S (IN REF. 2)
N -> F (IN REF. 2)
K -> N (IN REF. 2)
015431; 014963;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-QCT-2001 (Rel. 40, Last annotation update)
Synaptonemal complex protein 1 (SCP-1 protein)
                                                                                                                                                                                   Meuwissen R.L.J., Meerts I., Hoovers J.M.N.,
                                                                                                                                                                                                                                                                                                                  Kondoh N., Nishina Y., Tsuchida J., Koga M.,
Inazawa J., Taketo M., Nozaki M., Nojima H.,
                                                                                                                                                            TISSUE=Testis;
MEDLINE-97224467; PubMed-9119375;
                                                                                                                                                                                                                                                                                                      MEDLINE-98037449; PubMed-9371398;
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                                                                                                                                                                                                                                                   Genomics 39:377-384(1997).
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DNA-binding; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:11487; SYCP1
MIM; 602162; -.
                                                                                 (Human)
                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                             TISSUE=Testis;
                                                                  SYCPI OR SCPI
                                                                                 Homo sapiens
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TVLPKRGQRPKLSSKRE (IN REF 2).
LTSHCNKLSLENK -> YFTLQQASPPPN (IN REF.
2).
N -> I (IN REF. 2).
K -> T (IN REF. 2).
E -> D (IN REF. 2).
E -> D (IN REF. 2).
P -> S (IN REF. 2).
P -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 TNNKEVELEELKKVLGEKETLLYEN-----KQFEKIAEELKGTEQELIGLLQAREKEVH 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 ISAKVETKES-----TEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKE 438
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-> D (IN REF. 2).
                                                   KN -> NY (IN REF. 2).
K -> I (IN REF. 2).
K -> T (IN REF. 2).
E -> D (IN REF. 2).
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0.00023;
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20.7%; Pred. No. 0
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SEQUENCE
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NP_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 35092 / DSW 1617 / P2;
STRAIN-ATCC 3132296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N. Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,
Charlebois R.L., Sensen C.W., Van der Cost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                . 956 LKD&DTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015
                                                                                              ERLFDKKKTVGKYKMQIKKLT-LLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET 1074
                                                                                                                                                              1075 ENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKD 1134
                                                                                                                                                                                                                             1135 NLNLEKKKLSYL-SSGLHHLIAELKEVIKNKNYTGNSPS----ENNTDVNNALESYKK-- 1187
                                                                                                                                                                                                                                                  --GISKDKRDYLWTSARNTLSTPLP-----KAYTVKTPTKPKLQQRENLNIPIEESKKKR 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
 731
                                                               ------LGLYKSKEQEQSSL----RASLEIELSNLKAEL----LSVKKQLEI 769
                                                                                                                                                                                                                                                                                             -----FLPEGTDVATVVSESGSDTLEQ-SQPKKPASTHVGAES-----NTITT 1229
                                                                                                                                                                                                                                                                                                                883 KMAFEFDINSDSSETTDLLSMVSE--EETLKTLYRNNNPPASHLCVKTPKKAPSSLTT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006829; AAK42417.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003465; SMC_N.
Pfam; PF02463; SMC_N: 1.
Pfam; PF02483; SMC_C; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
-----KLQKEIDKRCQH-----KIAEMVALMEKHKHQYDKIIEERDSE----
                                                                                                                                                                                            --LLETPEIYWK-----LDSKAVPSQTVSR-----NFTSVDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                              864 AA
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                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAD50 OR SSO2249.
Sulfolobus solfataricus.
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                                                                                                                                                                                                            192 LNDVCANDYCQIPFNLKIR-----ANELDVLKKLVFGY-----RKPLDNI---KDNVG 236
                                                                                                                                                                                                                                                                                                             237 KMEDYIKKNKKTIENINELIEESKKTIDKN-----KNAT-KEEEKKKLYQAQYDLSIYNK 290
                                                                                                                                                                                                                                                                                                                                            SVTLYLSNEKDKIEIIRDIRSTTEDRLIRNQFPIARSATVVSNEIEKILGIDKDIAL--- 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----STIIVROGELD--KILENFOEIMGKI------STIIVROGELD--KILELI 154
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 IKNLEKRIKDIKDQFDEYEK-----KRNQYLKLTTTLKI-----KEGELNELNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 EEQLFEKKI-TKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELK-KTQLILK-----
                                                                                                                                                           Indels 357;
                                                                                                            Length 864;
                                 COILED COIL (POTENTIAL).
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                                                                                                                                                           Conservative 200; Mismatches 321;
            ATP (BY SIMILARITY)
                                                                                                          Score 331.5; DB
Pred. No. 0.00021
                                                           101601 MW;
                                                                                                            3.98;
                                                                                                                                 20.8%;
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37
701
                                                         864 AA;
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                                                                                                                                                           Matches 230;
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                                                                        ----LIAELKEVIKNKN 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Adductor muscle;

MEDLINE-92011955; PubMed-1917970;

MEDLINE-92011955; PubMed-1917970;

Nyitray L., Goodwin E. B., Szent-Gyoergyi A.G.;

"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence compearison with other heavy chains reveals regions that might be critical for regulation.";

J Blol. Chem. 266:18469-18476(1991).
-1: FUNCTION: MUSCLE CONTRACTION.
-1: FUNCTION: MUSCLE CONTRACTION.
-1: FUNCTION: MUSCLE CONTRACTION.
-1: FUNCTION: MUSCLE MUSCIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE
-1: SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT (CHAIN SUBUNITS (MLC)
-1: SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-1: SUBLEBRITY: CONTRAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-1: SIMILARITY: CONTRAINS 1 10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy chain, striated muscle.

Advipecten irradians (Bay scallop).

Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;

Pectinoidea; Pectinidae; Argopecten.
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MEDLINE-94173312; PubMed-8127365;
ALA X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V.N.
Szent-Gyorgyi A.G., Cohen C.;
"Structure of the regulatory domain of scallop myosin at 2.8-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Adductor muscle;
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"Structure of the regulatory domain of scallop myosin at 2-A
resolution: implications for regulation.";
Structure 4:21-32(1996).
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                                                                        NYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHH---
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01-WAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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1 777 MYOSIN HEAD-LIKE.
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THP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
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RODLIKE TAIL (S2 AND LMM DOMAINS)
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llarity 18.6%; Pred. No. 0.00051;
Conservative 249; Mismatches 466
                                                             PDB; 1SCM; 30-APR-94.
PDB; 1MDC; 11-JUL-96.
INTERTPO; 11-JUL-96.
INTERTPO; 11-JUL-96.
INTERTPO; 1PR000049; IQ_region.
INTERPO; 1PR00109; Myosin_tail.
INTERPO; IPR00109; Myosin_tail.
INTERPO; IPR00109; Myosin_tail.
Pfam; PF00063; myosin_head; 1.
Pfam; PF0012; IQ; 2.
Pfam; PF0012; IQ; 2.
Pfam; PF07376; Myosin_tail; 1.
Pfam; PF07376; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SWART; SM00242; MYSS; 1.
EMBL; X55714; CAA39247.1;
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A40997; A40997
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nes 261; Conserv
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QY ., 593 FEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNI	VI 647 OX	Gallus. Gallus. Gallus.
Db 1127 AKVEKQRAELNRELEELGERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEA	1184	11 SEQUENCE FROM N.A. CEDULCHE FROM N.A. CEDULCHE FROM N.A. CEDULCHE CETTELED.
Qy 648 HVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKK	690 RA RT RT RT	
691	743	
DO 1235 NWANNECESEN VMRQF ESQWSDLNARKLEDSQRSINELGSQRSKLQAENSDLFRQLEDD QV 744 VPVPVPEAKAOVPTPPAPVNNKTENVSKLDXLEKLYEFLNTSVTCHKYTLNSHS	1294	
-		Hayashida M., Maita T., Matsuda "The primary structure of skele"
QY 801 EKILKQYKITKEEESKLSSCDPLDLLFNIONNIPVMYSMFDSLUNNSLSQLFM	852	
Db 1338 DAIREQLEEEQESKSDVQRQLSKANNEIQQWRSKFESEGANRTEELEDQKRKLLG	1392	
QY 853 EIYEKEMVCNLYKLKDNDKIKNLLEESKSS ::	SS 893 RX RA NE 1452 RT	
QY 894 MQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELI	943	
Db 1453 WQAKVNSLQSELENSQKESRGYSAELYRIKASIEEYQDSIGALRRENKNLADEIHDLT	LT 1510 RP	
Qy 944GQKSSE	-NEYE 953 RX	
DD 1511 DQLSEGGRSTHELDKARRRLEMEKEELQAALEEAEGALEQEEAKVWRAQLEIATVRNEID	: ID 1570 RT	
QY 954 KILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSF	1005	Sequence of the 22 Abs fragments."; J. Biochem. 110:68-74(1991).
1006	1040	
: :: : 1 1 1		MEDLINE-92041770; museta 193903(Maita T., Yajima E., Nagata S.,
SKLNSLNNPKHVLQNFSVFFNKKKEA	1100	
Db 1681 EVEELRAALEQAERARKASDNELADANDRVNELTSQVSSVQGKRKLEGDIN	1732	
OY 1101 PLKT	1134	
Db 1733 AMQTDLDEMHGELKGADERCKKAMADAARLADELRAEQDHSNQVEKVRKNLESQVKEF	F 1790 RA	MEDULINE-0/052420; FULDREGU-340/300.
OY 1135KEVIKNKLSYLSSGLHHLIAELKEVIKNKN	YT 1167 RL	
Db 1791 QIRLDEAEASSLKGGKKMIQKLESRVHELEAELDNEQRRHAETQKNMRKADRRLKELAFQ	1850	
1168	iG 1203 RA	
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<pre>QY 1204 SDTLEGSQPKKPASTHVGAESNTITTS 1230</pre>	RN RP RP RP RX	
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MESS_CHICK ID MYSS_CHICK STANDARD; PRT; 1938 AA.	RL RL	
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DI 10-OCI-2001 (REI. 40, LGSL SEGUENCE UDGACE) DI 16-OCI-2001 (Rel. 40, LGSL BANDCIALION UDGACE) DE Myosin heavy chain, skeletal muscle, adult.	RA RT	Watanabe B.; "Amino-acid sequence of the hind subfragment-2.":
gallus (Chick		

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., Miyanishi T., Nakayama S., Matsuda G.;
letal muscle myosin heavy chaln: IV.
complete 1,938-residue sequence of the
Galliformes; Phasianidae; Phasianinae;
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and characterization of a full-length
y chain from adult chicken pectoralis
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cono K., Tanioka Y., Matsuda G.;
letal muscle myosin heavy chain: III.
t and the alignment of the 23 kDa, 50
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letal muscle myosin heavy chain: II.
it of subfragment-1.";
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ka Y., Komine Y., Matsuda G.;
myosin head.";
84:416-420(1987).
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METHYLATION

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                                                                                                                                                                                               --- FUNCTION: MUSCLE CONTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO

F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

--- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROFIEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MIC.). 2 ALKALL LIGHT CHAIN SUBUNITS (MLC.)

--- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

--- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

--- SUBCELLULAR RODLIKE ALL SUBUNITS (MLC.)

--- DOMAIN: THE RODLIKE ALL SUBUNITS (MLC.)

--- THE RODLIKE ALL SUBUNITY CONFOSED OF 4 HEPTAPEPTIDES,

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

--- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

--- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO I LIGHT

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LAFER BE

SPLIT PURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation;
Calmodulin-binding; Multigene family; 3D-structure.
                                                                                                                                              Holden H.M.; "Three-dimensional structure of myosin subfragment-1: a molecular
                                                                                                                                                                                                                                                                                                                                                                                    SUBFRAGMENT (S2).
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                    'Genomic clones encoding chicken myosin heavy chain genes.";
                           Richter H.E.,
                                                                                                                 Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R., Tomchick D.R., Benning M.M., Winkelmann D.A., Wesenberg G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843
                          Moriarity D.M., Barringer K.J., Dodgson J.B.,
Young R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN-BINDING.
ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQ.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612; IQ; 2.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB: ZMYS; 11-JAN-97.
InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_Lail.
InterPro; IPR001509; Myosin_Lail.
InterPro; IPR001609; myosin_head.
             MEDLINE=87217964; PubMed=3034534;
                                                                                                         MEDLINE-93303624; Pubmed-8316857
 SEQUENCE OF 1857-1938 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U87231; AAB47555.1; --
EMBL, M16575, AAA48970.1; --
PIR: PX0050; PX0051.
PIR: A26821; A26821.
PIR: S02082; S02082.
PIR: S04501; S04501.
PIR: S04515; S05515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                     Science 261:50-58(1993)
                                                                  DNA 6:91-99(1987).
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DOMAIN
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                                                                                                                                                                          motor.";
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MOD_RES
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                                                                                                                                                                                                                                                                                                      8).
METHYLATION (TRI-).
METHYLATION (MONO-).
ALKYLATION (SH-1).
ALKYLATION (SH-1).
C -> Q (IN REF. 7 AND 8
L -> F (IN REF. 1).
E -> D (IN REF. 5).
S -> A (IN REF. 5).
N -> QL (IN REF. 5).
I -> V (IN REF. 5).
I -> V (IN REF. 10).
IHG -> FH (IN REF. 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.9%; Score 331; DB 1; 19.1%; Pred. No. 0.00053;
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                                                                                                                                                                           | : : | |: : : | ||: : : |
LQAEVEELRGALEQTERSTRYVAEQELLDATERYQLLHTQNTSLINTKKKLE--TDIVQIQ 1740
                                              KYKM-QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILL 1085
                                                                                                                                  SESGSDTLEQS----QPKKPASTHVGAESNTITTSQ-----NVDDEVDDV---- 1240
                                                                                                                                                                                                                        -----IIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENE 1280
LSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV-----NNALESYKKFLPEGTDVATVV 1199
                                                                                                                                                                                                                                                                       1800 DEAEQLALKGGKKQLQKLEARVRELEGEVDSEQKRSAEAVKGVRKYERRVKELTYQCEED 1859
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                                                                                        1086 KHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craníata, Vertebrata, Euteleostomi,
Amphibla, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Xenopus laevis (African clawed frog).
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NCBI_TaxID=8355;
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PIR; JH0720; JH0720.

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W; 6502EAC9FE6C4E93 CRC64;
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18.0%; Pred. No. 0.00049;
ive 311; Mismatches 574;
                                                      coil; Neurone.
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LINKER 12.
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COIL 1A.
LINKER 1.
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LINKER 2.
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             Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled
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InterPro; IPR001664; IF
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myosin heavy chain

hypothetical prote purine NTPase [imp myosin heavy chain dystrophin, muscle tanabin - African	ALIGNMENTS		r - malaria parasite (Plasmodium falciparum)	2-Feb-1993 #text_change 09-Jun-2000	0000			96; PIDN:CAA33163.1; PID:g9897	id sequence of the qp195 (MSA-1) qene from Pl	ID:2668887		antigen	eywords: gtycoprotentn; merozolte; surrace antigen -19/Noomain: signal sequence #status predicted <sig> 0-1639/Product: major merozoite surface antigen #status predicted <mat></mat></sig>	8424; DB 2; Length 1639;	ed. No. 1.5e-253; Mismatches 0; Indels 0; Gaps 0;	MKIIFFLGSFLFFIINTOCVTHESYOELVKKLEALEDAVLTGYSLFOKEKMVLNEGTSGT 60 	AVITSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRINPSDNSSDS 120	SVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120	DAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTLCDNIHGFRYLIDGYEEINELLYK 180	TNHMLTLCDNIHGFKYLIDGYEEINELLYK 180	LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRRPLDNIKDNVGKMED 240 	YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300	KEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300	VLEKRIDTLKKNENIKELLDKINETRNPPPANSGNTPNTLLDKNKKIEBHEKEIKEIAKT 360	VLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEBHEKEIKEIAKT 360	IKENIDSLETDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNAL 420		NELNSFGDLINPFOYTKEPSKNIYTONERKKRINEIKRKIKIESDKKSYEDKSKS 480
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probable major surface antigen (83K, 19K, 42K) precursor - mal c; Species: Plasmodium falciparum C; Decies: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_chang C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_chang C; Accession: A24594
R; Holder, AAA: LocKyer, M.J.; Odink, K.G.; Sandhu, J.S.; Rive Nature 317, 270-273, 1985
A; Thiele: Primary structure of the precursor to the three major A; Reference number: A24594; MUID:86014355; PMID:2995820
A; Molecule type: DNA
A; Molecule type: DNA
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C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
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Q		C:Accession: A25120 B:Mackay, M.; Goman, M.; Bone, N.; Hyde, J.E.; Scaife, J.; Certa, U.; Stunnenberg, H.
oy.	AGSALEGDSVQAQAQEQKQAQPPVPVPVPRAKAQVPTPPAPVNNKTENVSKLDYLEKLYE 7	AMBO J. 4, 3823-3829, 1985 A.Title: Polymorphism of the precursor for the major surface antigens of Plasmodium f A;Reference number: A91030; MUID:86136024; PMID:3004972
QQ O	AGSALEGDSVQAQAQEQKQAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYQ	A;Accession: A25120 A;Molecule type: DNA
Qy Db	781 FLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLENIQNNIPVMYSMF 840 	A; Residues: 1-1631 <mac> C; Comment: The merozoite stages of different strains have strain-specific surface ant C; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The</mac>
Oy Db	841 DSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEERKKVSTSVKTLSSSSMQPLSLT 900 	<pre>C:Superramily: major merozoite surface antigen C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat; transmembrane pr F:1-19/Domain: signal sequence #status predicted <sig> F:20-1631/Product: major merozoite surface antigen #status predicted <mat></mat></sig></pre>
oy F	PODKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGGKSSENFYEKILKDSD	F:67-84/Region: 3 residue repeats (S-G-T/P) F:1614-1631/Domain: membrane anchor #status predicted <mbn> F:97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate (Asn</mbn>
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		QY 181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED 240
	EGGSDILEGGSGFARFASTHVGAESNIITTSQNVDDEVDDYIIVLIFGESEEDIDDLGGVV TGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKOLENNVMTFNVNVKDILNSRFN [QY 241 YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS 300
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•		QY 361 IKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGYTYPLSYNDINNAL 420
	81 DVLGIYALLESEKYRSDLDSIKKYINDRQGENEKYLPFLNNLETLYKTYNDKIDLEVIHLE I AKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLS 1	QY 421 NELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIESDKKSYEDRSKS 480
	ACVENTITIERSNVEVRIRELNILGUKLADFRKKNNNFVGIADDESTDYNHNNLLFRFLS I TGMVFENLAKTVLSNLLDGNL-QGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNY I	OY 481 LNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNL 540
	OI TGMVFENLLKBVLSNLLDUMKLARYVKHFTTPMRKKTMLQQSSGCFKHLDEKEECKCLLNY 60 KQEGDKCVENPUPTCNENNGCCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSS 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111	QY 541 EKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKD 600
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RESULT	ozi snrioisribindibisri 104	QY 661 PYYLIVLKKEIDKLKVFWPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQ 720
SAZUKI major merc C;Species: C;Date: 3C	merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st sies: Plasmodium falciparum s: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jun-2000	QY 721 AGSALEGDSVQAQAQEQKQAQPPVPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYE 780

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human malaria
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A; Accession: A.53300
A; Accession: A.53300
A; Molecule type: DNA
A; Residues: 1-1104 <WEB1>
A; Cross-references: EMBL: X0331
B; Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.;
Nucleic Acids Res. 16, 1206, 1988
A; Title: Merozoite surface protein sequence from the Camp strain of the human material merozoite surface protein sequence from the Camp strain of the human material merosoids. S06361; MUID:88143999; PMID:3278296
A; Recession: S06361
A; Molecule type: DNA
A; Residues: 1104-1726 <WEB2>
A; Residues: 1104-1726 <WEB2>
A; Comment: The merozoite stages of different strains have strain-specific surface (; Comment: The merozoite surface antigen merozoite, and gametocyte (; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte (; Superfamily: major merozoite surface antigen tandem repeat
E; 1-19/Domain: signal sequence #status predicted <SIG>
E; 20-1736/Product: major merozoite surface antigen #status predicted <MAT>
E; 21-19/Domain: signal sequence #status predicted <SIG>
E; 20-1756/Product: major merozoite surface antigen #status predicted <MAT>
E; 67-87, 91-96, 100-105, 109-120/Region: 3-residue repeats (7-E-E)
E; 133, 272, 501, 567, 638, 827, 839, 924, 944, 990, 1016, 1114, 1221, 1613, 1658/Binding site
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is 342;
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Andron merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) C. Species: Plasmodium falciparum C. Species: Plasmodium falciparum C. Species: Plasmodium falciparum C. Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000 C. Accession: A45948 R. Cession: A45948 R. M.; Kato, A.; Case, S. E.; Siddiqui, W. A. Exp. Parasitol, 67, 1-11, 1988 A. Title: Plasmodium falciparum: gene structure and hydropathy profile of the major mea. Reference number: A45948; MuID:89005525; PMID:3049134 A. Status: preliminary A. Status: preliminary A. Status: preliminary A. M. Status: Specimes: 1-1726 C-HA> A. Residues: 1-1726 C-HA> A. Status: C. Superfamily: major merozoite surface antigen C. Superfamily: major merozoite surface antigen
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RESULT 6 A54498

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major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum alciparum alciparum falciparum                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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61 AVTTSTPGSSGSVT---SGGSVASVASGG---SGGSVASGGSGNSRRTNPSDNSSDS
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A; Reference number: A26868; MUID:88011243; PMID:3079521
A; Accession: A26868
A; Molecule type: DNA
A; Residues: 1-1701 <TAN>
C; Superfamily: major merozoite surface antigen
C; Superfamily: major merozoite surface antigen
E; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-1701/Product: major merozoite surface antigen #status predicted
                                                                                                                            Length 1701;
                                                                                                                                                          Indels
                                                                                                                                                          338;
                                                                                                                             60.0%; Score 5053; DB 2; 60.1%; Pred. No. 2.9e-149;
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Matches 1042;
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                                                                                                                   SGPAVVEESHDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKNND
                                                                                                                                                                                                                                  KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTI
                                                        AND---DTSHS----TNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSD
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C;Species: Plasmòdium falciparum
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988
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R; Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. B401. 195, 273-287, 1987
A; Title: Allelic dimorphism in a surface antigen
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C:Superfamily: major merozoite surface antigen C:Keywords: surface antigen	Ouery Match Best Local Similarity 38.2%; Pred. No. 1.2e-88; Matches 704; Conservative 316; Mismatches 517; Indels 307; Gaps 4	QY 1 MKIIFFLGSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNBGTSGT 60	QY 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120 Db 51GENDIKVETNASANNNN 68	QY 121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLLDGYEEINELLYK 180 :	OY 181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRRPLDNIKDNVGKMED 240 11:: : :	241 YIKKNKKTIENINBL-IEESKK	262	OY 292 LEEAHNLISYLEKRIDTLKKNENIKELLDKINEIKNPPPANSONTPNTLLDKNKKIE 348	4 4	403YPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI-YTDNERKKFINE 45 : :: : : : :: : : :: 427 KETYPHGISYALAENSIYELIEKIGSDETFGDLQNP-DDGKQPRKGILINETKRKELLEK 48	QY 456 IKEKIKIEKKRIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGK 515	QY 516 RYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIE 575 1:	Qy 576 NEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQ 635 :	QY 636 LILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKK 690 11 :: ::	QY 691NIKTEGQSDNSEPSTEG	Qy 727 GDSVQAQAQEQKQAQPPVPVPV-PE-AKAQVPTPPAPVNNKTENVSK 771 :	Qy 772 LDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEBESKLSSCDPLDLLFNI 829	830
QY 867 KDNDKIKNLLEBAKKVSTSVKTLSSSSMQPLSLTPQDKPEVS 908	909 ANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL-IGQKSSENFYEKILKDSD : :: ::	933 SGFAVFESHIPFILTVISISNILAGITVSLENLÄNKTRVFNPITISITEMEKRYEN. 961 TFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKKKI 1::	1021 KKKTYGKYKWOIKKLTLLKEQLESKLNSLNNFKHVLQNFSVFNKKKEAEIAETENTLEN 11052 KKKEGODKWOIKKLTLLKEQLESKLNSLNNFKHVLQNFSVFNKKKEAEIAETENTLEN 11052 KKKEGODKWOIKKLTLKEQLESKLNSLNNFHNVLONFSVFNKKKEAEIAETENTLEN	TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLECKLKDNLNLEK			Qy 1247 GESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMT 1306	OY 1307 FNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYN 1366			QY 1467 QDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMYFENLAKTVLSNLLDGNLQGM 1524	1525 INISOHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDAD	1585 AKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSNFLGISFLLILMLILYSFI 1639		majory majory C;Species: Plasmodium vivax C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999	C;Accession: A45044 R;Gibson, H.L.; Tucker, J.E.; Kaslow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C.; Mol. Biochem. Parasitol. 50, 325-333, 1992 A;Title: Structure and expression of the gene for Py200, a major blood-stage surface ant	A; Reference number: A45004; MULD: YLISBULS; FMLD: 13/13/29 A; Accession: A45004 A; Status: preliminary A; Molecule type: DNA	A;Residues: 1-1751 <gib> A;Cross-references: GB:M75674; NID:g160608; PID:g457336 A;Note: sequence extracted from NCBI backbone (NCBIN:83591, NCBIP:83592)</gib>

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                                                                                                                                         tandem repeat
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A; Residues: 1-1086 < CoLA>
A; Cross_references: EMBL.X61930
A; Experimental source: isolate RO-71
C; Genetics:
A; Gene: MSA1
C; Superfamily: major merozoite surface antigen
C; Keywords: glycoprotein; merozoite; surface antigen;
                                                                                                                                                                                Query Match 35.6%; Score 2999.5; DB Best Local Similarity 57.3%; Pred. No. 5.9e-86; Matches 637; Conservative 147; Mismatches 238
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467 IESDKKSYEDRSKSLNDITKEYEKLLNEIVDSKFNNNIDLTNFEKMMGRRYSYKVEKLTH 526 :: :: ::	700 NSEPSTEGELTGQATTKFGQQAGSALEGDSVQAQEQKQAQPPVPVPVPEAKAQ 1	911 DDTSHSTNLNNSLKLFENTLSLGKNKNIYQELLGGKSSENFYEKIL 956 11
6 6 6 6 6 6		5
: NTQNG 936 YEKIL 956 YENIL 996 KLKLE 1016 : KLKLD 1055	-Nov-1999 lasmodium vivax reveal	; Gaps 43; 37SGT 60 57SGT 60 68SDS 120 61::: 68MBD 240 61::: 68MBD 240 61::: 68MBD 240 61::1 68MBD 240 61::1 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240 68MBD 240
:	RESULT 10 A39401 merozoite surface antigen 1 precursor - Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: Pas-1992 #sequence_revision 28-Feb-1992 #text_change 24-C;Accession: A39401 R;del Portillo, H.A.; Longacre, S.; Khouri, E.; David, P.H. Proc. Natl. Acad. Sci. U.S.A. 88, 4030-4034, 1991 A;Thle: Primary structure of the merozoite surface antigen 1 of Pl A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Reference number: A39401 A;Re	SINTEGE ANTIGEN 35.1%; Score 2959; DB 2; Length 1726 Similarity 37.0%; Pred. No. 1.8e-84; 100; Conservative 323; Mismatches 517; Indels 310 CONSERVATIVE 323; Mismatches 517; Indels 310 CONSERVATIVE 323; Mismatches 517; Indels 310 CONSERVATIVE 323; Mismatches 517; Indels 310 CIFFLCSFLFFINTOCVTHESYQEIVKKLEALEDAVIGGYELFHKKKL CAUDIKVDRY CIFFL 1 1 1 1 1 1 1 1 1 1

Db 467 ONKKLLEDYEKSKKDYEELLEKFYBMKFNNNENKDVVDKIFSARYTYNVEKORYNN 522 Db 523 KESSENNSYYNVOKLKKALSYLEDYSLRKGISEKBYNHYTLKTGLEADIKKLTEEIKSS 582 Qy 589 EEQLFEKKITKDENKPDEKILEVSDIVKQUQKVLLMKTGLEADIKKLTEEIKSS 582 Qy 589 EEQLFEKKITKDENKPDEKILEVSDIVKQUQKVLLMKTBELKKTQLILKNVELKH 645	Db 984 FVKNSKVITGLT ETGKNALNDEIKKLKDILLSFDLYNKKKELDRLFNKKKELGODK 1042 Qy 1030 MQIKKLTLLKEQLESKLN 1047	A; residues: 1.1.7, 2.12.0. R; Daly, T.M.; Burns Jr., J.M.; Long, C.A. R; Daly, T.M.; Burns Jr., J.M.; Long, C.A. Mol. Biochem. Parasitol. 36, 283-285, 1989 A; Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: A; Reference number: A45531; MUID: 90014982; PMID: 2797064 A; Accession: A45531 A; Status: preliminary A; Residues: 454-1094 < DAL> A; Residues: 454-1094 < DAL> A; Residues: 454-1094 < DAL> A; Cross references: GB: 03975; NID: 9160081; PID: 9160082 C; Superfamily: major merozoite surface antigen C; Keywords: surface antigen C; Keywords: surface antigen C; Keywords: Similarity 32.4%; Pred. No. 9.1e-72; Best Local Similarity 32.4%; pred. No. 9.1e-72; Matches 609; Conservative 331; Mismatches 589; Indels 349; Gaps 40;
Oy 1420 NIETLYRYVDKIDLEVIHLEAKVLNYTYEKSNVEVKIKELNYLKIJOKLADFKKNNNF 1479 1:1 1:1 1:1 1 1 1 1	Best Local Similarity 55.8; Prod. No. 16-80; Matches 609; Conservative 145; Mismatches 255; Indels 89; Gaps 22; QY 1 MKIIFELCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLEQKEKMYLNEGTSGT 60 1 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	X 4 X X-X X H X-

<u>ک</u> و	, L	MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60	
λ	61	AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120	
ą	55		
<u> </u>	121	DAKSYADLKHRVRNYLLTIKELKYPQLFDLFNHMLTLCDNIHGFKYLIDGYEEINELLYK 180 1.1.	
2 2	18	INPYENT I BAKI MNYCANDENIK TOBANI KIDANI KKI VECYDEDI DANIKNANYCKAPO	
. A	123	INFYYDVLRDKLNDMCANNYCEIPEHLKISEEFTEMLKKVILGYRKFIENIQDDIEKLEI	
Δ.	241	YIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKLYQAQYDLSIYNKQ :: :	
ą	183		
<u></u> ≵ 9	292	LEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSG 334	
2	335	NAC 116.	
, <u>a</u>	303		
λ	345		
ą	363	KKIAGLYAQIKEIAKTIKFNLEGIFVDPIELEYFKKEKKKESCNLSTSSC	
Ā.	0	PNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKF 45	
ð	423		
λ	453	INDIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIVDSKFNNNIDLINFEKM 512 - - - - - - - - - - - -	
ą	480		
≱ g	513	MGRRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS 572 :	
λį	573		
ą	598	::: :: : :: : : : : : :	
λi	633		
ą	647		
<u>~</u>	693	KTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEG 727	
q	707		
λ	728	DSVQAQAQEQKQAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYI 787	
ą	767		
λ	788	CHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVWYSMFDSLNN 845	
q	821		
λi	846	SLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLLEEA	
Q	881	GLQNIYTELYEKEMMYHIYKLKDENPSIKSLLVKAGVIEPEPVAAPTPVTPAATEQQQQQ 940	
λi	880		
ą	941	ATPDVQSDAPAPSDVSQQPETPVTSTTPEVTTSTEASSSAPGEGTPSGEAGASGTEGATA 1000	

Qy Ov	917	SNAATPAGTSASGSAASNASTTSDVTPPAAAAAVPSTSTPAPAQPPAANSQSGNPDSGIR 1060
g d	1061	E
Qy Db	993	DINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNP 1052
λο	1053	KHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIOT 1112 :: :
Qy Dp	1113	EDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPS 1172 1 : 1: : 1: :
Qy Dp	1173	ENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTI 1227 : : : : :
Qy	1228 1358	TTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVYTGEAVTPSVIDNILSK 1276 ::
Qy	1277	IENEYEVLYLKPLAGYYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPY 1336
Qy Db	1337	KDLTSSNYVKKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSD 1396 ::: ::: :
Qy	1397 1526	LDSIKKYIND-KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTY 1448 :: :
Qy	1449	EKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMV 1504
Qy	1505	
Qy Db	1561 1693	Q-EGDKCVENDNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFGSS 1619 :
Qy Db	1620	SNFLGISFLLILMLILYS 1637 : : : : : SSFMGLSILLITLIVFN 1770
RESU	RESULT 13	

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major merozoite surface antigen precursor - Plasmodium chabaudi chabaudi
major merozoite surface antigen precursor - Plasmodium chabaudi
C;Becies: Plasmodium chabaudi chabaudi
C;Becies: Plasmodium chabaudi chabaudi
C;Becies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: A45546
B;Delecersnijder, W.; Hendrix, D.; Bendahman, N.; Hanegreefs, J.; Brijs, L.; Hamers-Ca
MOL. Biochem. Parasitol. 43, 231-244, 1990
A;Title: Molecular cloning and sequence analysis of the gene encoding the major meroz
A;Reference number: A45546; MUID:91218805; PMID:2090945
A;Accession: A45546
A;Accession: A45546
A;Accession: A45546
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1785 < DEL>
A;Cross-references: GB:M34947; NID:g160597; PID:g160598
C;Superfamily: major merozoite surface antigen

C;Keywords: surface antiqen

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35; 540 334 437 617 647 677 707 757 827 888 TLKRCSELDVLLAIQNNMPTMYSLYENVVDGLQNIYTELYËKEMMYHIYNLKDKNPAVKA 947 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYK 180 EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRŠKSLNDITKEYEKLLNEIYD 497 Gaps 9 9 9 -----EFAQKLQPFILKFEELGFTEQTELVNLIKTLGPNKYGLKYLIESKEEFNELMHA LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRN : | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | | :: | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | | :: | | | :: | | :: | | | :: | | :: | | | :: | | | :: | | :: | | | :: | | :: | | :: | | | :: | | :: | | : | | :: | | | :: | | :: | | | :: | | : | | :: | | | :: | | :: | | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: KLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEWVCNLYKLKD-NDKIKN 61 AVTTSTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS YIKKNKKTIENINELIEESKKTI------DKNKNATKEEEKKKLYQAQYDLSIYNKQ LEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSG------303 SSNTKTTTTDKAVTTQTATKATGTETNTGTETNTGTETNTATGTTTATGTTTATGTPTVT ------KNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLRE-KNKNI DISA---KVETKESTEP--NEYPNGVTYPLS----YNDINNALNELNSFGDLINPFDYTK ITEDLITNEQARKNLIKAIKKKIEAEEQKLVELKDDYDTKLAAFNGQKTPFKEAAKKFYE 558 IVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKV **QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENĶQEPYYLIVLKKEIDKLKVF** PPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKOYKITKEEES--1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 61 PVDPF-----TNP----TNP-----TNP------MPKVESLINEEKKNIKTEG-QSDNSEPSTEGEITGQATTKPGQQA-------------PVPVPEAKAQVPT GTESTEETPAASKPAEGAASTGATTPTEQEAAPTEQEAQPAAPETPAEVPAPTTPAAPAT 29.8%; Score 2509; DB 2; Length 1785; llarity 31.6%; Pred. No. 1.5e-70; Conservative 324; Mismatches 605; Indels 366; --NTPNTLLD-----Local Similarity 598; Match Best Loca Matches 335 121 243 648 168 181 123 241 292 343 438 541 678 758 816 69 387 481 498 722 g ò õ g a ò QQ ò 임 q õ g ద ò g g g g g g g ò g g

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FUKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINF 1378
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LEKRNDFLDVLSYELALFKDINTNKFVVKNPYQLLDNDKKDKMINLKYAIKGVTEDIET 1521 ||||: | :: : : : : : | | | : | | : | | | STINVEGSTQV------RAESEDEMFVDDFEVDNFYKSYLQQVDG-NNTQFIDFIKSKK 1118 SVLKSRLLKRKKYINGTFYVLSGFANFFNKRREAEKQYVDNAIKNTDMLLKYYKARSKYF 1237 NGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIA 1155 ELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTD-----VATVVSESGSDTLEQS 1210 VVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSR 1318 NHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNI-SQHQCVKKQCPQNSGCFRHLD 1548 AESASTEPTPKAPTATPTSETVTQEGTTPAAPKAQEGASSSAPAQPAPAKPAPAQTVTGQ 1067 TLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYY 1095 LLVKAGVIDPEPVAPTPAVPAPETAPETAPETAPETPAQEAPQQFESAQAPEAATETTTP 1007 888 DDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKL --ASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQ ANDVLGYYKILSEKYKSDLDSIKKYI-----NDKQGENEKYLPFLNNIETLYKTVNDKID EREECKCLLNYKQ - - EGDKCVENPNPTCNENNGGCDADAKCTEEDSGSN - - GKKITCECT EEAKKVSTSVKT-STULINGLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTUFVKSKA LFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADF----KKNNNFVGIADLSTDY | |: |: || || : || || || EFSELLQHKLENYKIEKAGFDILMANLETYIRIDEKLEDFVESAEKNKHIASIA-----LSSSSMQPLSLTPQDKP-----1211 QPKKP----Ė 948 1008 1068 1036 1178 1096 1156 1298 1358 1259 1403 1379 1434 1582 1490 1636 1549 1605 875 916 916 1462 1522 1751 g QQ g q qq Db QQ g g qq g ò q δy qq ò g ò δy ò οy Qγ οy ŏ ò ŏ ŏ ò g

- malaria parasite (Plasmodium falciparum) (strain RO-71) RESULT 14 S47282 merozoite surface antigen 1

C;Species: Plasmodium falciparum
A;Variety: strain RO-71
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
C;Accession: S47282
R;Tolle, R.; Bujard, H.; Cooper, J.A.
Submitted to the EMBL Data Library, July 1994
A;Description: Plasmodium falciparum: recombination within the C-terminal region of A;Reference number: S47282

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Gaps

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glycoprotein 185 - malaria parasite (Plasmodium falciparum) (isolate Honduras C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jun-2000
C.Accession: A25814
R.Howard, R.F.; Ardeshir, F.; Reese, R.T.
Gene 46, 197-205, 1986
A;Title: Conservation and antigenicity of N-terminal sequences of GP185 from dA;Reference number: A25814; MUID:87106855; PMID:3542719
                                                                                                                                                                                                                                                                                                       VGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ 1539
                                                                                                                                                                                                                                                                                                                                                             NSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKI 1599
                                                                                                                                                     DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFRYLIDGYEEINELLYK 180
                                                                                                                                                                                                                                                                                                                                                                            VIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQ
                                                                                               LENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD
                                                                                                                                                                                            KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLN
                                                                                                                                                                                                            NIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNF
                                                                                                                                                                                                                                                                241 VGIADLSTDYNHNNLITKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVITISTPGSKGSVASGGSGGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMED
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                            Length 400;
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    Score 2101; DB 2; Le
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 Keywords: glycoprotein; merozoite; surface antigen;
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Pred. No. 1.2e-30;
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C;Superfamily: major merozoite surface
C;Keywords: glycoprotein
                           Similarity 100.0%; Pour Conservative 0;
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Best Local Similarity
Matches 232; Conserv
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A; Molecule type: mRNA
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                            Query Match
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                                                                                                                                                                                                                     ENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNL 1138
                                                                                                                                                                                                                                                                          1139 EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATV 1198
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                                                                                                                                                                                                                                                                                                                                 VSE------SGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVP 1244
                                                                                                                                                                                                                                                                                                                                                                                      1245 IFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNV 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGML 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                         PID:9535258
                                                                                                                                                                                                                                   180 VTPPQPDVTPSPLSVRVSGSSGSTKEETQIPTSGSLLTELQQVVQLQNYDEEDDSLVVLP 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                            651;
                                      NID:9535257; PIDN:CAA84558.1;
                                                                                                                                     Indels
                                                                                                             Length
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                                                                                                                                     82; Mismatches 114;
                                                                                                         Query Match 25.5%; Score 2146; DB 2; Best Local Similarity 64.5%; Pred. No. 8.3e-60; Matches 422; Conservative 82; Mismatches 114;
           A; Molecule type; DNA
A; Residues: 1-651 <TOL>
A; Cross-references: EMBL: 235329; NID:9535257; PIDN:C
A; Experimental source: strain RO-71
C; Superfanily: major merozoite surface antigen
C; Keywords: 91ycoprotein; merozoite; surface antigen
A; Accession: S47282
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merozoite surface antigen - Plasmodium vivax (fragment)
C;Species: Plasmodium vivax
C;Species: Jo.Sep-1993 #text_change 11-Jan-2000
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
C;Accession: A45949
R;del Portillo, H.A.; Gysin, J.; Mattei, D.M.; Khouri, E.; Udagama, P.V.; Mendis, K.N
Exp. Parasitol. 67, 346.353, 1988
A;Title: Plasmodium vivax: cloning and expression of a major blood-stage surface anti
A;Reference number: A45949; MuID:89052826; PMID:3056739
A;Accession: A4594
A;Accession: A4594
A;Accession: A4594
A;Retes preliminary
A;Molecule type: DNA
A;Residues: 1-636 <DEL>
                                                                                                                                     C;Species: Plasmodium falciparum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: B54498
R;Peterson, M.G; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V
Mol. Biochem. Parasitol. 27, 291-302, 1988
A;Title: Variation in the precursor to the major merozoite surface antigens of Plasmo A;Reference number: A54498; MUID:88142999; PMID:2449612
A;Stetus: preliminary
                                                                                                                   major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-281 <PET>
A; Residues: 1-281 <PET>
A; Cross-references: CB:M19144; NID:g160414; PIDN:AAA29654.1; PID:g552205
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 TSSGASPPADASDSDAKSYADLKHRVRNYLFTIKQLKYPESLDLPNHMLTLCDNIHGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 EITT-----KG--ASAQSGASAQSGASAQSGASAQSGTSGPSGPSGTSPSSRSNTLPRSN
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llarity 37.6%; Pred. No. 4.9e-25;
Conservative 113; Mismatches 194;
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C;Superfamily: major merozoite surface antigen
C;Reywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1096.5; DB Pred. No. 9.3e-28; 8; Mismatches 32
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Best Local Similarity 77.7%;
Matches 227; Conservative
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nes 245; Conserv
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                                                                                                                                                                         C;Species: Plasmodium yoelii
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YYKARTKYFTSEAVPLKTLSKASLDRESNYLKIEKFRAYSRLELRLKKNINLGKERISYV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LTNRQIRDLSILKARLEKRKQTLNGVFYILNGYVNEFNKRREAEKQYVDNALKNTDMLLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 GLYETVIGQAEEYSEELQNRLDNYKNEKAEFEILITKNLEKYIQIDEKLDEFVEHAENNKH 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAADAPATPEGAVPGAVPGAVPGAVPGAVPGSGTDTRVAGSSVDD-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDIPKNAGCFRDDNGTEEWRCLLGYKKGEGNTCVENNNPTCDINNGGCDPTASCQNAEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross-references: GB.J03612; NID:g160678; PID:g160679
A.Experimental source: strain 17XL
A.Note: the authors translated the codon GTA for residue 429 as Leu
C.Superfamily: major mercocite surface antigen
C.Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 680;
                                                                                                                                                 major merozoite surface antigen - Plasmodium yoelii (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                            C,Accession: A28121
R;Burns Jr., J.M.; Daly, T.M.; Valdya, A.B.; Long, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 602-606, 1988
A;Title: The 3' portion of the gene for a Plasmodium yoelli
A;Reference number: A28121; MUID:88124889; PMID:2448778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYS 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635 ENSKKIICTCKEPTPNAYYEGVFCSSSSFMGLSILLIITLIVFN 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 13.5%; Score 1135; DB 2; Local Similarity 36.2%; Pred. No. 1.6e-28; les 255; Conservative 142; Mismatches 247;
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-680 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A28121
229 YIKK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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                                                                                    RESULT 17
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Db 61 IGKLETFITKNKETISNINKLISDENAKRGGQSTNTTNGPGAQNNAAQGSTGNTETGTRS 120	Db 61 AVTTSTPGSGGSVTSGGSGGSVASVASGGSGGSVASGGSGNSRRTNPSDNSSDS 114
Qy 272 Qy 272 GPEKKRLYQAQYDLSIYNKQLEEAHNLI 299 :	OY 121 DAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEI 174
Qy 300 SVLEKRIDTLKKNENIKELLDKIN-EIKNPPPANSGNTPNTLLDKNKKIEEHEKE 353 : ::: ::: : : : 	RESULT 21 S03290
Qy 354 IKEIAKTIKFNIDSLFTDPLELEYYLREKNKNI-DISAKVETKESTEPNEYP 404 	glycoprotein, 190K - malaria parasite (Plasmodium falciparum) (isolate Bandia-Senegal C;Species: Plasmodium falciparum A;Variety: isolate Bandia-Senegal C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jun-2000
QY 405 NGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI-YTDNERKKFINEIKEKI 460 : :: :	C;Accession: S03290 R;Scherf, A.; Barbot, P.; Langsley, G. Nucleic Acids Res. 17, 1774, 1989 A;Title: Sequence and length polymorphism of a major malaria vaccine candidate analys
QY 461 KIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLINFEKMGKRYSYK 520 	A;Reference number: SU3290; MUID:89160345; PMID:2646601 A;Accession: S03290 A;Status: translation not shown A;Molecule type: DNA
QY 521 VEKLTHHNTEASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIET 580	A;Residues: 1-146 <sch> A;Cross-references: BMBL:X13782 C;Superfamily: major merozoite surface antigen C;Keywords: glycoprotein</sch>
QY 581 LVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKN 640	Query Match 8.4%; Score 710.5; DB 2; Length 146; Best Local Similarity 97.9%; Pred. No. 3.9e-16; Matches 143; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 641 VELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTE 695. :: :::	Qy 28 LVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVAS 84
Qy 696 GQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV 744	Qy 85 GGSVASGGSVASGGSGNSRRINPSDNSSDSDAKSYADLKHRVRNYLLTIKELKY 144
RESULT 20 A25522 major merozoite surface protein - malaria parasite (Plasmodium falciparum) (fragments)	QY 145 PQLFDLTNHMLTLCDNIHGFKYLIDG 170
C;Species: Plasmodium faloiparum C;Date: 06-Jan-1988 #sequence_revision 06-Jan-1988 #text_change 09-Jun-2000 C:Accession: A2552: A22828	RESULT 22
Richeung, A.; Leban, J.; Shaw, A.R.; Merkli, B.; Stocker, J.; Chizzolini, C.; Sander, C. Proc. Natl. Acad. Sci. U.S.A. 83, 8328-8332, 1986 A;Title: Immunization with synthetic peptides of a Plasmodium falciparum surface antiger A;Reference number: A25522; MUID:87041450; PMID:3534885	major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (isolate B N;Alternate names: gp195, PMMSA, PSA C;Species: Plasmodium falciparum C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jun-2000
A.FCCeSIOn: A.25s.z. A.Status: preliminary A.Molecule type: DNA	C:Accession: PQU125 R:Kimura E.: Mattei, D.; di Santi, S.M.; Scherf, A. Gene 91, 57-62, 1990
A.Residues: 1-168 <che> K.Cheung, A.; Shaw, A.R.; Leban, J.; Perrin, L.H. EMBO J. 4, 1007-1011, 1985</che>	A;Title: Genetic diversity in the major merozoite surface antigen of Plasmodium falci A;Reference number: PQ0120; MUID:90382698; PMID:2205540 A;Accession: P00125
le: Cl erence	A; Molecule type: DNA A; Residues: 1-138 <kin3 A; Cross-references: CR: M32116: NITD: 016010: DIDN. AAA29307 1: DID: 0552216</kin3
NA CCH3A CE VOLAGE CE MIAGAO. CE WASCOOL MITH AGOST. HITML CANAGES 1.	C; Superfamily: major merozoite surface antigen C;Keywords: glycoprotein; surface antigen
surface antigen	7.8%; Score 659.5; DB 2; Length 138;
Query march Query march Best Local Similarity 93.7%; Pred. No. 2.76-19; Matches 163; Conservative 2; Mismatches 3; Indels 6; Gaps 2;	MATCHES 132; CONSELVATIVE 2; MISMATCHES 4; INDELS 3; GAPS 1; Qy 30 KKLEALEDÀVLTGYSLFQKEKMYLNEGTSGTAVTTSTPGSKGSVASGGSVASGGSVA 89
1 MKIIFFLCSFLFFIINTQCVTHESYQEIVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT	1 KKLEALEDAVLTGYSLFQKEKMYLNEGTSGTAVTTSTPGSSGSVASGGSVASVGG 57
DD I MAINFILCSFLEFIINTGCVTHESTQELVKKLEALEDAVLTGYSLFÜKEKMVLNEGTSGT 60 Qy 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDS 120	QY 90 SGGSVASGGSVARKTRYBDNSSDSDARAFAKKYRILLIKKYLLIKKYLYLEVILDI 149 91 SGGSVASGGSGRAFKTRYBDNSSDSDARSTADLKHKYRYKYLLIKKYLEKYLEVILTI 149 11111111111111111111111111111111111

729 SVQAQAQEQKQAQPPVPVPEAKAQVPTPPAPVNNKTENV : : : :	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00	989KLEEDINKIKKTLQLSFDLYRK-YKLKERKEPKKKTV	09 1196 ATVVSESGEDTL-EQSOPKRPASTHVGAESNTITTSQNVDDEVDDIIVPIFGESEEDYD 1254 109 1-IRNKKGERATAELIKIKIKEKKSVKQNDESSANIITKDGDKTPEVVSNDDKIQKD 1555 09 1255 DLGQVVTGEAVTPSVIDNILSKIENEYEVLYL
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Qy 150 LTNHMLTLCDNIHGFKYLIDG 170 Db 118 LTNHMLTLCDNIHGFKYLIDG 138	In - Plasmodium chabaudi labaudi labaudi luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision 15-Oct-1999 luce_revision luce_revision luce_revision luce luce_revision luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revision luce luce_revisio	394; CORSELY SSDSDAACK SSDSDAACK SSEKDEKSKEEKF LIDGYEEINELLY : : : EYDDKINNMKEF PLDNIKDNVGKMEI :: : : EFI : : LISTYNKQLE LSKLNKEKDNIKNI	GGNTPWTLLDKNKKIEBHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNK

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	09 1001 1018 1019 1019 1019 1019 1019 1018 1019 1018 1019 1018 1019 1018 1019 1018 1019 1018 1019 1018 1019 1018 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 1019 10
Db 1829 INTLOTKVDLNQIN	QUELY MAICH Best Local Similarity 21.4; Pred, No. 2.1e-10; MATCHES 34; CONSETVATIVE 248; Mismatches 534; Indels 625; Gaps 81; MATCHES 384; CONSETVATIVE 248; Mismatches 534; Indels 625; Gaps 81; Db 155 XKVGYIENKMTIKNTIKSYPDQIYEGDIDTFYNELSSIVKEDPIDDIEDKTKLE 209 C23 GYRKPLONIKDWOKMA-DTIKKNKWTENINELESSKTTICNKNAATKEEKKKLVQA 201 [1]

	760 APVNN-KTENVSKLDYLEKLYEF-LNTSYICHKYILVSHSTMNEKILKQYKI 1	OY 1019 FORKTYGRYRMQIKKITLLKEQLESKINSLNNKHYLONESVFINKKKAEALAE 1073 1029 VYKKOSNAQOVDHKKKSWILLKDKSKERIKDKENQINVERNEERDLKRKDDEI- 1081 OY 1074 TENTLENTKILLKHYKGLVYYNGESSPLKTLSEBSIQTEDNYASLENFKVLSKLE 1129 OY 1074 TENTLENTKILLKHYKGLVYYNGESSPLKTLSEBSIQTEDNYASLENFKVLSKLE 1129 OY 1130 GKLKDRILNEELVKYKTILYNLKKDPLLQNODLLSKIDINSLTINEGMCVDKIE 1130 OY 1130 GKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNRNYTGNSPSENNTD 1177 I	OY 1238 DDVIIVPIEGESEEDVDDLGQUVTGEAVTPSVIDNILSKIEN-FYEVLYLKPLAGV 1292 1245 ::::::::::::::::::::::::::::::::::::
DD 1586 NNDIKVIEELENNYDSSEENNILGSKOKLKELINKFNAEIKKIDDKIIEKNDLIDKLIE 1645 QY 1439 LEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDY 1489 DD 1646 TRKNCMLFTHTLAETHITITISTKIKITDYSKEIESTKEKEKEKTIGTSNSLNDDIATLQLKY 1705 QY 1490NHNNLITKFLSTGMVFENLAKTVLSNLLDGN 1520 1100 DLHQINKYYTSKLSDATNDNNNLIEKEKEATQAIKNLTKLFTIDSNNIDAN 1756	RESULT 26 hypothetical protein PFB0145c - malaria parasite (Plasmodium falciparum) C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Accession: C71622 R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Fertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998 A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A; Reference number: A71600; MUID:99021743; PMID:9804551 A; Accession: C71622 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-1979 cGRP> A; Experimental source: clone 3D7 A; Experimental source: clone 3D7 A; Experimental source: clone 3D7 A; Genetics: A; Genetics:	Query Match G.68; Score 559.5; DB 2; Length 1979; Best Local Similarity 22.28; Pred. No. 3.4e-10; Matches 370; Conservative 314; Mismatches 609; Indels 373; Gaps 82; QY 110 RTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLID 169 : :	279 YQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKINEHLELDKILEYELEE 326DLENLNKKLLESKENVKELGGCVKEKNETHNSLNDHIEKEKKYKLLEYELEE 337 GNTPWTLLDKKKIEBHEKEIKETAKTIKFNIDSLETDPLELEYYLREKNKNIDI-S 338 HI

238 MEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEA	782 NKDYNNQNNQNIEN-NQNIENNQNNQNIENNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQNNQ	1074 481 1134 508 1194 556	1248 EKIILDEQINËKËKÏINIÏNEKYLILËKËYEEYQNKNIFINAQIËNLËKËKQLQËEI 1305 597 ITKDENKPDEKILEVSDIVKV-QVQKVLLMNKIDËLKKTQLILKNVËLK 644	726	787 1596 809 1656	1706 YEIKLEKHENNNLINEMNILKNKETENMNIKQKEEDYIKLIKKDKTNIQ 1707 TALANSIKLEFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESF
Db 1560 YSRYYGLREDLCKEEIVPSKIGNISNKNENNNKKNNTCDGYDEKVT 1605	RESULT 27 B25120 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st dy dy docuses: Plasmodium falciparum c; becies: Plasmodium falciparum c; becies: Plasmodium falciparum c; becies: Plasmodium falciparum c; bate: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jun-2000 C; Accession: B25120; A05263 E; Mackay, M. 38-3829, 1985 A; Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc d; A; Reference number: A91030; MUID:86136024; PMID:3004972 A; Residues: 1-115 AMCC A; Residues: 1-115 AMCC C; Superfamily: major merozoite surface antigen C; Keywords: merozoite; surface antigen tepeat F; 1-15/Domain: signal sequence #status predicted <amt> C; Superface cantigen #status predicted <amt> C; F; 20-101, 108-113/Region: 3-residue repeats</amt></amt>	Query Match 6.3%; Score 529; DB 2; Length 115; Db Best Local Similarity 91.7%; Pred. No. 1.2e-10; Matches 111; Gaps 2; Qy MATIFFLCSFLEFIINTOCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60 Db Db Db 1 MKIIFFLCSFLEFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60 Db Db 1 MKIIFFLCSFLEFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60 Qy 61 AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSGNSRTNPSDNSSDS 120 Db Chillill 11 111111111111111111111111111111111111	Qy 121 D 121 Db 115 D 115 RESULT 28 T18501 hypothetical protein C0760c - malaria parasite (Plasmodium falciparum) C; Species: Plasmodium falciparum C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C; Accession: T18501 R; Lawson, D.; Bowman, S.; Barrell, B. submitted to the BMBL Data Library, August 1997 A; Reference number: 218935	el331922; PIDN:CAB11140.1	Query Match 6.2%; Score 521.5; DB 2; Length 3394; QY Best Local Similarity 20.8%; Pred. No. 9.5e-09; Db Db Db Db Db Db Db Db Qy 108 SRRTNDSDNSSDSAKSYADLKHRVRNYLLTIKELKYPOLEDLYNHMLTL	Qy 158 CDNIHGFKYLIDGYEEINELLY

Best Local Similarity 20.8%; Pred. No. 1.6e-08; Matches 355; Conservative 306; Mismatches 552; Indels 494; Gaps 8	QY 132 VRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLN 182 : : : : : Db 9 VNLFLVSIVLEVYRQ-YDKRSRALDKIKKFVDLTKVNLEDFIEDKTKEINDLAVDME 64	Qy 183 FYFDLLRAKLNDVCANDYCQI	QY 213ELDVLKKLVFGYRRPLDNIKDNVGK-MEDXIKKNKKTIENINEL 255	QY 256 IESKKTIDKNKNATKEEKKKLYQAQYDLSIYNKQLEE 294 :	QY 295 AHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLL 341	Qy 342 -DKNKKIEEHEKEİKEIAKTIKEN	QY 371 DPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLI 430 1	Qy 431 NPFDYTKEPSKNIYTDNERKKFINEIKE-KIKIEKKKIESDKKSYED 476	QY 477 RSKSLNDITKEYEKLLNGIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENS 536	QY 537KHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIK 586 : : : : : : : Db 516 MESKYKSFTDKLTAGMDEFSLMYGEKFTLSQEATNNYGEQDLNKKLENEIESFYNMFE 575	QY 587 KDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQ 635 : ::: : : :	QY 636 LILKNVELKHNIHVPNSYKQENKQEPYZLIVLKKEIDKLKVFMPKVESLINEEKK 690	QY 691 NIKTEGOSDNSEPSTEGEITGOATTKPGQQAGSALEGDSV 730	OY 731 QAQAQEQKOAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTS 785 131 AAAAQEQKOAQPPVPVPPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTS 785 132 SLVIEKYKELKDMSYSQSDEAILGIKEFINRQTEIIKDKSVFMLEDLNKKFDDKN-N 794	Qy 786 YICHKDLLFNI 829 :	QY 830 QNNIPVMYSMFDSLNNSLSQLFMEIYEKEMYCNLYKLKDNDKIKNLLEEAK 880 : : :	Qy 881KVSTSVKTLSSSSMQPLSLTPQDK	Qy 913 TSHSTNLNNSLKLFENILSLGKNK
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9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Db 962 KKFR Qy 962 FYNE Db 1017 KYNE Qy 1005 Db 1077 KYQV Qy 1093 KYN Db 1137 ITNE Qy 1150 LHHL Qy 1150 E E CSO Db 1139 KYN Qy 1150 E CSO Db 1139 KYN Qy 1150 E CSO Db 1139 E CSO Db 1139 INSO Qy 1262 GEAV Qy 11433 DL Qy 11433 DL Qy 11433 DL Qy 11476 NNN Db 1139 MIFE Qy 11476 NNN Db 1139 KYN Qy 1150 E CSO CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SECIES: SSC CS SC CS SECIES: SSC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC CS SC	KKFAAVLNNSEEFVKEVDSLLQDKRTDIASFQANIDITLDSLNVKFNDINKEING 1016	FYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKRTLQLS 1004 : : : : :	FDL	-LTLLKEQLESKLNSLNN-PKHVLQNFSVFFNKKREAEIAËTENTKILLKHYKGLV 1092 	KYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSG 1149 :: :: :: :: :: :: :: :: :: :: :: :: ::	LHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTL 1207 ::	EQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIĘGESEEDYDDLGQVVT 1261 	GEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKOLENNVMTFNVNVKD 1313 :	ILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSID 1373 :: :: :	TDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIE-TLYKTVNDKI 1432 	DLFVIHLEAKVLNYTYEKSNVEVÄIKELNYLKTIQDKLADFKK 1475 : : : : : : : : : : : : : : : : : : : : : : : :	NNNFVGIADLSTDYNHNNLLT 1496 	SULT 30 8077 9077 Pothetical colled-coll protein - fission yeast (Schizosaccharomyces pombe) Species: Schizosaccharomyces pombe Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 Accession: T38077 Accession: T38077 Empirical to the EMBL Data Library, April 1996 Reference number: 221767 Reference number: 221767 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: DDA Residues: 1-1957 Cross-references: EMBL: 270690; PIDN: CAA94624.1; GSPDB: GN00066; SPDB: SPACIF3.06c Experimental source: strain 972h-; cosmid clF3 Genetics: Genetics: Map position: 1 Ouery Match Best Local Similarity 22.2%; Pred. No. 2.1e-08; Matches 352; Conservative 253; Mismatches 617; Indels 361; Gaps 67; 105 SGNSRRTNPSDNSSDSDAKSYADLKHRVRYLLIKELKYPQLEDLTNHMLTLCDNIHGF 164 115 GANFARAMECHER CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACT
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165 KYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGY 224
                                                             RKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYD 284
                    779 -KQSFTSLVNSYQSISNLYHELRDDH------VNMQSQNNTLL------ESESKLKTD
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Db 241 KKIAELYAQIKEIAKTIKFNLDGIFVDPVELEEF 274 RESULT 32 \$67593 transport protein USO1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein D255; protein YDL058w C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000 C;Accession: \$67593; A38455; \$30782 R;Bloecker, H.; Brandt, P. submitted to the Protein Sequence Database, July 1996 A;Recence number: \$67587 A;Accession: \$67587 A;Molecule type: DNA	A; Residues: 17190 (BLC)> A; Residues: L1790 (BLC)> A; Cross-references: EMBL: 274106; NID: 91431058; PID: e253003; PID: 91431059; MIPS: YDL058 A; Experimental source: strain \$288C R; Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M. J. Cell Biol. 113, 245-260, 1991 A; Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transpector number: A38455; MUID: 91185402; PMID: 2010462 A; Reference number: A38455; MUID: 91185402; PMID: 2010462 A; Residues: 1-389, 'TA, '392-724,'S', 726-1790 (ANAK) A; Residues: 1-389, 'TA, '392-724,'S', 726-1790 (ANAK) A; Residues: 1-389, 'TA, '392-724,'S', 726-1790 (ANAK) A; Cross-references: GB: X54378; NID: 94777; PIDN: CAA38253.1; PID: 94778 A; Note: the authors translated the codon ACT for residue 768 as Ile R; Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E submitted to the EMBL Data Library, Februamy 2093 A; Description: An integrin analogue in Saccharomyces cerevisiae. A; Reference number: \$30782	A; Molecule type: DNA A; Readuces: 71-1846, E., 848-923, K', 925-1252, I', 1254-1318, V', 1320-1460, S', 1462-1580 A; Cross-references: BMBL:L03188 C; Genetics: A; Genetics: AC: 1001 C; Genetics: SGD:SO002216; MIPS:VDL058w A; Map position: 4L C; Keywords: colled coil; transmembrane protein F; 326-342/Domain: transmembrane #status predicted <tm1> F; 336-4410/Domain: transmembrane #status predicted <tm2> F; 617-633/Domain: transmembrane #status predicted <tm3> Query Match Best Local Similarity 20.6%; Pred: No. 5.48-08; Matches 314; Conservative 278; Mismatches 561; Indels 368; Gaps 66; Qy 98 GSVASGGSGNERRINESDNSSDSAKSYADLKHRVNYLLITKELKYPQLFDLTHHMLTL 157</tm3></tm2></tm1>	Db 456 GDNAKENGGSNKSDKEDGKDCTEYEGSFKANLEEUL-LNYDAELINPFKLFF 514 Qy 158 CDNINGFKYLIDG-YEEBINELLYKLNFYFDLLRAKLN-DV 195
Qy 1161 IKNKNYTCNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHV 1220 Db 1	Qy 1357	RESULT 31 A45518 merozoite surface antigen 3103 - Plasmodium chabaudi adami C;Species: Plasmodium chabaudi adami C;Species: Plasmodium chabaudi adami C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 11-Jan-2000 C;Accession: A45518 R;Lew, A.M.; Beck, D.J.; Thomas, L.M. Mol. Biochem: Parasitol. 41, 289-291, 1990 A;Title: A second region recognized by the protective monoclonal antibody 5C10/66 iA;Reference number: A45518; MUID:90377298; PMID:2398918 A;Accession: A45518 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-284 ALEM>A;Cross-references: GB:M32980 C;Superfamily: major merozoite surface antigen C;Superfamily: major merozoite surface antigen	QUETY MATCH QUETY MATCH QUETY MATCH QUETY MATCH QUETY MATCH Best Local Similarity 39.4%; Pred. No. 3.7e-09; MATCHES 108; Conservative 36; Mismatches 57; Indels 73; Gaps 3; QY 178 LYKLNFYFDLLRAKLNDVCANDYCOIPFUKITRANELDVLKKLVFCYRRPLDNIKDNVGK 237 1:

KEQAWKRDEDTVKKTTDSC IHLEAKVLNYTYEKSNVEVKI : : :: :	Db 1749 TDLDEKNAKYRSKLKDLGVEI 176	RESULT 33 T28317 ORF MSV156 hypothetical protein - M	C;Species: Metanopius sanguinipes e C;Date: 21-Jan-2000 #sequence_revis C;Accession: T28317 R;Afonso, C.L.; Tulman, E.R.; Lu, Z	J. Virol. 73, 533-522, 1999 A.Title: The genome of Melanoplus S. Reference number: Z20484; MUID:99 A.Accession: T28317	A;Status: preliminary; translated f A;Nolecule type: DNA A;Residues: 1-1127 <a;coss-references: embl:af063866;<="" th=""><th>C;Genetics: A;Note: MSV156</th><th>Query Match 5.7%; S Best Local Similarity 19.7%; P Matches 287; Conservative 247;</th><th>Qy 132 VRNYLLTIKELKY-PQLFDLTNHML</th><th>Db 54 IKNYNKIVEKIFYMHNQFKINDYNI Ov 101 KINDVCANDYCOIDFNIKIRANFID</th><th>100</th><th>Qy 247 KTIENINELIEESKKTIDKNK</th><th>Db 150 NNIHSDNETIITGKETLIDILNKLL Ov 303 EKRIDTLKKNENIKELLDKINEIKN</th><th>199</th><th>Qy 363 FNIDSLFTDPLELEYYLREKNKN</th><th>Db 240 KKQEELIKKLNDKEINFUDEKÇKL Qy 418 NALNELNSFGDLINPFDYTKEPSKN</th><th>Db 295 NLQNETLNKDSTIKSLD</th><th>Qy 478 SKSLNDITKEYEKLLNEIYDSKFNN</th><th>ZK.</th><th>Qy 538 HNLEKLTKALKYMEDYSLRNIVVEK</th><th>Db 357 ININELKS Ov 595 KKITKDENKPDEKILEVSDIVKVOV</th><th>400</th><th>Qy 655 QENKQEPYYLIVLKKEIDKLKVFMP</th><th>Db 426 KIDEQTEXY</th><th>715 TKPGQQA</th><th>DD 446IELKNNNLQKLEEENKK</th></a;coss-references:>	C;Genetics: A;Note: MSV156	Query Match 5.7%; S Best Local Similarity 19.7%; P Matches 287; Conservative 247;	Qy 132 VRNYLLTIKELKY-PQLFDLTNHML	Db 54 IKNYNKIVEKIFYMHNQFKINDYNI Ov 101 KINDVCANDYCOIDFNIKIRANFID	100	Qy 247 KTIENINELIEESKKTIDKNK	Db 150 NNIHSDNETIITGKETLIDILNKLL Ov 303 EKRIDTLKKNENIKELLDKINEIKN	199	Qy 363 FNIDSLFTDPLELEYYLREKNKN	Db 240 KKQEELIKKLNDKEINFUDEKÇKL Qy 418 NALNELNSFGDLINPFDYTKEPSKN	Db 295 NLQNETLNKDSTIKSLD	Qy 478 SKSLNDITKEYEKLLNEIYDSKFNN	ZK.	Qy 538 HNLEKLTKALKYMEDYSLRNIVVEK	Db 357 ININELKS Ov 595 KKITKDENKPDEKILEVSDIVKVOV	400	Qy 655 QENKQEPYYLIVLKKEIDKLKVFMP	Db 426 KIDEQTEXY	715 TKPGQQA	DD 446IELKNNNLQKLEEENKK
DD 779 QILNSSHSSLKENFSILETELKNVRDSLDEMTQLRDVLETKDKENQTALLEYKST 833 QY 453 INEIKEKIKIEKKKIESDKKSYEDRSKSLNDIȚKEYEKLLNEIYDSKFNN 502		QY 503 NIDLTHFEKMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEK 562 1:	QY 563 ELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIV 615	Qy 616 KVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYRQENKQEPYYLIVLKKEIDKLK 675 	Qy 676 VFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQ 735	736 EQKQAQPPVPVPVPEAKAQVP :	Db 1080 LTKTRE1117 Oy 796 HSTMNEKILKQYKITKEEESKLSSCDPLDLLENION	Db 1118NEEHLKEEKIQLEKEATETKQQLNSLRANLESLEKEHEDLAAQLKKYEEQIANKER 1173	QY 842 SLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEBAKKYSTSVKTLSSSSMQPLSLTP 901 : : :	902 ODKPEVSANDDTSHSTNLFENILSLGKNNI	Db 1231 QIK-ELKKKNETNEASLLESIKSVESETVKIKELQDECNFKEKEVSELEDKLKASEDKNS 1289	QY 939 -YQELIGQKSSENFYEKILKDSDTFYNESFTNFVKŠKADDINSLNDESKRK 988 	989 KLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNS	DD 1346 NAEEQLEKLKNEIQIKNQAFEKERKLLNEGSSTITQEYSEKINT 1389	QY 1049 LNNPKHVLQNFSVFFNKKKBABIAETENTLENTKILLKHYKGLVKYYNGESSPLK-1103	QY 1104TLSEESIOTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKE 1159	DD 1446 KITRNDEKLLSIERDNKRDLESLKEQLRAAQESKAKVEEGLKKLEEESSKEKAELEKSKE 1505	1160 VIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSE	Db 1506 MMKKLESTIESNETELKSSMETIRKSDEKLEQSKKSAEED 1545	OY 1220 VGAESNTITISONVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIEN 1279 1	1280 EYEVLYLRPLAGVYRSLK-KQLENNVMTFNVNKDILNSRFNKRENFKNVL	DD 1594 AQEKIRINAEENTVLKSKLEDIERELKDKQAEIKSNQEEKELLTSRLKELE 1644	QY 1330 ESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGY 1385	1645QELDSTQQKAQKSEEERRAEVRKFQVEKSQLDEKAMLLETKYNDLVN-	QY 1386 YKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV 1436 ::
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entomopoxvirus
.sion 21-Jan-2000 #text_change 21-Jul-2000
EIEKLAKELDNLKAENSKLKEANEDRSEIDDLMLLV 1748
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CLKLVSSDEKQLIEQIYKNIN--NKEIE------ 198
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SNTKITNIQQLL------ESSLTDFNNAN 356
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Pred. No. 4.2e-08;
'; Mismatches 430; Indels 490; Gaps
                                                                                                                                                                                                                                        Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
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99102612; PMID:9847359
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reticulocyte-binding protein 1 - Plasmodium vivax C;Species: Plasmodium vivax C;Species: Plasmodium vivax C;Species: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995 C;Accession: A42771 R;Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W. Cell 69, 1213-1226, 1992 A;Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites. A;Reference number: A42771; MUID:92315338; PMID:1617731 A;Accession: A42771 MUID:92315338; PMID:1617731 A;Accession: A42771 A;Status: preliminary A;Molecule type: DNA A;Residues: 1~2829 <GAL> A;Residues: 1~2829 <GAL> A;Note: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)
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	1655		805	ον
	804	PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL	745	η γ ₀
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	1545		1486	Db
	687	MPKVESLINE	665	Qy
	664 1485	E-KKROLILKNV-ELKHNI	630 1428	ду Фу
	1427	::: : : : : : : : :	1368	Db
	629	ETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKID	(JI	Qy
	577 1367	HHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLIS-KIENE :: : : : : : :	526 1309	Qy Db
	1308	AGKVVEEMNSLKTKIEKLIQETSDDS-QNELVTTSITKHLENAKGYEDVIKRN	1257	дb
	525		467	Qy
	466 1256	VTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKK	407 1222	Qy Db
	1221		1174	Db
	406		358	Оу
	357 1173	NENIKELLDKINEIKNPPPANSGNTPNTLLDKNKK-IEEHEKEIKEI- :: : : : : : : : : : : :	312 1114	Qy Db
	1113	NYQVISENKVTLFKNNSVTYIEAMHSHINTVAHGI-TSNK	1075	дb
	311	EEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKK	254	Оу
	1074	: : :: : RIDEWEDIKRDVDELNV	1015	DЪ
	253		207	Qy
	1014	: :	955	Db
	206		174	Оу
	954		898	Дb
	173	LKHRVRNYLLTIKELKYPQLF-DLTNHMLTLCDNIHGFKYLIDGYEE	115	Qγ
87;	Gaps	Query Match 5.7%; Score 477; DB 2; Length 2829; Best Local Similarity 20.9%; Pred. No. 1.8e-07; Matches 372; Conservative 300; Mismatches 617; Indels 490; Ga	Query M Best Lo Matches	7 H 0

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RESULT 35
T18427
T18427
T18427
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18427
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: 218935
A;Accession: T18427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3724 <LAW>
A;Cross-references: EMBL:298547; NID:e1325376; PID:e1325379; PIDN:CAB11104.1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYT----KEPS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEHPDEQNQS-----LNKNKCLTGTNKKEK------YMIPKGTEYQDKEKES 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNATKEEEKKKLYQA--QYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYK--LNF----YFDLLRAKLNDVCANDYCQIPFNL----KIRANELDVLKK---
                          KLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNF---SVFFNKKKE--
                                                                                            ESKRKKLEEDINKL-
                                                                                                                           DNNINNIYDESINNIYDE$INNIYDESI----NNIYDESINNIYDENINNIYDENINNIYD
                                                                                                                                                         ----NIYQELIG---QKSSENFYEKILKDSDTFYNESFTNFVKSKA-----DDINSLND
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                                                          ENTINNIYDEGINKICDDN LENKNIKTTNDIVQVEENNESIEKNELMISLNKDINNTYNM
                                                                                                                                                                                                                                                                                                                                                           ----YLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNI
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RESULT 36
S38173

Myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae)
MyAlternate names: protein YKR095w; protein YKR415
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C; Accession: S38173; S40647; S31207
R; Baladron, V; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcianterista.
A:Experimental source: strain S288C
R:Koelling, R.; Nguyen, T.; Chen, E.Y.; Botstein, D.
Mol. Gen. Genet. 237, 359-369, 1993
A:Title: A new yeast gene with a myosin-like heptad repeat structure.
A:Reference number: S31207; MUID:93247549; PMID:8483450
A:Accession: S31207
A:Molecule type: DNA
A:Residues: 1-300,'A',302-1875 <KOE>
                                                                                                                                                                                      A;Residues: 11875 <BAL>
A;Cross-references: EMBL;Z28320; NID:g486586; PID:g486587; MIPS:YKR095w
A;Experimental source: strain $288C
R;Bou, G; Esteban, P.F; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, Yeast 9, 1349-1354, 1993
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae A;Reference number: $40644; MUID:94205265; PMID:8154186
A;Accession: $40647
                                                                                                                        A;Cross-references: EMBL:X73541; NID:g450550; A;Experimental source: strain S288C
                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1875 <BOU>
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A; Accession: S38173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDE 1549
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Database, March 1994
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     IQIYTAADKEVNNSTNGPGLNNIL-----ITLRRERDILDTKVTVAERDAKMLRQKISL
                                     DKPEVSANDDTSHSTN---LNNSLKLFENILSLGKNKNIY--QELIGQKSSENFYEKI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENKPDEKILEVSDIVKVQVQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 289;
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A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g171959
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                                                                                                     QNNNKEVEAVKSEYESKLSKIQNDLDQQTIYANTAQNNYEQELQKHADVSKTISELREQL
                                                                                                                                                                                                                                                                  VPEAKAQVPTPPAPVNNKTENVSKLDYL-EKLYEFLNTSYICHKYILVSHSTMNEKIL--
                                                                                                                                                                                                                                                                                                                                                                     EKKNIKTEGOSDNSEPSTEGEITGOATTKPGOQAGSALEGDSVQAQAQEQKQAQPPVPVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNEIYDSKFNNNIDLTNFEK-MMGKRYSY-----KVEKLTHHNTFASYENSKHNLEKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLCDNIHGFKYLIDGYE-EINELLYKLNFYFDLLRAKLNDVCANDY----CQIPFNLKIR
                                                 YEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVK-----TLSSSSMQPLS-----LTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                         QTDIEKLQYKVKSLEKEIEEDKIRLHTYNVMDETINDDSLRKELEKSKINLTDAYSQIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKSKQSLQKIESETVNEAKEAIITLKSEKMDLESRIEELQKELEEL-KTSVPNEDASYS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLK------KN
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                                                                                                                                            KQYKITKEE-ESKLS----SCDPLDLLFN-IQNNIPVMYSMFDSLNNSLSQLFMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SNTLDLTKAENDQLRKRFDYLQNTILKQDSKT-HETLNEYVSCKSKLSIVE
                                                                                                                                                                                                              -TDEKTSLEDKISLLKEQMFNLNNELDLQKKGMEKEKADFKKRISIL
                                                                                                                                                                                                                                                                                                                      ------LQQTNSKLD-ESFKDFTNQIKNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 474.5; DB 2; Pred. No. 1.4e-07;
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					Quer Best Matc	C; Speci C; Date: C; Date: C; Agalin R; Galin Cell 69 A; Title A; Tefer A; Access A; Statu A; Rolec A; Molec A; Molec A; Cross A; Exper C; Genet A; Gene:	Db RESULT B42771 reticu	₽				
616 250	186 556 217	441 138 496	385 85	272 1	he T	C;Species: Pl C;Date: 12-Ma C;Accession: A C;Accession: A R;Galinski, M Cell 69, 1213 A;Title: A re A;Reference n A;Accession: A;Actaus: pre A;Molecule ty A;Residues: 1 A;Cross-refer A;Genetics: A A;Genetics: RBP2	471 39	02	964 412	904 361	886 301	,828 241
KVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLK 675 :: :	TTQNALGERENA LKYYKNLISKIENEIETLVENIKKDEEQLFEKK	KNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEI 495 :: : : :	NIDISAKVETKESTEDNEYPNGVTYPLSYNDINNALNELNSFGDLINFDYTKEPS 440	VLEKRIDTLKKNENIKELLDKINEIKNPPPÄ 	Match 5.4%; Score 457.5; DB 2; Length 1252; Ocal Similarity 21.1%; Pred. No. 2.9e-07; Similarity 228; Mismatches 458; Indels 455; Gaps 71;	asmodium vivax r-1933 #sequence_revision 12-Mar-1993 #t B42771 .R.; Medina, C.C.; Ingravallo, P.; Barnw -1226, 1992 ticulocyte-binding protein complex of Pl umber: A42771; MUID:92315338; PMID:16177 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771 B42771	QIEAANQKVKEI 482 .te-binding protein 2 - Plasmodium vivax (fragment)	VGKYKMQIKKL 1	NESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKK 1023 : : :	KPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFY 963	VKTLSSSSMQPLSLTPQD 903	-NIQNNIPVMYSMEDSLNNSLSQLFMETYEKEMVCNLYKLKD-NDKIKNLLEEAKKVSTS 885

	.531QCVKK 1535 : : 169 TLESIKK 1175	Оу 15 рь 11	
LLDGNLQGMLNISQH- 1530 : ::: IVTNQHSINNVKDKLKGKLQELIDADSSF 1168	SHÖN	Qy 14 Db 11	
NYLKTIQDKLADFKKNNNFVGIAD ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	1429 NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTI	Qy 14 Db 10	
	DVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPF- ; ; ; ; ; ; ; ; ; ; NVKAYLAYIKKNYEDTVQDVLTLNEHFNTKQVSNHEPTNFD	Qy 13 Db 10	
LNKEKRDKFLSSYNYIKDSIDTDINFAN 1380	1329 LESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSI- : : : :	Qy 13 Db 9	
NNVMTENVNVKDILNSRENKRENFKNV 1328 : : HEHVQSKSEPVNPAL-SEIEKEET 952	1273 ILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENF 	Qy 12 Db 8	
PIFGESEEDYDDLGQVVTGEAVTPSVIDN 1272	1219 HVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN	Oy 12	
SDTLEOSOPKKPA-ST 1218 : : : NQIYLKVVLINQYKNKISSIKSKEEAVSV 845	1182 LESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPA-ST	Qy 11 Db 7	
IAELKEVIKNKNYTGNSPSENNTDVN-NA 1181 : : :	1123 KVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVN-	Qy 11 Db 7	
YYNGESSPLKTLSEESIQTEDNYASLENF 1122 ; : YVGIKITPELALTE744	074TENTLEN-TKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENF	Qy 107 Db 70	
KLNSLNNPKHVLQNFSVFFNKKKEAEIAE 1073 : :	034 KLTL	Qy 10 Db 6	
K-LKLERLFDKKKTVGKYKMQIK 1033	AQKE	Qy 9 Db 5	
KILKDSDTEYNESETNEVKSKADDINSLND-ESKR 987 : : : : : : : : SINSTVGNESSLENNEDLNQYDENKNINDYENKM 580	951 FYEKILKDSDTFYNESFTNFVKSKADDINSLND-ESKR 	Qy 9 Db 5	
SLGKNKNIYQELIGQKSSEN 950	G :	Qy 9 Db 4	
NILEEAKKVSTSVKTLSSSSMQPLSLTPQ 902 	GG	Оу 8 Db 4	
KLSSCDPLDLLFNIQNNIPVMY-SMFDSL 843	CDPLD	Qy 7 Db 3	
PTPPAPVNNKTENVSKLDYLEKLYEFLNT 784	, Š	Qу 7 рь з	
SDNSEPSTEGEITGQATTKPGQQAGSA 724 : : : : IEDAEKQASTKVELFHKHETTISNIF 351	676 VFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPG	Qу 6 Db 2	

Qy 662 YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQA 721 ::: :: : : :	604 PDEKTLEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEP 661 : : : : : : ::::::::::::::::::::::	QY 560 VEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENK 603	QY 505 DLTNFEKMMGKRYSYKVEKLTHHNTFAS-YENSKHNLEKLTKALKYMEDYSLRNIV 559	476 DRSKSLNDITK-EYEKLLNEIYDSKFNNNI	Qy 418 NALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINE-IKEKIKIEKKKIESDKKSYE- 475	QY 384KNIDISAKVETKESTEDNEYPNGVTYPLSYNDIN 417	QY 325 IKNPPPANSGNTPNTLLDKNKKIEBHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN- 383	QY 265 KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINE 324	QY 214 LDVLKKLVEGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTID 264 Db 648HIKCVSSFNNTSDDISSHSSVNKKEPFFALKNNSIRHIPKENNIIYTSGKSFNHVQD 704	QY 162 HGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANE 213	QY 102 SGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNI 161	Query Match 5.4%; Score 453.5; DB 1; Length 2485; Best Local Similarity 20.7%; pred. No. 8.5e-07; Matches 361; Conservative 257; Mismatches 579; Indels 543; Gaps 84;	A;Gene: PFB0150c C;Superfamily: malaria parasite serine/threonine-specific protein kinase PFB0150c; prote C;Keywords: phosphotransferase F;2087-2352/Domain: protein kinase homology <kin></kin>	Residues Cross-ref Experimer Genetics	99021743; PMID:9804551 Id sequence not shown; translation not	er, M.J.; Tettelin, H.; Carucci, D.Jer, M.; Salzberg, S.; Zhou, L.; Sutt 282, 1126-1132, 1998 : Chromosome 2 sequence of the human	H71621 H71621 H71621 H71621 H71621 H71621 H71621 H71621 Serine/threonine-specific protein kinase (EC 2.7.1) PFB0150c - malaria parasite (Plasm C; Species: Plasmodium falciparum C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: H71621	RESULT 40
RESULT 41 T18444	QY 1557 LNYKQEGDKCVENPNTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDG 1614 :: : :: : : : :	QY 1497 KFLSTGMVFENLAKTYLSNILDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCL 1556	1438 HLEAKVLNYTYEKSNY-FYKIKELNYLKTIQDKLADFKKNNNFYGIADLSTDYNHNULTT	1378 FANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVI	OY 1319 FNKRENFKNVLESDLIPYKDLTSSNYVVKDPYK-FLNKEKRDKFLSSYNYIKDSIDTDIN 1377	QY 1259 VVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSR 1318	QY 1221 GAESNTITTSQNVDDEVDDVIIVPIFGESEEDXDDLGQ 1258	QY 1164KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHV 1220 DD 1619 NGTCNSVGDKETEKNNEKNNEKNNEKNNEKNNEKNNEKNNEKNNEKN	1124 V 1568 I	7 TLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK : : : : :	4 SKLNSLNIP	0 0	943 IGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDIN : : : : : : : : : : : :	QY 883 STSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL 942 : : : : : : : :	Qy 836 MYSMFDSLNUSLSQLF-MËIYEKEMVCNL-YKLKDNDKIKNLLEEAKKV 882 :: :: :: :: :	Qy 782 LNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLENIQNNIPV 835 :: : : : : :	Db 1134	

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hypothetical protein C0385c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18444
R;Lawson, D.; Bowman, S.; Barrell, B.
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A;Introns: 1597/3; 1625/3
A;Note: C0385c
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A; Accession: T18444
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EKKKYVHDHRKDNIIKRNKEFINIYKGKRNYANVEIGSEVCNNKVNVKGDDNKMMVENKQ
                                                                       DMLQKENKILTNNDKKKTFLLSKSKNITS-NVLSSKIPGTLSTKKLNATIKTIKKDVTDN
                                                                                               --YKQENK------QEPYYLIVLKKEIDKLKVFMPKVESLINEEKKN--IKT--EGQSDN 700
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                                  SEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQ-EQKQAQPPVPVPVPEAKAQVPTPP
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20.3%;
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Pred. No. 7.9e-07;
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.y, August 1997
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Qy	Qy Db	Дb	Оу	Qy	Оу	Оу	Оy	Qу	Qу	Оy	Оy	Qу	Qу
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IDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIODKLADFKKNNNFVGIAD 1484	IDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDK 1.	KDILNSRFNKRENFKNVLESDLIPYKDLISSNYVVKDPYKFLNKEKROKFLSSYNYIKDS 1 -	- '	QPKKPASTHYGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQ 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	TGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQS	SIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNY 1: :	NPKHVLQNESVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEE 1	RLEDKKKTVGKYKM-QIKKLTLLKEQLESKLNSLN 1 : :	FTNFVKSKADDINSLNDESKRKLEEDINKLKKTLQL-SFDLYNKYKLKLE 1:	ANDDTSHSTNL-NNSLKLFENILSLGKNKNIYQELIGQKSSENFYE-KILKDSDTFYNES 966 : : :	LYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVS- 908	QYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCN 862	APVNN-KTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILK 805
	1431 1508	1458	1311 1428	1258 1380	1210 1323	1166 1268	1108 1222	1050 1169	1016 1109	966 1049	908	862 933	805 895

RESULT 42 S28261

S28261

Centromere protein E - human

N;Alternate names: centromere 312K protein; kinesin-related protein CENP-E

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001

C;Accession: S28261

R;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.

Nature 359, 536-539, 1992

A;Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis

A;Accession: S28261; MUID:93024922; PMID:1406971

A;Accession: S28261

A;Accession: S28261

A;Residues: 1-2663 <YEN>

A;Cross-references: EMBL:Z15005; NID:g29864; PIDN:CAA78727.1; PID:g29865

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A;Gene: GDB:CENPE
A;Cross-references: GDB:361164; OMIM:117143
A;Cross-references: GDB:361164; OMIM:117143
A;Map position: 4q24-4q25
C;Superfamily: centromere protein E; kinesin motor domain homology
C;Superfamily: centromere protein E; kinesin motor domain homology
C;Reywords: APP; colled coll; microtubule binding; mitosis; nucleotide binding;
F;7-335/Domain: kinesin motor domain homology <KMOT>
F;86-93/Region: nucleotide-binding motif A (P-loop)
F;486-2183/Domain: colled coll #status predicted <COI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 LIDGYEEI-----NELLYKLNEYFDL--LRAKLNDVCANDYCQI-----PFNLKIR-ANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 5.3%;
Local Similarity 18.4%;
                                                                                                                                                                      ILKN----VELKHNIHVDNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEK---
QTKEELKIAHIHLKEHQETIDELRRSVSEKTAQIINTQDLEK-----
                                   EQKQAQPPVPVPVEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVS 795
                                                                                                                                                   LSRTCDRLAEVEEKLKEKSQQLQEKQQQ----LLNVQEEMSEMQKKINEIENLKNELKNKE 1171
                                                                                                                                                                                                                                                                  VENIKKDEEQLFEKKITKDEN-----KPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQL
                                                                                                                                                                                                                                                                                                        TGETKDEFQQKMVGIDKKQDLEAKNTQTLTADVKDNEIIEQQRKIF-SLIQE-KNELQQM
                                                                                                                                                                                                                                                                                                                                             ---SKHNLEKLTKALKYMEDYSLRNI------VVEKELKYYKNLISKIENEIETL
                                                                                                                                                                                                                                                                                                                                                                                  KSDIHDT-VNMNIDTQ------EQLRNALESLKQHQETINTLKSKISEEVSRNLHMEEN 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEQLKEQLENRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESLQIERDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INEIKEKIK-----IEKKK-----IESDKKSYEDRSKSLNDITKEYEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEQKYKMVLEENERMNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQEYIDSQK--LENIKMDLSYSLESIEDPKQMKQTLFDAETVALDAKRESAFLRSENLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINLLREIDESVCSESDVFSN
                                                                        LTLEHMETERLELAQKLNENYEEVKSITKERKVLKELQKSFETERDHLRGYIREIEATGL 1231
                                                                                                             ---KNIKTE----GQSDNSEPSTEGEITGQATTKPGQQAGSALEGD-----SVQAQAQ
                                                                                                                                                                                                                             LESVIAEKEQL --- KTDLKENIEMTIENQEELRLLGDELKKQ - QEIVAQEKNHAIKKEGE 1114
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•		w	RESULT 43 B71612	RES
	KIKEEQHECI 2153		2144	DЬ
	KQEGDKCV 1567	;	1560	Оу
2143	MESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFHRIMKKLKYVLSYVT		2088	Db
1559	SGCFRHLDEREECKCLLNY	. E	1525	Qy
2087	IRIVAKERDELRRIKESLKMERDQFIAT LREMIARDRQNHQVKPEKRLLSDGQQHL	E	2030	Вb
1524	MVFENLAKTVLSN	NH	1490	Qy
2029	NFQLTKKLHESL		1973	Db
1489	LADEKKNNNEVGIADLSTDY		1437	Qy
1972	EIQQE-LKTARMLSKEHKETVDKLREKISEKTIQISDIQKDLDKSKDELQKKI		1921	Db
.1436	GENEKYLPFLNNIETLYKTVNDKIDLFV		1377	Qy
1920	VMKERDNLRRVEETLQETKARDL	ro -	1886	Db
1376	NYIKDSIDTDI		1317	Qy
1885	KANEHOLITIKKDVNETOKKVSEMEOLKKOIKDOSLTLSKLEIENLNLAQELHENLEEMK		1826	Дb
1316			1279	Qy
1825	KAQDLKIQEELRIAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEKIQEL		1766	Db
1278			1241	Qy
1765	KENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEISNMQKDLEHSNDAL		1706	₽.
1240			1196	Qy
1705	ETENIRLTQI LHENLEEMRSVTKERD	н.	1663	Db
1195	GLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDV		1136	Qy
1662	LKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCEIEHLKEQFETQKLNLEN		1609	DЬ
1135	ILLKHYKGLVKYYNGESSPLKTLSEESI-QTEDNYASLENFKVLSKLEGKLKDN	1-3	1077	Qy
1608		15 •	1549	DЬ
1076		٠ 🛪	1034	Qy
1548	/NLSEKETETSTIQKQLEAINDKLQNKIQEIYEKEEQLNIKQISEVQENVN		1489	Ъ
1033			990	Qy
1488	-QESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIVAKHLETEEELKVAHCCLKE	,	1431	рь
989		G	944	Qy
1430	KQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLGLSKRL	ω –	1384	Db
943	EVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELI		893	Qy
1383	LRLNEKFQESQEEKSLTKERDNLKTIKEALEVKHDOLKEHIRETLAKIQESQ		1331	Db
892	KVSTSVKTLSSS		847	Qy
1330	HTKLQEEIPVLHEEQELLPNVKKVSETQETMNELELLTEQSTTKDSTTLARIEMER		1275	Db
846	ILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNS		796	Qy

o 4	VQVQK-VLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLVQVQK-VLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYL		Qy G
	KITKDENKPDEKILEVSDIVK	y 596 b 863	P 29
FEK 595 VRK 862	KALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEK : : : : :	у 545 b 803	Db Qy
KLT 544 LE 802	NNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKH-NLEKLT	y 501 b 748	DB Qy
F 500 	RSKSLNDITKEYEKF : : :	y 477 b 688	P Q
ED- 476 : NEM 687	NELNSFGDLINPFDYTKEPSKNIYTDNERKKF-INEIKEKIKIEKKKIESDKKSYED- ::	y 421 b 631	ρ δ
NAL 420 NIL 630	YLREKNKNIDI-SAKVETKESTEPNEYPNGVTYPLSYNDINNAL	y 378 b 572	рb
LEY 377 KEY 571	TNODVNININISLVKNMKKHIEOKEFFKRNINKNLFLNVCILLFKKONFLLYTHDIKKEY	y 354 b 512	Db Qy
353 RYK 511	KELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKE	y 316 b 459	Дb
ENI 315 † 3NI 458	KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENI 	y 265 b 420	DP QA
264 LFD 419	LDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTID	y 214 b 376	Db dq
213 HYF 375	YLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANE	y 166 b 323	dg VQ
3FK 165	SDSDAKSYADLKHRVRNYLLTIKELKYDQLFDLTNHMLTLCDNIHG	y 118 b 273	Оу
Gaps 94;	1tch 394	Query Ma Best Loc Matches	
21-Jul-2000 21-Jul-2000 .; White, O.; Smith, H.O. asmodium falciparumion not shown .ion pro:9384521	1998 #sequence_revision 13-Nov-1998 #text_change 1612 ; Tettetlin, H.; Carucci, D.J.; Cummings, L.M.; Ar Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R. 26-1132, 1998 some 2 sequence of the human malaria parasite Plaber: A71600; MUID:99021743; PMID:9804551 1612 1612 1612 1612 1612 1613 1612 1613 1614 1615 1615 1615 1616 1617 1618 1618 1619 1619 1619 1619 1619 1619	C; Date: 13-Nov- C; Accession: B7 R; Gardner, M.J; Pertea, M.; Science 282, 11 A; Title: Chromo A; Reference num A; Accession: B7 A; Status: preli A; Molecule type A; Residues: 1-3 A; Cross referen A; Experimental C; Genetics: A; Gene: PFB0555 C; Superfamily:	C>C>D>D>D>D>D>D

1573	6 LLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT	151	Qy
1808	60NEEQKNNELISYPYNNMLQNNIIFVKFFLYTQNLLQIIFQNNYIFFLSD	176	Db
1515	_	146	Qy
1466 1759	PELNNLETLYKTYNDKIDLEYIHLEAKVLNYTYEKSNVEYKIKEL-NYLKTI : : : :	1416 1712	Оу
1711	9 VFNKPFDNNNNNNNNNNNFMLNYFNYIPENNNNNYRMDIKKRYPPESYDNNYYM	• 0	ga
1,415	YIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYL	136	Qy
1658		162	Db
1359	LENNYMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD	1300	Qy
1623	O DVFNEIMRNIIINHNSLIKDHNDMCTKKKRINIFQISSPATSEQ	158	Db .5
1579	6 SYRGEEKDTLDVINGETATIONINGSINGL	154	Ov Db
1243	4 SYKKFLPBGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIV	118	QΥ
1545	EHNIMMDVHMKSHLHHDIDVYYGHDNSYNNI-YQKIIK	149	Db
1183	DNLNLEK-KKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALE	1134	Qy
1496	NEDNEFESIESKYINKIEVEIYSSSSSSTSSNSSEVENVSKEYMMKMCISIINNMIGVVK	1437	마
1133	3TLLKHY-KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLK	108	Qγ
1436	91 NREKNINIKKLVKLEFISFYKYLKNYFLQIYYHFFYNQIYNRKNY	139	дд
1082	MQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTK	1030	Qy
1390	ICTSLLLKIFKRIIKKKSNSYFLFNIYKAFENDIKLILDSINILIKKWYVWTFKNCDNIF	133	da ;;
1029	KKKTVGKYK	992	Ωу
1330		1271	ДĎ
991		96	Qy
1270	NNSSNNSSNNSSNNSSNNSSGRNNSSDEVVVDPYDYNNYYECKDSNKFGVVVNYFYA	1213	рь
965	SHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNE	914	Ωу
1212	DNNKYNDGNTFLSSQDEEKSKSFDSSDSCSVDEKESSKGLYGNDFVNSSDHN	1161	ф
913	EEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDT	86	Qy
1160	DIKENFRIDISFLKIFFLLNDVRQINLNESNGRKDKLESKAKRRIQKLDVHRYTYNEN	1103	DЬ
867	DLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLK	824	Qy
1102	4VSNLYRDIENEYDENHLERRKDRNVFSSNMNDDKKYNNLSDFKYTKEN	105	Db
823	DYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPL	773	Qy
1053		1028	DЬ
772	13 ATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKL	7]	Qy
1027	RFQIMIVRCLSFLLKKKNINKLNAYIFQLFSYLENDQININEKGM	983	Db
711	669	0	V

Db

1809 FL-----FINYKKKEYIEEKKNGNQNV-----INIKDEDKHITNIK-DGDKHITNIKDG 1856

Cipectes; Mycoplasma genitalium Cipectes; Oneseria, MSC18 - Mycoplasma genitalium Cipectes; Oneseria, MSC18 - Mycoplasma genitalium Riffaser; C.M.; Godoyne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Pielschmann, R.D.; K. A.; Mychert, J. Guyden, D.; Utctarback, T.K.; Saudek, D.M.; Philips, C.A.; Merrick, J. C.A.; Mychret, J. Guyden, D.; Utctarback, T.K.; Saudek, D.M.; Philips, C.A.; Merrick, J. Science 270, 397-403, 1995 A.; Pielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Pielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Canaritalia; Gene complement of Mycoplasma genitalium. A.; Science 270, 397-403, 1995 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Canaritalia; Gene complement of Mycoplasma genitalium. A.; Science 270, 397-403, 1995 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Canaritalia; Gene complement of Mycoplasma genitalium. A.; Science 270, 397-403, 1995 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce and A.; Fielsernce not shown; translation not shown A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce and A.; Fielsernce not shown; translation not shown A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028346; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028340; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028340; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028340; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028340; PMID:91045903; PIIG:MSC118 A.; Fielsernce number: A64200; MUID:96028340; P	Qy 1574 CNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLPDGIFCSSSNFL 1623 Db 1857 DKNITNIKDDDKNITNMKKKNNKNYLTILMYNSQECSFYYSIFNTLI-NDYNFL 1909 RESULT 44
VSHSTMNEK	694 K 705 T 750 N

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A;Reference number: Z18248; MUID:98365468; PMID:9700162
A;Accession: T14867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1738 <RIV>
A;Cross-references: EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC34582.1
C;Genetics:
A;Gene: abpD
A;Introns: 173/2; 1680/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interaptin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14867
R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J. Cell Biol. 142, 735-750, 1998
A;Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in
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Best Local Sim:
Matches 302;
1011 IQQLQSQLNEQRQ-----QQSNQLSEKDQQLNQLIEKNQFDQKEQQLKQQSIENDLFEK 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYQAQYDLSIYNKQLE-EAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNT
                                               MPKVESLINEEKKNIKTEGQSDNSEPSTEGEIT-----GQATTKPGQQAGSALEGD----
                                                                                                                                                                                                                                                                                                                                                                                                           SKSLN-DITKEYEKL---LNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFDYTKEPSKNIYTDNERKKFINEIKEK----IKIEKKK----IESDKKSYEDR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND----INNALNE---LNS-FGDLIN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQTLNQQETHRLTQQLYQINTDYNEKQTQLQSEIKD-NQTIN-----EQLNKQLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEEINELLYKL-NFYFDLLRAKLNDVCANDYCQIPFNLKIRA-----NELDVLK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THLQDQLTEQQ-QQYQEKSLKLVHLELELQE-KSHQLVDKSHQLSTM-------
                                                                                                                                                                                  NOQIEKIQFDQQEFSKQNSINIELVNEKNEKLIQLQQDYDQLKQQNRSNDEKDENDLIEK
                                                                                                                                                                                                                                                                            KDHQDQLELLEKQLKQLQQEYDQLNETNQSIENQLNQQNLINKENLNEKEQELLKLQNQL
                                                                                                                                                                                                                                                                                                                                                                 QLSSNSNIDQQLQSTIIELSELKEQKELNDSKLIEKEKQL-QQLQQEFDQLNEKN----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKDKEIE----KLSNQQEQQQDEKINNLLLEIKEKDCLIERINQQLLENIDLNSKYQQLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLTIEQTSQLQDRIKQLINELQERDDKFIEFTNSSNQSLADNQRVIDQLTN----EKQSI 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QATNSELMEKIGGLMNDLTDIPTQDIKEKD--EIIANLKIESEKNLKCFQDDFNALQSRY
                                                                                         ENQLKSIQNELN-----QLIEKN-ESDHK------EQQLKQQSIENDLIEKENQ-----
                                                                                                                                      QVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVF
                                                                                                                                                                                                                               ETLVENIKKDEEQLFEKKITKDE--NKPDEKILEV-----
                                                                                                                                                                                                                                                                                                                         ENSKHNLEKLTKALKYME------DYSLRNIVVEKELKYYKNL-----ISKIENEI 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFENFK-----LNSSKEKENQLNELQSKQDERFNQLNDEKLEKEKQLQSIEDEFNQYKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%; Score 438; DB 2; 1 ilarity 21.0%; Pred. No: 1.7e-06; Conservative 254; Mismatches 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1738;
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729SVQAQAQEQKQAQPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
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RESULT 46

R:Kimura, E.; Mattei, D.; di Santi, S.M.; Scherf, A. Gene 91, 57-62, 1990
A;Title: Genetic diversity in the major merozoite surface A;Reference number: PQ0120; MUID:90382698; PMID:2205540
A;Accession: PQ0120. major merozoite surface antigen - malaria parasite (Plasmodium falciparum) N;Alternate names: gp195, PMMSA, PSA C;Species: Plasmodium falciparum C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jun-2000 C; Accession: PQ0120 - malaria parasite (Plasmodium falciparum) (isolate PSAantigen of Plasmodium

A; Molecule type: DNA A; Residues: 1-144 < KIM>

PID:g552211

falcı

C;Superfamily: major meroz
C;Keywords: glycoprotein; A;Cross-references: GB:M32111; NID:g160490; PIDN:AAA29701.1; C;Superfamily: major merozoite surface antigen Query Match Best Local Similarity 5.2%; surface antigen 8; Score 435.5; Pred. No. 1.2 5; DB 2; 1.2e-07; hes 24; Indels Length 144; 21;

30 KKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGS-VASGGSV 88

Mismatches

Gaps

5

Qy

Matches

Conservative

	MATCHES 317; CONSERVATIVE 255; MISMATCHES 530; Indels 458; Gaps 70; MATCHES 317; CONSERVATIVE 255; MISMATCHES 530; Indels 458; Gaps 70; OY 118 SDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFKYLIDGYEEINEL 177	references: EMBL: X95601; N references: EMBL: X95601; N cs: Imp3 c code: SGC3 c code: SGC3 amily: surface-located men ds: duplication; membrane omain: signal sequence #st 2/product: surface-locatec 2/product: surface-locatec 2/product: surface-locatec 2/product: stratricopeptic 26/Domain: tetratricopeptic 120/Domain: tetratricopeptic	RESULT 47 JC6009 JC6009 JC6009 Surface-located membrane protein lmp3 precursor - Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 21-Jul-2000 C;Accession: JC6009 R;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. J;Bacteriol. 178, 2775-2784, 1996 A;Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system A;Reference number: JC6009; MUID:96213016; PMID:8631664 A;Accession: JC6009	Db 1 KKLEALEDAVLTGYGLFHKEKMILNEEEITTKGASAQGSGPSGTPSGTSG 51 Qy 89 ASGGSVASGGSGNSRRINPSDNSSDSDAKSYADLKHRVRNYLL 137
Qy 1310 NVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE- 1356 Qy 1310 NVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE- 1356	1080NTKILLKHYKGLYKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLK	Qy 886 VKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNI-YQELIG 944 Qy 886 VKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNI-YQELIG 944 Qy 886 VKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNI-YQELIG 944 Qy 945 QKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINK 996 Qy 945 QKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINK 996	483 -S 711 GQ 716 Q 528 NQ 766 TE 1: 579 TD 826 LF	550 MEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKI

1164		, ;
0	558 IVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKD 600 : :: : :: ::	p Qy
557 1104	KMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRN	Db Qy
0	462 IEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFE 510 	Db Oy
161	417 NNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIK 41	Db Qy
A 4	384 KNIDISAKVETKESTEPNEYPNGVTYPLSYNDI 416	Db Qy
& W	353EIKEIAKTIKFNIDSLFTDPLELEYYLREKN 383 	Qy Db
ω Ν	322 INEIKNPPPANSGNTPNTLLDKNKK	Фу
8 1	263 IDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLI-SVLEKRIDTLKKNENIKELLDK 321 	ОУ
ω Ν	226 -KPLDNIKDN VGKMED YIKKNKKTIENINELIEESKK 262 : : : :	Оy
5 25	172 EBINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANEL-DVLKKLVFGYR 2: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	ОУ
.71	119 DSDAKSYADLKHRVRNYLLTIKELKYPQLEDLTNHMLTLCDNIHGFKYLIDGY 171	pb Qy
88 8 ,	ery Match 5.2%; Score 434.5; DB 2; Length 2819; st Local Similarity 19.7%; Pred. No. 3.8e-06; tches 371; Conservative 299; Mismatches 614; Indels 599; Gaps	Quer Best Matc
(Strain UAB CT	RESULT 48 A90551 A90551 C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Cate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Cate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Cate: A00551 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Myco A;Reference number: A99551 A;Accession: A90551 A;Accession: A90551 A;Accession: A90551 A;Residues: 1-2819 < KUR> A;Cross-references: GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:GN0015 A;Cross-references: GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:GN0015 A;Genetics: A;Genetic code: SGC3	RESULT A90551 CONSETV C. Speci C. Date: C. Date: C. Chambs R. Chambs Nucleic A; Title A; Macces A; Statu A; Molec A; Resid A; Cross A; Exper C. Genet A; Gene: A; Genet

1516	LNYLKTIODKLADFKKNNNFVGIADLSTDYNHNNLLTKFLS-TGMVFENLAKTVLSNL	1460	Ov
2223	KOSLSKIVALIASDPOTINLVNKVIDDIFKNHKNYA-SKANLNEILAEFLTTHKN	2170	Db
1459	PFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKE	1411	Qy
2169	LFEKLLKNTSVQNFVKDKFIENISKSIPIEQNN	2137	DЬ
1410	(F)	1351	Qy
2136	: : ::: : : : LFEVLSIILKSNILDSKSINNKEYIQKVKT	2080	Ъ
1350		1296	Оу
2079	GFALNLLQEQNLELSKDELSLVSNITSGAIDALSTSNIVEKILEVFLAEVKKQ	2027	Db -1
1295		1250	Qy
2026	EFFKSLVNNIISNNQNYKNANNYLDLIVSFIEKNKNLVTQYFKKIAPKIASDSMLKTEVN	1967	Db
1249		1197	Qy
1966	GQMLLRVFKNTDLLNKFLDPVLQNINFIDQDQKDSKTKNENLRNASKQILVFVLQNEDTL	1907	Db
1196	HHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVA	1151	Qy
1906	TKVEIFNFSSLLKPIMDQKDNYFSLVKTLATINWKLMESQNTDALKNAL	1858	дb
1150	KLSYLSSGL	1099	Qy
1857	-LKKSKITLQNDEIDSIVNFVNESLVVLEKTDLIDKLYDLVVSSFNAKVSDK	1807	Db
1098	KKEAEIAETENTLENTKILLKHYKGLVKYYNGE	1048	Qy
1806	VVSQKE-EYSKLNSYQEILYKFLSSNKNETLNFFKKQIGEIKNSKLINPLAKSFIESE	1750	Db
1047	z	997	Оу
1749	SISSILRVELRKEKALELMLKKQFRNFELHDIKVDDAINLIKFIFRDNQVIDFIETTINR	1690	Дb
996		955	Оy
1689	KDSKSTSLEFSTFMKKSISEFLDAENNYLALFKKVLSSNLLSTQSDQSSFTK	1638	Db
954	GKNKNIYQELIGQKSSENFYEK	912	Qy
1637	FKNIIKSFITKNLMTSDSSITEEEINTIVKSAHELISIVDSSNFLNQLLKDFFALLEKNK	1578	ДĎ
911		872	Qy
1577	KFSAQIIDTIFANKNKYLAYENLNDFLIDALVDNKENIINLSSNTLGKIKTDDE	1524	Db
871		817	Оу
1523	IVDKTIDFDSATKSSIVKLIKNVLSDEQNL	1464	ДĎ
816		770	Qy
1463	FGKTNIISNLYDLVLSALSINQESSSVLTKVENITHKALDQQNSYFAVIKTLLSVKEGDV	1404	дь
769		741	Qy
1403	NKETVVNYLKELSFEIKSSNIIQRLLGQTINALVTPNGEKIFSDTELQSLSTLINESLDL	1344	дь
740	QAGSALEGDSVQAQAQEQKQA	690	Qy
1343		1284	рь
689		678	Qy
1283	SQNSESIKNLLKTFTKSALSRDEFYEKTIKVF	1224	Db
677		653	Qy

Qy 561 EKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQ 620		129 KHRVRNYLLTIKELKYPOLFDLTNHMLTLCDNIHGFKYLIDGYBEIN 175		
RESULT 50 REP11606 hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: E71606 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E. R;Gardner, M.J.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.	Db 1111 RAKRLKQEILNAK-NDLSNFTLNHQKNQFTAKDITPKISLLENKLNEINQYLLPIIKEKA 1169 Qy 1359 DKFLSSYNYIKDSIDTDINFANDVLGYKILSEKYKSDLDSIKKYINDKQGENEKYLPFL 1418	Qy 1114 DNYASLENFKV	856 656 892 716 945 776 1005 808	Db 502 QADNLAKSIKEQL

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A; Accession: E71606
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-980 <GAR>
A; Cross-references: GB:AE001417; GB:AE001362; NID:g3845271; PIDN:AAC71942.1; PID:g38
A; Experimental source: clone 3D7
C; Genetics:
A; Gene: PFB0765w
C; Superfamily: hypothetical protein MJ1322
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                                                                                                                           648
                                                                                                                                                       746 VPVPEAKAQVPTPPAPVNN--KTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKI 803
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--INNKKLTTATNMANNNMLMDENLKEKD--KKI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEIKEIAKTIKFNIDSLFTDPLELEYYLREK--NKNIDISAKVETKES--TEPNEYPNGV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KD-----NVGKMEDYIKKNKKTIENINEL---IEESKKTIDKN---KNATKEEEKKKL 278
                                                   KKKEEINKLVEEKSKLEHSH-----VKIQNEMSLLVEQNEKL------KEEMGL 729
                                                                                      LKOYKITK--EEESKLSSCDPLDLLFNIONNIPVMYSMFDSLNNSLSQLFMEIYEKEMVC 861
                                                                                                                                                                                                EIQNKEME-----
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                                                                                                                                                                                                                                                                                                    DELKKTQLILKNV---ELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLI 685
                                                                                                                                                                                                                                                                                                                                       EE-LNEKEIIL-KNKYDK---EINMIIEQYNKKIQEEKDMLNNKIKSMDQTHKNQIEEMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEQLLKDIKDENEKMNEHVNKLQNELIKRELQNKCISKDIEFCKKEKEDKIKNLEDDLLE 396
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EKTIKEKELEIQSLQEKLDETEVEKEDAEKKKKEIEKEMKALQEEKENVESSKNSTEKDK 1262	· K - K F	EYYLREKNKNIDISAKVETKESTEPNEYPNGYTYPLSYNDINNA 419	PPANSGNTPNTLLDKNKKIBEHEKBIKEIAKTIKFNIDSLFTDPLEL 375	LSIVNKQLEEAHNLISVLEKRI-DTLKKNENIKELLDKINEIKNP 328 :	PLDNIKDNYGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEBEKKKLYQAQYD 284 : : : : : :	LIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRK 226 : : : EELKETIDNLKGDLKDSKLKGEDLEV966	RRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYP-OLFDLTNHMLTL-CDNIHGFKY'166 :: :: : : : : : KREBAENALASATAKTGELEAKIQDLEDKISELESKLSAAELDKQELNLKIENLEEDK- 940	atch 5.1%; Score 428.5; DB 2; Length 2139; cal Similarity 20.5%; Pred. No. 4.2e-06; 307; Conservative 233; Mismatches 554; Indels 405; Gaps 58.	C;Senermity: myosin heavy chain; myosin motor domain homology C;Superfamily: myosin heavy chain; myosin motor domain homology kmyosin motor mailto:kmyosin motor mailto:kmyosin motor mailto:kmyosin motor mai	e type: DNA s: 1-2139 <gui> eferences: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB48065.1</gui>	A;Retelence number: Arono A;Retelence number: Arono A;Retelence number: A;Status: preliminary; translated from GB/EMBL/DDBJ	, N. To number: 718865 Co number: 718865	myosin heavy chain - Entamoeba histolytica C;Species: Entamoeba histolytica C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000 C;Accession: T18296		: :: : EEVYKIFSVEKYDMLKKEVGE	TRILLRHYKGLVKYYNGESSPLKTLSBESIOTEDNVASLENFKVLSKLEGK 1131	Y-KMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAE-IAETENTLEN 1080	EHQKEDRKRKDKKKGHSSDKEKYNKEKTKEKSSNILFDEEYIIQLEELRDTGENCFI 873	NSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK 1027	KKKNEEERKKNEEEKKKLEKDKHQFEEEKERMEIY 813	LNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDI 978	SRIAIKDMEEIKKOMEKYEEEKKKNEEERKKNEEERKKNEEERKKNEEE 778

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                                                                                                     SYNYIKDSIDTDI----NFANDVLGYYKILSEKYKSD---LDSIKKYIND-----
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EIGKTQAELKKYQQQVRDDETRMSSLEDEIKKGTDALANKQLELDKVNKQYEKLKKQYK 2126
                                 ----KQGENEKYLPFLNNIETLYKTVNDKID-----LFVIHLEAKVLNYTYEKSNVEVK 1456
                                                                   SIAKVKAKYEAEIEELTTEAEDALKAKMKAEKKAKTSQKKLDELQKTIADYETKEASFNT
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RESULT 52 S48385 hypothetical

protein

YIL149c

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yeast (Saccharomyces

cerevisiae)

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A;Cross-references: GB:Z47047;
C;Genetics:
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A;Cross-references: SGD:S0001411
A;Map position: 9L
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A; Residues: 1-1679 <
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                                                                                                                      CKKKTTLEDFENFKGLAKEKERMLEEAIDHLKAELEKQKSWVPSYIHVEKERASTELSQS
                                                                                                                                                                                       YKLLASTEENKANTNSVTSMEAAREKKIRELEAELSSTKVENSAIIQNLRKELLIYKKSQ
                                                                                                                                                                                                                                                                                                                                                            HNTFASYEN-SKHNLEKLTKALKYMEDYSLRN----IVVEKELKYYKNLISKIENEIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YNKFLLNQNKQLSQSVEEKVLEMKNLKDTASVEKAEFSKEMTLQKNMNDLLRSQLTS 289
                                                   RIKIKSLEYEISKLKKETASFIPTKESLTRDFEQC------CKEKKELQ----M
                                                                                                                                                      YKQENKQEPYYLI-----VLKKEIDKLKVFMPK----VESLINEEKKNIKTE-GQS
                                                                                                                                                                                                                                                          LNCIRILADKLENYEGKODKTLOKVENOTIKEAKDAIIELENINAKMETRINILLRERDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKQLLDES----SEQKNTAKEELNGLKDQLNEERSRYRREID--ALKKQLHVSHEAMREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEFLNVPFE-SLQGVTYPVLRKL---YKKIAKFERSEEEVTKLNVLVDEIKSQYYSRISK
                                                                                 DNSEPSTEGEI - -
                                                                                                                                                                                                                                                                                                                                                                                                 KSLEHELKRSTELLETVSLTKRKQEREITSLRQKINGCEANIHSLVKQRLDLARQVKLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                  KSLNDITKEYEKLLNEIYDSKFNNNIDLT-----NFEKMMGKRYSY-KVEKLTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --------LNELNS----FGDLINPFDYTK---EPSKN-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSVQEKELMLQSKKLIEEKLSSFSKKTLTEEVTKSSHVENLEEKLYQMQSNYESVFT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - SGNTPNTLLDKNKKIEE - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TMTTSAVSPTVGKLFSDIKVLKRQLIKERNQKFQLQNQLEDFILELEHKTPELISFKERT
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                                                                                                                                                                                                                                                                                            -VENIKKDEEQLFEKKITKDENKPDEKILEVSDI-VKVQVQKVLLMNKID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IYTDNE--RKKFINEIKEKIKIEKKK----IESDKK-----SYEDRS
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19!7%; Pro
vative 296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 423; DB 2; I
Pred. No. 4.8e-06;
96; Mismatches 583;
                                                                                 TGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------HEKEIKEIAKTIKFNIDSLFTDPL 373
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                                                                                                                                                                                                                         -ELKKTQL----ILKNVELKHNIHVPNS
 -YLEKLYEFLNTSYICHKYILVSHSTM 799
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RESULT 53 \$41649 DNA polymerase - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 20-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jun-2000 C;Accession: \$41649 R;White, J.H.; Kilbey, B.J.; de Vries, E.; Goman, M.; Alano, P.; Cheesman, S.; McAleese, Nucleic Acids Res. 21, 3643-3646, 1993 N;Tile: The gene encoding DNA polymerase alpha from Plasmodium falciparum. A;Reference number: \$41649; MUID:93376482; PMID:8367280	OY 1520 NLQGMLNISOHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQE-GDKCVENPNP-TCNEN 1577 : : : : : : : :	1296 KLDASKKQOAALTNELNELKAIKDKLEQDLHFENAKVIDLDTKLKAHELQSEDVS 1 1407 KQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSN-VEVKIKE 1	QY 1243 VPIEGESEDVDLIGG - VVIGENTPSYLDILISKIENTYEVIXIKPLAGVYRSLKKQL 1300 QY 1301 ENNVMTENVINCKIENTKEQV-:SINSNKILVYESEMEQCKQRYQDLSQQQ 1250 QY 1301 ENNVMTENVINCKIILNSRFNKRENFKNYLESDLIPYKDLTSSNYVVKDPYK 1351	1037 SSLYSAODLLDKHERKWMEEKADYERELISNIEQTESLRVENSVLIEKVDDTAAN 1135 NINLEKKKLSYLSSGLHHLIABLKEVIKNKNYTGNSPSENNTDVNNALES :	946 1019 995 1076	916 STNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKI-LKDSDTFYNESFTNFVK	Db 754 RLKESEISHNENKMDFSSKEGQYKAKIKELENNL 787 Qy 800 NEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEM 859 :-
Qy 568KNLISKIENBIETLVENIKKDEBQLF	494 558 544 601	378 FLLNKNYYYENGEEIKFNHEKFKIHIMSEFLEEFKIIRE 402 EYPNGYTYPLSYNDINNALNELNSFGDLINPFDYTKEP :	Qy 337 PNTLLD		QY 59 GTAVTTSTPGSKGSVASGGSGSVASGGSVASGGSVASGGSGNSRRTNPSDNSS 118 I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	Query Match 5.0%; Score 423; DB 2; Length 1855; Best Local Similarity 19.3%; Pred. No. 5.3e-06; Matches 385; Conservative 303; Mismatches 667; Indels 638; Gaps OY 1 MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTS 58	A;Accession: S41649 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-1855

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                                                                                                                                                                                                                                                                                                               VIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                PINRLCQYIEGTSAEKLSSCFNIYDVKE-----IKTDKQIEE-NYLETNVLSLLNESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDVNNALESYK-----KFLPE-----GTDVATVVSESGSDTLEQSQP---KKPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YASLENFKYLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENN
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                                              DSGSNGKKITCEC
                                                                                       EAKDPNGSISNIHDDINNEHSEKNNHNIYKK-----NNSNNNNNNNNKDIENEEYCND-
                                                                                                                                   KKQCPQNSGCFRHLDEREECKCLLN---YKQEGDKCVENPNPTCNENNGGCDADAKCTEE
                                                                                                                                                                              PLISKKYIYLILEYFLF - - LLKDNL - KKIPSNLVEKNKSEQLNETQDTNNENDITSNQKE 1686
                                                                                                                                                                                                                                                                      IHHLCNTFYKQLYICQGCTLKTRRI - -
                                                                                                                                                                                                                                                                                                                                                           ERFKDIHLKGFLVCS----NCMHNVKPNIFIKYFKCNKCLTYLS----IEQIRNYIFSF
                                                                                                                                                                                                                                                                                                                                                                                             INFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLES 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANNINNYKESFKLAHLIKNSINKNYKKLEL----DLECIFSKLL-LLKKKKYACAKVIDNN
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    -FIVCLC
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myosin heavy chain - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR023w; type II myosin
C;Species: Saccharomyces cerevisiae
C;Date: 07-Oct-1994 #sequence_revision 11-Aug-1995 #text_change
C;Accession: S46773; S05806; S12323
R;pu, Z.
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A; Rolecule type: DNA
A; Residues: 1-45,'T', 47-58,'S', 60-329,331-342,'S',344-528,'ARGHDR',536-
A; Cross references: EMBL:X06187; NID:94015; PIDN:CAA29550.1; PID:94016
A; Sweeney, F.P.; Watts, F.Z.; Pocklington, M.J.; Orr, E.
Nucleic Acids Res. 18, 7147, 1990
Nucleic Acids Res. 18, 7147, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: actin binding; TrP; coiled coil; nucleotide F;78-779/Domain: myosin motor domain homology <MMOT> F;78-779/Domain: nucleotide-binding motif A (P-loop) F;459-528/Domain: actin binding #status predicted <ACB> F;186/Binding site: ATP (Lys) #status predicted
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C; Superfamily: myosin heavy chain; myosin motor domain homology
C: Superfamily: myosin heavy chain; myosin motor domain homology
C: Superfamily: myosin heavy chain; myosin motor domain homology
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A;Title: The MYO1 gene from Saccharomyces cerevisiae:
A;Reference number: S12323; MUID:91088308; PMID:226348
A;Accession: S12323
A;Status: translation not shown; significant sequence
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A;Title: The yeast MVO1 gene encoding a myosin-like A;Reference number: S05806; MUID:88111539; PMID:3322 A;Accession: S05806
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EMBO J. 6, 3499-3505, 1987
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A; Cross-references: EMBL:U10399; NID:g500689;
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A; Residues: 1-1928 <
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A; Accession: S46773
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64 pp pp

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RESULT 55
T18440
hypothetical protein C0425w - malaria parasite (Plasmodium falciparum)
c;Species: Plasmodium falciparum
c;Species: Plasmodium falciparum
c;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
c;Accession: T18440
C;Accession: T18440
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A;Molecule type: DNA
A;Residues: 1-4550 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Lawson, D.; Bowman, S.; Barrell, F
submitted to the EMBL Data Library,
A:Reference number: Z18935
A:Accession: T18440
2282 NNNSNSNHSNHNNNSNH--INLSDLKKKININKYTYLFYRLPLFLFGDKYINDIDDVKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1683 SCSSRSFWGSLYNTSDNISESEISNNLSFSSDKSEN-YCSSISDHEIEKDVTIYRNTYHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 VRNYLLTIKELKYPQLFDLTN------HMLTLCDN------IH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 SVASGGSGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNDNNNSGEDQLINEDNKKRKINNLSTHEHTHNMSDHNKEPKKKKNKSNETQINDDTNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKI-----RANELDVL
                                                                                                                                                  ASYENSKHNLEKLTKALKYMEDYSL-RNIVVEKELKYYKNLISKIENEIETLVENIKKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYND
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                                                       EQLFEKKITKDENKPDEKILEVSDI-VKVQVQKVLLM-----
                                                                                                                                                                                                                               ETKCIMKNNVCDGIYYLIRQENGLNICQKVNNNI----IKNKMKQEKFYKKKKQNKNN--
                                                                                                                                                                                                                                                                                      EDRSKSLNDITKEYEKLLNEIYD----SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTF
                                                                                                                                                                                                                                                                                                                                                   NDDDNNNNNN-----NDDDNNKDPT----LDGETRSYIDEINQKEINIFSKYIDKIIENV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKLVFGYRKPLDNIKDNVGKMEDYIKKNKKTIENIN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 420.5; DB 2;
Pred. No. 1.8e-05;
38; Mismatches 679;
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1340 VIIINEPROYNDYNYTSNNILYVIDLIKKNNINJIKKNNINJOSPKKYLEEDOSNOEP 6.0 1 1 1 1 1 1 1 1 1
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Match

4.98;

Score

414;

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phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium in C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: B71616 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koon.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Sm. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falcipa A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: B71616 A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Cessidues: 1-2010 <GRP>
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 57
B71616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-89 < HUI>
A; Residues: 1-80 < HUI>
A; Experimental source: FVO isolate
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:89242, NCBIP:89243)
C; Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Roles of conserved and allelic regions of the major merozoite surface protei A;Reference number: A43854; MUID:92192814; PMID:1548068
A;Accession: A43854
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      major merozoite surface protein gp195 - malaria parasite (Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000 C;Accession: A43854 R;Hui, G.S.; Hashimoto, A.; Chang, S.P. Infect. Immun. 60, 1422-1433, 1992
                                                                 A; Experimental source: clone C; Genetics:
                                                                                           A; Cross-references: GB:AE001391; A; Experimental source: clone 3D7
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87; Conserv
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97.8%;
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                                                                                                                GB:AE001362; NID:g3845168; PIDN:AAC71865.1; PID:g384
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R.; White, O.; Smith
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	-NNSLKLFENTLSLGKNKNIYQELIGQKSSENFYEKIL 956	EVSANDDTSHSTNL	906	Qy
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	QATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKA 753 :	TEGQSDNSEPSTEGEITGQATT	694 1285	g 9
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4.9%; Score 412; DB 1; Length 3259; est Local Similarity 19.8%; Pred. No. 2.2e-05; atches 314; Conservative 301; Mismatches 592; Indels 376; Gaps 72;	A;Gene: GDB:GOLGB1; GCP; GCP371 A;Gene: GDB:GOLGB1; GCP; GCP371 A;Cross-references: GDB:454958 A;Map position: 3q13.31-3q13.31 C;Superfamily: giantin C;Superfamily: giantin C;Keywords: coiled coil; Golgi apparatus; transmembrane protein F;3238-3254/Domain: transmembrane #status predicted <tmn></tmn>	ACCESSION: ADD399 MOlecule type: mRNA MOlecule type: mRNA Residues: 1-3259 <see> Cross-references: EMBL:X75304; NID:g405714; PIDN:CAA53052.1; PID:g405715</see>	Mol. Cell. Biol. 14, 2564–2576, 1994 A;Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protei A;Reference number: A56539; MUID:94187728; PMID:7511208	r, H.; Wiemann, C.; Griffiths, G.; Re	RESULT 58 A56539 A56539 giantin - human giantin - human N;Alternate names: macrogolgin C;Species: Homo sapiens (man) C;Species: Homo sapiens (man)	1967 DKKIKKRKKKLQKKNYENENIVCLDCLISYLKKMLRIYGND 2007	1518 DGNLQGMLNISQHQCVKKQCPQNSGCFRHLDEREEC-KCLLNYKQEGDKCVENP 1570	1936NKNNQIIGYSIKYDKNVVSENSCSDVITSLK 1966	VFENLAKTVLS	1902 QKKINDH NNINSYDNNINNGLINEHKNVLHNECK 1935	3ENEKYLPFL	851 INNILLHTYK-QHKKKKSTIISSDNNNNNNNAEDDISSRKLKFKDIKGNTK	1342 SNYVYKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIK 1401	1288 PLAGVYRSLKKQLENNVMTFNVNVKD-ILNSRFNKRENFKNVLESDLIPYKDLTS 1341 :: :: : : : : : : : : : :	1238 DDVITVPIFGESEEDYDDLGQVVIGEAVIPSVIDALLSKIENEYEVLYLK 1287	710 NNICLKNNKNNIMHEDINANKRESLKKKKKKKKNCIQKNNNICERK	ASTHVGAESNTITTSQNVDDEV 123	1660	1118 SLENFKYLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTD 1177	:: : 13 THIKKNMQLKEGKKHGKRNF	1066KKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYA 1117	1566 NKKYESYLPKCLNKIHDFK-NLFYLLCYKNNNIQDLIQLYDICLNNNY 1612	KKKTVGKYKMQIKKLTLLKEQLESKLNSL	:	957 KDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYN 1009	1459 HASSRSVHVNQTDRTDVLSFIYHNNTANIFCCKDDCVWKVRETENEKKFEKCR 1511

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773	34 EDIKNQIDEVTQECYRNNDIIRDTHDKSDIFKNIKIDNN	7:	Db
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733	74 LINKDLSKNTDNINIKDYNVLQKKKSKKKKKKELNDILNTYNFTTESKYQDLYVKGEESK	6	DЬ
658	09 LEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENK	6	Qy
673	.16 KEEWYTDNRIKAIKSKDDMDVFSQVQLETYVRMIKTDFEIEKLKIKMAENIQSVEGEL	6.	рь
809	LKYYKNLISKIEN	56	Qy
615	64 LDTSNIFLEGKDEYKVYYVNKEEIRIPLFKEINKEIFEKLPLKLQYQILQDI	5	Db
561	04 IDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVE	5(Qy
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1356	06TFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE 1356	Qy 1306	
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2, Appli
20, Appl
5231168
                                                                                                                                SEQUENCE ..... SEQUENCE ..... SEQUENCE ..... A TYPE: amino acid STRANUSDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: C-termina ORIGINAL SOURCE: ORGANISM: Plasmodium STRAIN: WEL

US-08-195-705-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-08-195-705-5
; Sequence 5, Application
; Patent No. 6420523
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PATENTIA! Release #1
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/195
FILING DATE: 14-FEB-1994
CLASSIFICATION: 4 35
FILING DATE: 14-FEB-1994
CLASSIFICATION: 4 35
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 1188
REFERENCE/DOCKET NUMBER: 1188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPHONE: 212-757-2200
TELEPHONE: 212-756-1461
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FENUTH: 377 mino. 26446
                                                                                                                        Query Match 21.7%;
Best Local Similarity 93.6%;
Matches 353; Conservative;
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APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                         1324
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CITY: New YORK
STATE: N.Y.
COUNTRY: USA
ZIP: 10111
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45 Rockefeller
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US-08-463-483A-23
US-08-471-046A-23
US-08-470-566B-23
US-08-469-334-23
US-09-300-529-23
US-08-477-831C-11
                                                                                                                        Score 1824.5;
Pred. No. 8.8e
6; Mismatches
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8.8e-90;
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Sequence 3, Appril-
No. 6420523
 Best Local Similarity Matches 345; Conserv
                           Query Match
                                                                                                                                                                                                            TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Pla
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/06
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                            MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1563
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                              NAME: Jacobs, Seth H
REGISTRATION NUMBER:
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45 Rockefeller Pl.
20.9%; ilarity 91.5%; Conservative
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                                                                                                                                                                  single
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Score 1763.5; DB 4;
Pred. No. 1.5e-86;
7; Mismatches 22;
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                           Length 375;
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             TOPOLOGY: 1
MOLECULE TYPE:
 HYPOTHETICAL:
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                                                                                                                                                                                  NAME:
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Sequence 2, Application US/08195705 Patent No. 6420523
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Chang, Sandra
                                                                                      TELEFAX: 212-586-1461 INFORMATION FOR SEQ ID NO:
                                                                                                     REGISTRATION NUMBER: 32140
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPAX: 212-586-1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1324 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVL 1383
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1264 AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRE 1323
                                                                                                                                                                                                                                                       FILING DATE: 14-FEB-1994 CLASSIFICATION: 435
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULO
TITLE OF INVENTION: FALCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Applic Patent No. 6420523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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FRAGMENT TYPE: C-termi
ORIGINAL SOURCE:
ORGANISM: Plasmodium
STRAIN: falciparum u
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ATTGRNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 321
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1490
                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                     STATE:
                                                                         APPLICATION NUMBER: FILING DATE: 14-FEE
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                 ADDRESSEE:
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les 243; Conserv
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 MDNILSGFENEYDVIYLKPLAGVYRSLKKQIEKNIFTENLNLNDILNSRLKKRKYFLDVL 65
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Plasmodium uganda palo
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Pred. No. 2.5
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2.5e-61;
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TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        APPLICANT: Hundt, Erika
APPLICANT: Enders, Burkhar
APPLICANT: Kuepper, Hans
TITLE OF INVENTION: Protec
TITLE OF INVENTION: Hybrid
TITLE OF INVENTION: Antige
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS
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ORIGINAL SOURCE:
                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                           STATE:
                                                                                  STREET: 1300 I Street Washington
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                                                                                                                  ADDRESSEE:
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                                                        E: D.C.
20005-3315
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                                                                                                    E: Dunner
1300 I Street,
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Enders, Burkhard
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                                                                                                                                 Finnegan,
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   compatible
PC-DOS/MS-DOS
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Protective Plasmodium Falciparum
Hybrid Proteins which Contain Part-Sequences of the Malaria
Hybrid Proteins which Enterparation and Use Thereof
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                                                                                                     Suite 700
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US-09-134-001C-3159
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                                                                                                                                                                                                                                                                                                   ORGANISM: Staphylococcus epidermidis US-09-134-001C-3159
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                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3159, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EDIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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LENGTH: 115 amino acids
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REFERENCE/DOCKET NUMBER: 02.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,408-4000
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PRIOR APPLICATION NUMBER: US 07/806,471
                                                         8014 TMSHDEIENAINNIKHAINALDGEHKLQQAKENAN----LLINSLND------
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                      208
                                                                                                                                                                             107 NSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLF--DLTNHMLTLCDN----
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FILING DATE: 13-DEC-1991
CLASSIFICATION: 424
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                                                                                                                                                                                                                                         Local Similarity
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                    KIRANELDVLKKLV--FGYRKPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDK 265
                                                                                                                                      NKAKALNNDMKKLKDIVAQQDNVRQSNNY - - - INEDSTPQNMYNDTINHAQSIIDQVANP
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Einaudi, Carol P.

On Number: 32,220
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20.6%;
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                                                                                                                                                                                                                                         Score 448; DB 4;
Pred. No. 6.9e-15;
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DEKQIQGLKQVIEDTKDALNGIQRLSKAKAKAIQYV----QSLSYINDAQRHI-----
                                     SEESIQ-----TEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEV 1160
                                                                            DELNNQAFPVQASSNYINSDEDLK-QQFDHALSNARKVLAKE-----
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Query Match 4.6%; Score 387; DB 4; Length 3696; Best Local Similarity 20.9%; pred. No. 3.4e-12; Matches 314; Conservative 231; Mismatches 592; Indels 368; Gaps 67; 114 SDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTN 152 114 SDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTN 152 115 HMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQ 202 153 HMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQ 202 153 HMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQ 202 154 HMLTLCDNIHGFKYLID	RRENT FILING DATE: 1998-1 TOR APPLICATION NUMBER: UI TOR FILING DATE: 1997-11-1 TOR APPLICATION NUMBER: UI TOR APPLICATION NUMBER: UI TOR APPLICATION NUMBER: UI TOR SEQ ID NOS: 5674 TID NO 5080 SINGTH: 3696 TPE: PRT TRANSEN: Staphylococcus el TAM-001C-5080	SULT 7 -09-134-001C-5080 Sequence 5080, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION OF AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: GENERAL INFORMATION OF AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE REFERENCE: GENERAL INFORMATION OF AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE REFERENCE: GENERAL INFORMATION OF AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE REFERENCE: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INF	1516 LLDGNLOGMLNISOHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCV-ENPNP 1572 : :	431KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTI 1 :: : : ::::::	1265 VIPSVIDNILSKIEBYEVLYKPLAGVYRSIKKQLENVAMTENVANVEDLNISKENKREN 1324 1265 VIPSVIDNILSKIEBYEVLYKFLAGVYRSIKKQLENVAMTENVANVEDLNISKENKREN 1324 9170KVN 9202 9170KVN 9202 1325 FKNVLESDLIPYKDLTSSNYVVKDBYKFLNKEKRDKELSSYNYIKDSIDTDINFAND 1381 1325 FKNVLESDLIPYKDLTSSNYVVKDBYKFLNKEKRDKELSSYNYIKDSI	161 IKNKNYTGNSPSENNTDVNNALESYKKFLDEGTDVATVVSESGSDTLEQSQPKKPASTHV
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Patent No. 559991
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                              TELEPAX: (215) DO TELEPAX: (215) TELEPAX: 1: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 1.FNGTH: 3248 amino acids
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APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED
TITLE OF INVENTION: AND METHODS OF USE
                     Matches
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
NAME: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILLING DATE: 09-DEC-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
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                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                   LENGTH: 3248 amino TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIKKRÉAIAEIQELADKK - - -
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                 Score 356.5; DB 1
Pred. No. 1.2e-10;
)4; Mismatches 631
                                                     DB 1;
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KINETOCHORE PROTEIN,
                     631;
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                                                     Length 3248;
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                                    CSSLQEENLTRKETPSAPAKGVEELESLCEVYRQSLEKLEEKMESQGIMKNKEIQELEQL
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FD-----KKKTVGKYKMQIKKLTLLKEQLESKLNS-----
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                                                                                                                                                KNKNIYQEL-----IGQKSSENFYEKILK---DSDTFYN-ESFTNFVKSKADDI- 978
                                                                                                                                                                                     GDMSLLSNLEGAVSANQCSVDEVFCSSLQTYVDSLKAENLVLSTNLRNFQGDLVKEMQLG
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                                                                           -NSLNDESKRKK-
                                                                                                           LEEGLVPSLSSCVPDSSSLSSLGDSSFYRALLEQTGDMSLLSNLEGVVSANQCSVDEVF 1623
                                                                                                                                                                                                                                                              AENLVLSTNLRNFQGDLVKEMQLGLEEGLVPSLSSSCVPDSSSLSSLGDSSFYRALLEQT 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIMTLKEEQNKMQKEVNDLLQENEQLMKVMKTKHECQNLESEPIRNSVKERESERNQCNF 1190
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                                                                                                                                                                                                                         -PLSLTPQDKPEVSAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESL 684
                                                                         -LEEDINKLKKTLQLSFDLYNKYKLKLERL 1018
                                                                                                                                                                                                                       DDTSHSTNLNNSLKLFENILSLG 933
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-LNNPKHVLQN 1058
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Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
COUNTRY: USA
ZIP: 19103-2307

ZIP: 19103-2307

COMQUTER READABLE FORM:
MEDIUM TYFE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                    APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 36,252
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
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Best Local Similarity
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APPLICATION NUMBER: PC'
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INEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAG
                                          QDMQSQEISGLKDCEIDAEEKYISGPHELSTSQNDNAHLQCSLQTTMNKLNE-LEKICEI 1309
                                                                                                                                     KPQMDLEVKEISLDSYNAQLVQLEAMLRNKELKLQESEKEKECLQHELQTIRGDLETSNL
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PCT-US95-16216-1

CITY: Philadelphia

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LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN LSGIN 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                                                                                          Sequence 8, Application Patent No. 6191270 GENERAL INFORMATION:
                 APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION
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NUMBER: US/08/973,462B
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Best Local Similarity
Matches 269; Conserv
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LENGTH: 1786
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EARLIER APPLICATION NUMBER: 05-12
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2
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                                                                                                                                                     YE-KEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDT
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                                                                                         -SH--STNLNNSLKLFENILSLGKNKNIYQELIGQKSS-ENFYEKILKDSDTFY
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20.0%; Pred. No. 1.2e-10;
ative 243; Mismatches 437;
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US-08-328-254-6
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GENERAL INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                           STREET: 43.C
CITY: San Diego
STATE: California
                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
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                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A NO.
NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Best Local
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
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                      FQGDLVKEMQLGLEEGLVPSLSSSCVPDSSSLSSLGDSSFYRAL---LEQTGDMSLLSNL
                                                                                                                                     CHKYILVSHSTMNEKIL---KQYKITKEEESKLSS-----
                                                                                                                                                                            DIPGGEFGEQPNEQHPVSL------APLDESNS-----YEHLTLS--
                                                                                                                                                                                                                                                          LQAEKYELVTELNDSRSECIT-----ATRKMAEEVGKLLNEVKILNDDSGLLHGELVE
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19.8%; Pred. No. 1.8e-10;
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                                                                                                                               Sequence 1, Application US/09310187A Patent No. 6358751
GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE.OF INVENTION: Involvement of Autoani
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-090
CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Wildows Ve
; SEO ID NO 1
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                      QLEE-----KEALISQLTRGKLSYTQQMEDLKRQLEEEGKAKNALAHALQSAR 1339
                                                                   YLEKLYEFLNTSYICHKYILVSHSTMNE----KILKQYKITKEEESKLSS------
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                                                                                                         KVSR-----TLEDQANEYR-----VKLEEAQRSLNDFTTQRAKL--QTENGELAR 1291
                                                                                                                                                                              RKKHADSVAELGEQIDNLQ ----RVKQKLEKEKSEFKLE--LDDVTSNMEQIIKAKANLE
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   --CDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD-NDKIKNLL
                                                                                                                                        PGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV----PTPPAPVNNKTENVSKLD
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1669
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                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              979
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                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 80203
                                                                                                                                                                                                                                                                                           STREET: 1700
CITY: Denver
                                                                                           FILING DATE:
                                                                                                           APPLICATION NUMBER:
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   NUMBER:
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Best Local Similarity
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LENGTH: 1886 amino acids
TYPE: amino acid
TYPE: amino acid
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                 PVNNKTEN----VSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKL 817
                                                     HMEQIIKAKANLEKVSR-----TLEDQANEYR-----VKLEEAQRSLNDFTTQRA
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                                                                                                                            QHEA----TAAALRKKHADSVAELGEQIDNLQ----RVKQKLEKEKSEFKLE--LDDVTS 1182
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                                                 COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/09/104,324B
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
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TITLE OF INVENTION:
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CITY: New Y
STATE: New
ZIP: 10103
                 FILING DATE: 2 CLASSIFICATION:
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APPLICATION DATA:
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And Methods For Identifying Pathogenic M
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FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6232460
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                                                                                                                                                                                                                                                                                                                                                                                  DEKILEVSDIVKVQVQKVLLMNKIDELKKTQL---ILKNVELKHNIHVPNSYKQENKQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYDSKFNNNIDLTNFE------KMMGKRYSYKVEKLTHHNTFASYENSKHN--LEKLTKA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSENLKQSIEKQHHLTKELEDIKVSLQRSVSTQKALEEDLQIATKTICQLTEEKETQMEE
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PLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKI 955
                                       ----ESAKQKFGEITDTYQKEI------EDKKISEENLLEEVEK----AKVIADEAV-
                                                           DSLNNSLSQLFMEI---YEKEMVCNLYKLKDNDKI--KNLLEEAKKVSTSVKTLSSSSMQ
                                                                                                                                                 FLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMF
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                                                                                                                                                                                                                                                                                                       YYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQA 721
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                                                                                                                                                                                                                                                                      ----LTQETSDMTLELKNQQEDINNNKKQEERMLKQIENLQETETQLRNE
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20.7%; Pred. No. 5
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5.6e-10;
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THHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENE 577 :::::::::::::::::::::::::::::::::::	KKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKL 524 	SYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEK 464	TIKFNIDSLFTDPLELEYYLREKNKNIDISAKVET-KESTEPNEY-PNGVTYPL 411	RIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEHEKEIKEIAK 359 :	INELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEK 304 :	7 Match 3.7%; Score 314.5; DB 4; Length 1151; Local Similarity 19.7%; Pred. No. 5.8e-09; es 268; Conservative 225; Mismatches 485; Indels 379; Gaps 63;	TYPE: PRT ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3242	APPLICATION NUMBER: US 60/055,779 FILING DATE: 1997-08-14 OF SEQ ID NOS: 5674 NO 3242 H: 1151	CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08	APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007	:-09-134-001C-3242 Sequence 3242, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:		***FLPEGTDVATVVSESGSDTLEQ-SQPKKPASTHVGAESNTITT 1229	NIPIEESKK	NLNLEKKKLSYL-SSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKK 1187		ERT-EEKET-KLKREAKENTATLKEKKDKKTQTF799 ENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKD 1134	GKYKMQIKKLT-LLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAET	LGLYKSKEQEQSSLRASLEIELSNLKAELLSVKKQLEI 769
RES US-	Db	Db QY	B 5	S B 2	0 p 4	. g. 4	5 g 4	Q	Оу Db	ОУ	Qy Db	Db	Qy Db	Qy	DЬ	Qy	Ωу	Db	Qy
RESULT 17 US-09-134-001C-4820 ; Sequence 4820, Application US/09134001C	1456 KIKELNY-LKTIQDKLADFKKNNFVGIADLST 16		KSVFNSQMTQNNDFNEEKKIS	905 DNAKLSARQHKLNHYKNQTLLNQELIDTTAQRT	1200 YIGGAYLGA LUMLUGA LEMULUK LANG :			1100 SPLKTLSEESIQTEDWYASLENFKVLSKLE 1100 SPLKTLSEESIQTEDWYASLENFKVLSKLE 1100 SPLHTVSLEELKKWSAEDEVATFVKTV 1100 SPLHTVSLEELKKWSAEDEVATFVKTV	1050 NNPKHVLQNFSVFFNKKKEAEIAETENTLE	991 EEDIN-KLKKTLQLSFDLYNKYKLKLERLFDKK	932 LGKNKNIYQELIGQKSSENFYEKILK-DSDTFY : : :: :: : : : : : : : : : :	510 SHNYKHYYIHLDDSLDKLIGRTETHFELKQENS	465 ENESTPLFEEAVNHVQVN 872 IKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDK	EEESKLS	422ILNQEYDVVPSLISELYQTQ		698 SDNSEPSTEGEITGQATTKPGQQAGSALEGDS- : ;		638 LKNVELKHNIHVPNSYKQENKQEPYYLIVLKKE

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1456 KIKELNY-LKTIQDKLADFKKNNNFVGIADLSTDYNH 1491 :: :: ::	019 VMKKLNQIHVIINAKFNVEPSLVDTALLQIELNSMLQSLPRQ	KOSIDTDINFANDYLGYYKILSEKYKSDLSIK	LNSRFNKRENFKNVLESDLIPYKDLTSSNYVXKOP 	1260 VTGEAVTPSVIDNILSKIENEYEVLYKPLAGVESLKKQLENNWMTFNVNVKDI 1260 VTGEAVTPSVIDNILSKIENEYEVLYKPLAGVESLKKQLENNWMTFNVNVKDI 1260 VTGEAVTPSVIDNISKIENEXEVLKPLAGVESLKKQLENNWMTFNVNKDI 1260 VTGEAVTPSVIDNIKTENEXEVLKPLAGVESLKKQLENNWMTFNVNKDI 1260 VTGEAVTPSVIDNIKTENEXEVLKPLAGVESLKKALLENGTH 1260 VTGEAVTPSVIDNIKTENEXEVLKTAGVESLKALLENGTH 1260 VTGEAVTPSVIDNIKTENEXEVLKTAGVESLKKALLENGTH	LEQSQPKKPASTHYGAESNTITTSQNYDDEVDD	1152HLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDT :: : :: : : : : : :	O SPLKT	ı z	991 EEDIN-KLKKTLQLSEDLYNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSL	932 LGKNKNIYQELIGQKSSENFYEKILK-DSDTFYNESFTNFVKSKADDINSLNDESKRKKL	872 IKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILS	812 EEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK	752 KAQVPTPPAPVNIKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITK	698 SDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPVEA : :	638 LKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQ :: :	578 IETLVENIKADEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLI ::::::::::::::::::::::::::::::::::::
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4820
LENGTH: 1211
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                  KKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQK-QAQPPVPVP
                                                                                               TQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMP-----KVESLINEE
                                                                                                                                    \tt QRGLGRATFLPLNVIQPRHVAADIKDVARGSQGFINIASDAINVSAK---YQNIIENLLG
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                                                        NTIIVEN--LKHANELARAIRYRTR----IVTLEGDVVNPGGSMTGGGARKTKSILSQK
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Pred. No. 1.1e-08;
3; Mismatches 471;
                                                                                                                                                                                                                                                                                                                                     THHNTFASYENS-KHNLEKLTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1211;
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US-08-687-080-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/08687080 Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                            APPLICATION NUMBER: US 0: FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:

NAME: Sholts Charles K
                                                                                           APPLICATION NUMBER: U$/00 FILING DATE: 17-JUL-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1190 GVSKLVSVNLNTIDEV 1205
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  NAME: Sholtz, Charl REGISTRATION NUMBER:
                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AESNTITTSQNVDDEV 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNSPSENNTDVNNALES --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~-TEDDYLS-AGVDIIVQPPGK-----KLQHLSLLSGGERALSAIALLFAILKVR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPEAKAQVPTPPAPVNNKTENVS----KLDYLE-----KLYEF-LNTSYICHKYI 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SAPFVILDEVEAALDEANVIRYAQYLNELSTETQFIVITHRKGTMEFSDRLYGVTMQES 1189
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                                                                                                                                                                                                                                                                                                                                                         Palo Alto
                                                                                                                                                                                                                                                                                                                                       CA
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350 Cambridge Avenue, Sui
                                                                                                                                                                                                                                                                                                                    USA
                  Charles
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38,615
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                                                                             08/592,126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERENCE/DOCKET NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: pr
                                        1033 K-KLTLLKEQLESKLNSLNNPKH------VLQNESVFFNKKKEAEIAETENTLENTKI 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TRYIKALETLROVROTOGOKVKEYOME-----LKYLKOYKEKACEIRDQITSKEAQLTSS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 EIDREMISSLGVSKAVLNNVIFCHQEDSNWPLSEGKALKQKFDEIFS------A 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 LSYNDINNALNELNSFGDLI----NPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKI 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 LQFRDVN------GELIAVQRSMVCTQKSKKTEFKTLEGVITRTKHGEKVSLSSKCA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: TRANS. OF RAD50 cDNA (SEQ. 54), NT INDIVIDUAL ISOLATE: 389 TO 4324
                                                                                                                                                                                                                                                                          VSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSL-----GKNK 936
                                                                                                                                                                                                                                                                                                                                                       NIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDK-----IKNLLEEAKK 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDY-----SLRNIVVEKE--LKYY 567
QSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSII--DLKEKEIPELRNKLQNVNR 759
                                                                                 LDRLKEEIEKSSKQRAMLAGATAVYSQFITQLTDENQSCCPVCQRVFQTEAELQEVISDL 701
                                                                                                                                                               EINQTRDRLAKLNKELASSEQNKNHINNELKRKE----EQLSSYEDKLFDVCGSQDFESD 641
                                                                                                                                                                                                                                              LNH--HTTTRTQMEMLTKDKADKDEQIRKIKSRHSDELTSLLGYFPNKKQLEDWLHSKSK 585
                                                                                                                                                                                                                                                                                                                                                                                                            ILSK-----KQNELKNV-----KYELQQLEGSSDRILELDQELIKAERELSKAEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLF 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKLVRERQEGEAKTANQLMNDFAEKETLKQKQ------IDEIRDKKTGLGRIIELKSE 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTKPGQQAGSA-----LEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTE 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVE 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEIVKSYENELDPLKNRLKEIEHNL--SKIMKLDNE----IKALDSRKKOMEKDNSELE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESDKKSYEDRSKS---LNDITKEYE------KLLNEIYDSKFNNNIDLTNFEKMMG 514
                                                                                                                       RKKLEEDINKLKK---TLQLSFDLYNKYKLKL-----ERLFDKKKTVGKYKMQI 1032
                                                                                                                                                                                                      NIYQ------ELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESK 986
                                                                                                                                                                                                                                                                                                                               -----NSNVETLKMEVISLQ-----NEKADLDRTLRKLDQEMEQ 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLLNQEKSELLVEQGRLQLQADRHQEHIRARDSLIQSLATQLELDGFERGPFSERQIKNF 396
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	SEQUENCE CHARACTERISTICS: LENGTH: 1312 amino acids		
• .	NE: (415) 324-0880 : (415) 324-0960		
	ATION INFORM	٠. ٠.	
	NUMBER: 38,615		
	Charles		
	ILING DATE:		
	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,126	·. ·.	
	ARE: PatentIn Release	٠. ٠	
	IBM PC compatible		
	COMPOTER READABLE FORM: MEDIUM TYPE: Floppy disk		
	94306		
	TATE:		
	Palo Alto	٠.	
	TREET: 350	٠. ٠.	
	PONDENCE ADDRESS:	•. •	
	••		
	TITLE OF INVENTION: Transcripts Encoding Immunomodulatory		
	ADDITIONT GREGORY		
	O. 5821091		
	-08-592-126 Sequence 141	SO	
		,	
	1172 NVSASDKRRNYNYRVVMLK 1190	рь	
	1480 -VGIADLSTDYNHNNL	Qy	
1171	1120 DLDIYYKTLDQAIMKFHSMKMEE	дь	
1479	. 1431 KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNF	Qy	
1119	1060 LEENI	Д	
1430	, 1393 YKSDLDSIKKYINDKOGENEKYLPFLNNIETLYKTVND	0γ	
1059	1000 DMRLMRQDIDTQKIQERWLQDNLTLRKRNEELKEVEEERKQHLKEMGQMQVLQMKSEHQK	ДĎ	
1392	1364 SYNYIKDSIDTDINFANDVL	Ωу	
999	949 EKVKNIHGYMKDIENYIQDGKDDYKKQKETELNKVIAQLSECEKHKEKINE	В	
1363	1320 NKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLS	Qy	
948	908 -AKEQVSPLETTLEKFQQEKE	ф	
1319	1260 VTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRF	Qy	
907	854 QDQQEQIQHLKSTTNELKSEKLQISTNLQRRQQLEEQTVELSTEVQSLYREIKD-	фd	
1259	1204 SDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEEDVD	Qy	
853	810 AQQAAKLQGIDLDRTVQQVNQEKQEKQHKLDTVSSKIELNRKLI	ДD	
1203	1144 SYLSSGLHHLIA	Qy	
809	760 DIQRLKNDIEEQETLIGTIMPEEESAKVCLTDVTIMERFQMELKDVE	Db	
1143	TO84 FERHAGEVARIANGESSPERTESEESEQTEDNASSEESARVESAFEGARADULULEARAL	γ	

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В
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                                                                                  1144
                                                                                                                                                                  1084
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1204 SDTLEQSQPKKPASTHVGAESNTITTS----QNVDDEVDDVIIVPIFGESEEDYDDLGQV 1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 KRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDY-----SLRNIVVEKE--LKYY 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 LQFRDVN-----GELIAVQRSMVCTQKSKKTEFKTLEGVITRTKHGEKVSLSSKCA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKLVRERQEGEAKTANQLMNDFAEKETLKQKQ-----IDEIRDKKTGLGRIIELKSE 448
                                                                               SYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESG 1203
                                                                                                                       DIQRLKNDIE---EQETLIGTIMPEE---ESAKYCLTDVTIMERFQMELKD----VERKI 809
                                                                                                                                                                                                                                       K-KLTLLKEQLESKLNSLNNPKH------VLQNFSVFFNKKKEAEIAETENTLENTKI 108:
                                                                                                                                                                                                                                                                                                                                                                       EINQTRDRLAKLNKELASSEQNKNHINNELKRRE----EQLSSYEDKLFDVCGSQDFESD 641
                                                                                                                                                                                                                                                                                                                                                                                                             NIYO------ELIGOKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESK 986
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                                       AQQAAKLQGI--DLDRTVQQVNQEKQEKQHKLDTVSSKIELNRKLI--------
                                                                                                                                                               LLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKL 1143
                                                                                                                                                                                                       QSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSII--DLKEKEIPELRNKLQNVNR 759
                                                                                                                                                                                                                                                                                                                               RKKLEEDINKLKK---TLQLSFDLYNKYKLKL------ERLFDKKKTVGKYKMQI 1032
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	513	6 DRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKM	Ov 47	2
	392	7 THNGQRSSMAPHDQTNGIYIQNLQEFHITHAMEGLHLLQKGLKHRQVASTKMHDFS	Db 33	
	475	KIESDK-KS	Оу 42	0
	336	9 RSLNDLTPKAALLRKRLRTKSLPNTIKQQYQQQQAVNSRNNSSSNSGSTTNNASSNTN	Db 27	ь
	421	IDISAKVET	Qy 37	Ω
	278	2SNSNGSSNTGFDGQFMKKLRIFASSTANNTTSNSASSSRSNSRNSSP	Db 23	-
	372	IKEIAKTIKFNI	Qy 32	n
	231	F -	Db 17	п
	322	- ₩	Оу 279	р
	173		Db 132	п
	278	VFGYRKPLDNIKDNVGKMEDY	Qy 221	Ω
50;	ps); Conservative 169; Mismatc	atch	
		3.6%; Score 303.5; I	Query	
		ORGANISM: Saccharomyces cerevisiae 99-541-782-4	s-	c
		38	9	
		FastSEQ for		
		NT FILING DATE: 2000-04-03 R OF SEO ID NOS: 10	A CO C	
		WENTION: Antitungal Assay	FILE	٠. ٠.
		Sakowicz, Roman Beraud, Christophe	APF	
		L INFORMATION: CANT: Nislow, Corey	GENE	
		41-782-4 nce 4, Application US/09541782 nt No. 6284480	S-09-5 Seque Pater	·· ·· a :
			ESULT	ובי
		2 NVSASDKRRNYNYRVVMLK 1190	Db 117	п
		-VGIA	Qy 1480	Ω
	1171	0 DLDIYYKTLDQAIMKFHSMKMEEINKIIRDLWRSTYRGQDIEYIEIRSDADE	Db 1120	
	1479	KIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKT	Qy 1431	n
	1119	0 LEENIDNIKRNHNLALGROKGYEEEIIHFKKELREPOFRDAEEKYREMMIVMRTTELVNK	Db 1060	ь
	1430	3 YKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND	Qy 139	Ω
	1059	O DMRLMRQDIDTQKIQERWLQDNLTLRKRNEELKEVEEERKQHLKEMGQMQVLQMKSEHQK	Db 1000	ь
	1392		136	Qy
	999	KOKETELN	Db 94	6
	1363	TSSNYVVKDPYKEKR	Qy 132	Ø
	948	8 -AKEQVSPLETTLEKFQQEKEELINKKNTSNKIAQDKLNDIK	90	Db
	1319	/IDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDI	Оу 126	0
	907	4 QDQQEQIQHLKSTTNELKSEKLQISTNLQRRQQLEEQTVELSTEVQSLYREIKD-	Db 85	D

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APPLICANT: NISLOW, COTEY
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,82/
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR TILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.
; ORGANISM: Saccharomyces cerevisiae US-09-723-820-4
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US-09-723-820-4
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                              SEQ ID NO 4
LENGTH: 1038
TYPE: PRT
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                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09723820 Patent No. 6468760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        QFEQLINKHNMLKDNIKNSITSTHSHITNVDDIYNTIENIMKNYGNKENATKDEMIENIL
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QFEQLINKHNMLKDNIKNSITSTHSHITNVDDIYNTIENIMKNYGNKENATKDEMIENIL 983
                                                                                                                                                                    ADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGK-----YK 1029
                                                                                                                                                                                                                                         NLNNSLKLFENILSLGKN----KNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSK 974
                                                                                                                                                                                                                                                                                                            VCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSAN--DDTSHST 917
                                                                                                                                    NDHL----DENKKLIMHNLTTATSAVIDQEMDLFEPKRVKWENSFDLINDCDSMNNEFYN 874
                                                                                                 MQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENT ---LENTKILLK 1086
                                                                                                                                                                                                         EENNNMKQYL-----KNHFFKNNHQELL-NRHVDSTYENIEKRT----NEFVENFKKVL
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                                                                   -ESISVM-----KGQVEESENAISLLKNNTKFND
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Qy 85 GGSVASGGSVASGGSVASGGSGNSRTINPSDNSSDSDAKSYADLKHRVRNYLLTIKELKY 144	Query Match 3.6%; Score 302.5; DB 4; Length 3169; Best Local Similarity 18.7%; Pred. No. 8.8e-08; Matches 392; Conservative 277; Mismatches 596; Indels 829; Gaps 97; Qy 25 YQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSGGSVAS 84	મિંત્ર ઉજન વર્ષ	ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J. REGISTRATION UNMBER: 27386 REFERENCE/DOCKET NUMBER: 960296.95017 TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 251-5000 TELEPHONE: (608) 251-9166 INFORMATION FOR SEO ID NO: 257:	CORRECTION SYSTEM: CC-DOS/MS-DOS CORRENT APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-Dec-1999 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998	PONDENCE PONDENCE DDRESSEE: DTREET: 1 ITY: Madi ITY: Madi ITY: WI OUNTRY: U OUNTRY: U OUNTRY: U OUNTRY: U	RESULT 22 US-09-453-702B-257 US-09-453-702B-257 Sequence 257, Application US/09453702B Patent No. 6365723 Patent No. 6365723 Patent No. 6365723 Patent No. 6365723el Sequences of E. coli 0157 NIMBER OF INVENTION: No. 6365723el Sequences of E. coli 0157	Qy 1133 KDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFL 1189 : : : : : : : : : : : :
: :		QY 633 KTQLILKNVELKHNIHVPNSYKQENYQEIVLKKEIDKL	LPTSLYYEIDSRSFF LMNXIDELK : : ISSKIDNPLALRSIR	512 - MMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME	453 KFGDRFQLRDINTLESFKKPQDYFFYQQEMLLRWNYAAASDQVRINILKEYGGIYTDTDI 423 LNSFGDLINPFDYTKEDSKNIYTDNERKKFINE-IKEKIKIEKKKIESD 423 LNSFGDLINPFDYTKEDSKNIYTDNERKKFINE-IKEKIKIEKKKIESD 1 :	Qy 300 SVLEKRIDILK	OY 251 NINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLI 299 :: :: : : : : : : :

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RESULT 23
US-08-290-919-3
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ZIF: 2000 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLKTLSE-----ESIQTEDNYASLENFKVLSKLEGKLKDNL-------
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                                                                                                                                                                RY: U.S.A.
20005-3918
                                                                                                                                                                                                                                                        D.C.
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                                                                                                                                                                                                                                                                                                                                               1100 NEW YORK AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                           CUSHMAN DARBY & CUSHMAN, L.L.P.
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RESULT 24
US-08-480-604A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 6, Application US/08480604A Patent No. 5736139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                           APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-FEB-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-FEB-1993 ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                OPERATING SYSTEM: PC-DU5/ms COPTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /Label= X
OTHER INFORMATION: /note= "X = M and N, or
                                                                                                                                                                                                        CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
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FILING DATE: 04-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                  CLASSIFICATION:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                          220 MONTGOMERY STREET,
                                                                                                                                                                                       UNITED STATES
                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                   Floppy disk
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                                                                                    Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
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APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
APPLICATION NUMBER: US 08/405,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 --- NKY-RIPERLKNK---- EKVKVTFIGHGKDEFNTSEFARLSVDSLSNEISSFLDTIK 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 ISYEATCHLESKNPKNSIIIQRNMNESAKSYFLSDDGESILEL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538 TGGSLSEDNGVDFNKNTALDKNYLLNNKIPSNNVEEAGSKNYV------HYIIQLQGDD 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2710 amin
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
  KLTKALK---YMEDYS--LRNIVVEKELKYYKNLISKIENE-----
                                                                   TKEYEKLLNEIYDSKFNN---NIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLE
                                                                                                                          Y---ELKK-LNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEHI 927
                                                                                                                                                         YTDNERKKFINEIKEKIKIEKKKIESDKKSYEDR-----
                                                                                                                                                                                                                ------EKLEP------VKNIIH--NSIDDLIDEFNLLENVSDEL
                                                                                                                                                                                                                                          KNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI 443
                                                                                                                                                                                                                                                                                                   KNIPGLASISEDIKTLLLDASV-----SPDTKFILNNLKLNIESSIGDYI---YY----
                                                                                                                                                                                                                                                                                                                                           GNTP-----NTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN 383
                                                                                                                                                                                                                                                                                                                                                                                GANQYEVRINSEGRKELLAHSGKWINKEEAIMSDLSSKEYI--FFDSIDNKLK----AKS
                                                                                                                                                                                                                                                                                                                                                                                                            YQAQYDLSIYNKQLEE--AHN--LISVLEKRIDTLKKNENIKELLDKI-NEIKNPPPANS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDISPKNVEVNLLGCNMFSYDFNVEETYPGKLLLSIMDKITSTLPDVNKNSI-----TI 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCANDYCQIPENLKIRANELDVLKKLVFGY------RKPLDNIKDNVGKMEDYIK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKYPQLFDL-----TNHMLTLCDNIHGFK--YLIDGYEEINELLYKLNFYFDLLRAKLND 194
                                           TKEISTIKNSIITDVNGNLLDNIQLDHTSQVNTLNAAFFIQSL-----IDYSSNKDVLN 981
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----- IETLV 582
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-MVFENLAKTV 1512 : :	LTKFLSTGMVF	32 IADLSTDYNHNNL	Qy 148
KTVNDKIDLFVIHLEÅKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVG 1481	EAKVLNYTYEKSNVEV	2 ETLY : 1 VTGW	Oy 142 Db 185
KKYINDKQGENEKYLPFLNNI 1421 	FG : -	34 GYYKILSEKYKSDLDSI- : : : : 	Oy 1384 Db 1791
LIPYKDLTSSNYVVKDPYKFLNKEKRDKFLS-SYNYIKDSID-TDINFANDVL 1383 	DLTSSNYVVKDPYKFLNKEKRDKFLS- 	s D	Qу 1332 рь 1733
VYRSLKKQLENNVMTFNVNVKÖILN-SRFNKRENFKNVLES 1331 : :	QLENNVMTFNVNVKD-	6 LKPLAG 7PLYG	Qy 1286 Db 1677
QNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLY 1285 : :: :: :: :: ::: ::: ::: :::	PIFGESEEDYDDLGQV	6 TITTS : : 9 SSSKS	Qy 122 Db 163
LESYKKFLPEGTDVATVVSESGSDTLE-QSQPKKPASTHVGAESN 1225 :	DKY	SENNTDVNNA : :: NFMNLFLDN-	Qy 1172 Db 1580
KLSYLSSGLHHLIAELKEVIKNKNYTGNSP 1171 	SIDESISLVSKNOVKVN	24 VLSKLEGKLKDNLNLEKK- ::: : : 21 -INTITGKYYVDNNTDKSI	Qy 1124 Db 1521
KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK 1123 ::::	KKDS	58 EAEIAETENTLENTKILLKHY :: : :: 1 :: : :: 71 FGAISKTSQKSII-HY	Qy 1068 Db 1471
YNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKK 1067	DKKKTYGKYKMQIKKLTLLKEQ : : : DKNYLISNLSNTIEKINTLG		Qy 1008 Db 1426
FTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDL 1007	SETNEVKSKADDINSLNDE	18 SENFYEKILKDSDTFYNES : : : : 90 IDFSGDIDNKDRYI	Qy 948 Db 1390
NSLKLFENILSLGKNKNIYQELIGQKS 947 ::: : :: KLIKDVLSKIDINKNKLIIGNQT 1389	LTPQDKPEVSANDDTSHSTNLNNSLKLFENILS-	SSSMQPLS	Qy 891 Db 1365
NNIPVMYSMFDSLNNSLSØLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLS 890	QLFMEIYEKEMVCNLY	р р	Qy 83 Db 131
DYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQ 830 : : : : : : : : :	CHKYILVSHSTMNEKIL : : EDYAITTLKPVYEDIN	DYLEKLY : DSIRDLYPG	Qy 773 Db 1254
VPVPVPEAKAQVPTPPAPVNNKTENVSKL 772 : : :	ZEQKQAQPPVPVPVPEA	18 GQQAGSALEGDSVQAQAQAQËQKQAQPPVPVPVPEAKAQV : :: :: SLSIYSAIGIETENLDFSKKIMMLPNAPSRV	Qy 718 Db 1201
EKKNKTEGQSDNSEPSTEGEITGQATTKP 717	LGTCNILAMEGGSGHT	9 PKVESLINE : : : 8 PIDDLVISE	Qy 67 Db 114
LMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFM 678 :	LMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPY	LPIAG	Qy 624 Db 1096
KDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVL 623 :	- KD	3 ENIK : 9 DGINLGAAIKELL	Qy 58 Db 103
: -VNLISNAVNDTINVLPTITEGIPIVSTIL 1038		: :: :: : 32 DLSTSVKVQLYAQLFSTGLNTIYDSTQL-	Db 982

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US-08-405-496A-6
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                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION NUMBER: US 07/429,791
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,496A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1905 FAPANT - QNNNIEGQAIVYQSKFLTLNGKKYYFDNNSKAV 1943
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
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                     244
                                                                                                                                  591
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                                                                                                                                                                                                                                        84 SGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIK--E 141
                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                        ---NKY-RIPERLKNK----EKVKVTFIGHGKDEFNTSEFARLSVDSLSNEISSFLDTIK 685
                                                                                           VCANDYCQIPFNLKIRANELDVLKKLVFGY------
                                                                                                                                  ISYEATCHLFSKNPKNSIIIQRNMNESAKSYFLSDDGESILEL------
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T: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
CALIFORNIA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                     262; Mismatches
-NINE------LIEESKKTI-DKNKNATKEEEKKKL 278
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Pred. No. 1.2e-07;
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 NFMNLFLDN-ISFWKLFGFENINFVIDKYFTLVGKTNLGYVEFICDNNKNIDIYFGEWKT 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SENNTDVNNALESYKKFLPEGTDVA----TVVSESGSDTLE-QSQPKKPASTHVGAESN
                                                                         -INTITGKYYVDNNTDKSIDFSISLVSKNQVKVNGLYLNESVYSSYLDFVKNSDGHHNTS
                                                                                                                                                 FGAISKT-----SQKSII-HYKKDSKNILEFYN--DSTLEFNSKDFIAEDINVFMKDD--
                                                                                                                                                                                      EAEIAETENTLENTKILLKHY----KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFK 1123
                                                                                                                                                                                                                                                                YNKYKLKLERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKK
                                                                                                                                                                                                                                                                                                                                          SENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDL 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLS 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSIRDLYPGKFYWRFYAFFDYAITTLKPVYEDTNIKIKLDKDTRNFIM----PTITTNEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDDLVISEIDFNNNSIKLGTCNILAMEGGSGHTVTGNIDHFFSSPSISSHI-----P 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKEYEKLLNEIYDSKFNN---NIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLE 541
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                                                                                                          VLSKLEGKLKDNLNLEKK---KLSYLS----SGLH---HLIAELKEVIKNKNYTGNSP
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Length Indels

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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,136
FILING DATE:
CLASSIFICATION.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1905
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                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                     PRIOR APPLICATION DATA:
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-
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APPLICANT: STAFFORD, DOUGLAS C.

TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT

TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
CITY: S
STATE:
                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
 APPLICATION NUMBER: 51-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF
 JMBER: US 07/429,791
31-OCT-1989
                                                      JMBER: US 07/985,321
04-DEC-1992
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Best Local Sin
Matches 339;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: OP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
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NAME: INGOLIA, DIANE E
REGISTRATION NUMBER: 40,
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LENGTH: 2710 amino acids
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GQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV---PTPPAPVNNKTEN--VSKL 772
                                                                                                                                                                                                                                                                                     DLSTSVKVQLYAQLFSTGLNTIYDSIQL---VNLISNAVNDTINVLPTITEGIPIVSTIL 1038
                                                                                                                                                                                                                                                                                                                         KLTKALK---YMEDYS--LRNIVVEKELKYYKNLISKIENE----
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                                                        PIDDLVISEIDFNNNSIKLGTCNILAMEGGSGHTVTGNIDHFFSSPSISSHI-----P
                                                                                           PKVESLINEEKKN----
                                                                                                                                 LPIAGISAGIPSLVNNELICHD-KATSVVNYFNHLSESKKYGP-----LKTEDD--KILV 1147
                                                                                                                                                                    -----LMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFM 678
                                                                                                                                                                                                             DGINLGAAIKELLDEHDPLÄKKEL---EAKVGVLAINMSLSIAATVASIVGIGAEVTIFL
                                                                                                                                                                                                                                              ENIK-----KDEEQLEEKKITKDENKPDEKILEVSDIVKVQVQKVL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Y --- ELKK-LNNLDEKYLISFEDISKNNSTYSVRFINKSNGESVYVETEKEIFSKYSEHI
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20.4%; Pred. No. 1.2e-07;
Live 262; Mismatches 573;
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                                                                                                                                                                 Sequence 6, Application US/08957310 Patent No. 6365158
                                                                                                                 GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Kink, John A.
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                                                                  TITLE OF INVENTION: IDENTIFICATION TITLE OF INVENTION: OF TOXIN A AND TITLE OF INVENTION: DISEASE
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                                  NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                      ADDRESSEE:
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220 Montgomery Street,
                 Medlen & Carroll
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FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diana
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino aci
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STATE:
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FILING DATE: 24-OCT-1994
APPLICATION NUMBER: US 08/161,907
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COMPUTER: II
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                 YTDNERKKFINEIKEKIKIEKKKIESDKKSYEDR--
                                                                                                                 KNIPGLASISEDIKTLLLDASV----SPDTKFILNNLKLNIESSIGDYI---YY----
                                                                                                                                            GNTP-----NTLLDKNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKN
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                                                                  KNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Applic Patent No. 5733772
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-JAN-1
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
1654 QLEEVIYNDIESLELK---
                                                                                                                                                                                                                     1502 LKNNLANF--TYKHQFNYMEIPALMDNDISFKCICVDLKKKKYNVKSPLGPKVLRALYKK 1559
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                                                                                                                                                                                                                                                       128 LKHRVRNYLLTIKE----LKYPQLFDLTNHMLTLCDNIHGFKYLID---GYEEINELLYK 180
                                   291 QLEEA-HNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTL----LDKNK
                                                                                                                                                                                                                                                                                            Local Similarity hes 347; Conserv
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Quine, Jonathan REGISTRATION NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Kaslow, David C.
Cloning and Expression of Plasmodium
AVENTION: faliciparum Transmission-Blocking Tax
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-DIEQYVLQVN-LKAPKLMMSAQIHNNRHVCDFSKNN
                                                                                                                                                                                                                                                                                            Score 298; DB 1;
Pred. No. 1.5e-07;
0; Mismatches 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -INGKHFYFNNDGVMQLGVFKGPDGFEY 1904
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                                                                                                                                                                                                                                                                                                                             Length 3135;
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                                                                                                                                                                                                                                                                                               582;
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                                     345
                                                                                                                                                                                    235
                                                                          1653
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	.232	1175 NTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQN 1232 :::: :	Qy 11 Db 25	
	74	1116 Y-ASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN 1174	Qy 11 Db 25	
	15	1056 LQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSDLKTLSEESIQTEDN 1115 	Qy 10 Db 25	
	55	1016 ERLFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHV 1055	Qy 10 Db 24	
	43 5	964 NESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015 	Qy 9 Db 23	
	87	925 LFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFY 963 	Qy 9 Db 23	
	28	869NDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLN-NSLK 924	Qy 8 Db 22	
	80	813 EESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKD 868 :	Qy 8 Db 22	
:	26 :	753 AQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKE 812	Qy 7 Db 21	
	67	699 DNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPDEAK 752	Qу 6 Db 21	
	29	639 KNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFWPKVESLINEEKKNIKTEGQS 698	Qу 6 рь 20	
	93	592LFEK-KITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLIL 638 : ::	Qy 5 рь 20	
		559 VVEKELKYYKNLISKI	Qy 5 Db 19	
	2	519 YKV	Qy 5 Db 19	
	8	468 ESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMM-GKRYS 518 	Qy 4 Db 18	
	7	435 YTKEPSKNIYTDNERKKFINEIKEKIKIEKKKI 467 	Qy 4 Db 18	
	19	393ETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFD 434	Qу 3 рь 17	
	54 2	346 KIEEHEKEIKEIAKTIKFNIDS-LFTDPLELEYYLREKNKNIDISAKV 392 	Qy 3 Db 17	

	INFORMATION FOR SEQ ID NO: 2:	
	TELEFAX: (415) 576-0300	
	TELEPHONE: (415) 576-0200	
	REFERENCE/DOCKET NUMBER: 015280-1131100S	
	440	
	NAME: Einhorn, Gregory P.	
	FILING DATE: 29-JAN-1993	
	APPLICATION NUMBER: US 08/010,409	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 08/323,170	
	PRIOR APPLICATION DATA:	•. •
	FILING DATE: 20-00T-199/ CLASSIFICATION: 424	
	APPLICATION NUMBER: US/08/954,441	•••
	CURRENT APPLICATION DATA:	
	DOS	
	PC compat	
	COMPUTER READABLE FORM:	
	-	
	COUNTRY: USA	
	- ED	
	τ.	
	PONDENCE ADDRESS:	
	R OF SEQUENCES: 4	
gen, Pfs230	TITLE OF INVENTION: Cloning and Expression of Plasmodium TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen,	
	Kaslow, David C.	
	Patent No. 6316000	
	Sequence 2, Application US/08954441	
	RESULT 29 US-08-954-441-2	C 24
	b 2994 HLFTYSKKPLPNDDDICNVTIG 3015	ДĎ
	y 1546 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNG 1579	Оу
2993	2953 NSLSLTK-QNQNIIYGNVAKIFIHINQGYKEIHGCDFTGKYS	Db
1545	1491 HNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFR	Οv
2952	2904 NYNKPINIEHILPGAITTDIYDTRTKIKQYILRIPPYVHKDIHFSLEFN	da
1490	1447 TYEKS-NVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYN	. Оу
2903	2845 TCEIIDTIDSSVLKEHHTVHYSITLSRWDKLIIKYPTNEKTHFENFFVNPFNLKDKVL-Y	ф
1446	1417 FLNNIETLYKTV	УО
2844	Db 2787 EKFEEELIDTKKVLACTCDNKYIIHMKIEKSTMDKIKIDEKKTIGKDICKYDVTTKVA 2	
1416	1369KDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLP	γo
2786	2730 CFDEVYYVKQEDVPSKTITADKYNTFSKDKIGNILKNAISINNPDEKDNTYTYLILP	Db
1368	1324 NFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYI	у
2729	Db 2670 CDFLYLENQTNDAISNNNNNSYSIFTHNKNTENNLICDISLIPKTVIGIKCPNKKLNPQT 2	Г
1323	1281 YEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSFENKRE : : : : : : :	у
2009	DD 201/ DGASSIFIERIADE DILLUME CONSTINUE MUNNISHMETHITIES NUNHTHE C	
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1280	Qy 1233 VDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENE 1	_ ი

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Best Local S
Matches 347
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LENGTH: 3135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                        2168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1993
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                                                                                                                                                                                                                                                                                                                                                                             2053 VHLCNFFDNPELTFDNNK----------IVLCKIDAELFSEVIIQLPIFGT 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1820 KFFEKVINEYDDTEEEKDLESILPGAIVSPMKVLKKKDPFTSYAAFVVPPIVPKDLHFKV 1879
                                                                                                                                                                                                                                                                                                                                                                                                                      592
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                                                                                                                                                                                                                                                                                                                                          639
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---NDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLN-NSLK 924
                                                                                                                                                                                                                    KN-----EVSISLALK-----GVYGNRIFTFDKNGKKGEGISFFIPPI-----
                                                                                                                                                                                                                                                           DNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQ-----PPVPVPVPEAK 752
                                                                                                                                                                                                                                                                                                                                                                                                                -----LFEK-KITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNKKKVAYAKVPLDYINKLLFSCSCKTSHTNTIGTMKVTLNKDEKEEEDFKTAQGIKHNN 2052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECNNTEYKDENQYISGYNGIIHIDISNSNRKING--CDFSTNNSSILTSSVKLVNGETKN 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVPESLKKKEELGGNPVNIHCYALLKPLDTLYVKCPTSKDNYEAAKVNISENDNEYELQ 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIEEHEKEIKEIAKTIKFNIDS-LFTDPLELEYYLREKNKNIDISAKV-------
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                                                         KKCTVKIKKGD----IFGLK--CPKGFAIFPQACFSNVLLEYYKSDYEDSEHINYYIHKD 2280
                                                                                                                                      -KQDTDLKFIINETIDNSNIKQRGLIYIFVRKNVSENSFKLCDFTTGSTSLMELNSQVKE
                                                                                                                                                                                                                                                                                                                                      KNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQS 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESDKKSYEDRSKSLN-----DITKEYEKLLNEIYDSKFNNNIDLTNFEKMM-GKRYS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTKEPSKNIYTDNERKKFINE----IKEKIKIEKK------KI 467
                                                                                             EES--KLSSCDPLDLLFNIQNNIPVMYSMFDS--LNNSLSQLFMEIYEKEMVCNLYKLKD 868
                                                                                                                                                                           AQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKE 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TDANPESII-ESLSINESNESGPFPTGDVDAEHLILEGYDTWESLYDE 1653
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07261 LARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES '	11, Application PC/TUS93 INFORMATION: PfEMP3 MA OF SEQUENCES: 23 PPONDENCE ADDRESS: RESSEE: John H. C. Blasd ET: One Giralda Farms FE: New Jersey TE: Wadison TE: New Jersey TES: USA 07940-1000 TER READABLE FORM:	RESULT 30 PCT-US93-07 ; Sequence ; GENERAL ; TITLE ; NUMBEI ; CORRES ; ADDJ STRR CCITY ; COUD ZIP- ; COMPUT
PTCNENNG 1579 DICNYTIG 3015	46 HLDEREECKCLLNYKQEGDKCVENPNPTCNENNG	Qy 15 Db 29
LDGNLQGMLNISQHQCVKKQCPQNSGCFR 1545 :: :	91 HNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQ :: : : : : 53 NSLSLTK-QNQNIIYGNVAKIFIHINQ	Qy 14 Db 29
VKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYN 1490 : : : : : : : : TKIKQYILRIPPYVHKDIHFSLEFN 2952	TYEKS-NVE	Qy 1447 Db 2904
NNIETLYKTV 1446	7 FL 5 TC	Qy 141 Db 284
EKYKSDLDSIKKYINDKQGENEKYLP 1416 : : :: : : : :	69KDSIDTDINFANDVLGYYKILS	Qy 13 Db 27
VVKDPYKFLNKEKRDKFLSSYNYI 1368 	24 NFKNVLESDLIPYKDLTSSNY :: : : : : : : : : : :	Qy 13 Db 27
FNVNVKDIL	81 YEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDIL	Qy 12 Db 26
DDLGQVVTGEAVTPSVIDNILSKIENE 1280 : :: : : DITFHLFCGKSTTKKPNKKNTSLALIHIHISSNRNIIHG 2669	33 VDDEVDDVIIVPIFGESEEDY :: 7DGVSSILIPPYVKE	Qy 12 Db 26
YKKELPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQN 1232 :	5 NTDVNNALES	Qy 117 Db 258
KLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSDSEN 1174	16 Y-ASLENFKVLS :: 45 YGVSLDHLNQIK	Oy 11 Db 25
NFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQFEDN 1115 	56 LQ 02 FP	Qy 10 Db 25
LFDKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHV 1055	16 ER	Oy 10 Db 24
SLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKL 1015 - : : : 	64 NESFTNFVKSKADDIN	Qy 9 Db 23
NKNIYOELIGOKSSENFYEKILKDSDTFY 963 	925 LFENILSLGKNKNIYOELIGOKSSENFY	Qy 9 Db 23
LMDENFRELQ-NIQQYTGISNITDVLHFKNFNLGNLP 2328	2281 KKYNLKPKDVIELMDF	Db 22

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; MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
LENGTH: 1588 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201-822-7398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
    488
                                                                                                                                                                               393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 KKNKKTIENINE--LIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLIS
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REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/927,531 FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 EKNEKARNALKEKKLKEQKKNDAQKAKDLTKKESQD-----SSSEKSLKEKVNGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                LILKNVELKHNIHVPNSYKQENKQEPYYL-----IVLKKEIDKLKVFMPKVESLINEE 688
                                                                                                                                                                                                                                                                                                                                                             ---KLKEDK----EKKLIAAEEPDDEKKIKLKDSDDKVVVPVN---
                                                                                                                                                                                                                                                                                                                                                                                                       LVENIKKDEEQLFEKKITKDENKPDEKILEVSD-----IVKVQVQKVLLMNKIDELKKTQ
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  DYQL-EHEPPTKLPEYEKGHVSREYQLDHEPPTKLPEYE---
                                       KYILVSHSTMNE-----KILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDS
                                                                                      REKRENPDGEPLNTPEIHV---IRPSDLMDKGENKSAGHPFKYQPTKGLKEY-EESHVSK 487
                                                                                                                                QEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVS-----KLDYLEKLYEFLNTSYICH 789
                                                                                                                                                                                                                       KKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQ------AQA
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                                                                                                                                                                                                                                                                    -KNKSSFPDKFRAPDKKRTMFYRLSELFPIVPRKD-NELAVCGDSMDSKVNGK 392
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                                      CTEEDSG-----SNGKKIT 1600
                                                                               TGLKNTPSKGQQNTGLKNTPNERQQNTGLKNTPSEGQQNTGLKNTPSEGQQNTGLKNTPN 1310
                                                                                                                                                                                                                                                                                      DLFVIHLEAKVLNYTYEKSNVEVKIKEL------NYLKT--IQDKLADFK- 1474
                                                                                                                                                                                                                                                                                                                                                                     NFANDVL---GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND-KI 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVYRSLK---KQLEN-----VL 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLENFKYLSKLEGKLKDNL---NLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN 1174
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                                                                                                                      CVKKQCP----QNSGCFRHLDEREECKCLLNYKQEGDKCVENPN-PTCNENNGGCDADAK
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                                                                                                                                                               MKNKELLNKDISNKDMKNKELLNKDLSN----EDMKNKELLNKDIRNKDLKSIGNMEQQN 1250
                                                                                                                                                                                                      -KNNNFYGIADLSTDYNHNNLLTKFLSTGMVFENLAKTVLSN--LLDGNLQGMLNISQHQ
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Gaps

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RESULT 31

PCT-US93-07261-16

; Sequence 16, Application PC/TUS9307261

; GENERAL INFORMATION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES

; TITLE OF INVENTION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS: STREET: COUNTRY: STATE: CITY: Madison New Jersey One Giralda Farms

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PCT-US93-07261-16
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TELEFAX: 201-822-7039
TINFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FRIGHT: 1663 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.5%; Score 296; DB 5; Length 1663; Best Local Similarity 20.3%; Pred. No. 8.8e-08; Matches 308; Conservative 248; Mismatches 601; Indels 362; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMBER: PCT/US93/07261
APPLICATION UNMBER: 19930805
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,531
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERRNCE/DOCKET NUMBER: 31,895
REFERRNCE/DOCKET NUMBER: DX0288K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.
SOFTWARE: Microsoft Word 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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432 REKRENPDGEPLNTPEIHV---IRPSDLMDKGENKSAGHPFKYQPTKGLKEY-EESHVSK 487
                                      735 QEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVS-----KLDYLEKLYEFLNTSYICH 789
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                                                                                        393 KL----
                                                                                                                               689 KKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQ-----
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TOPOLOGY: linear
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                                                                                                                                                                        -----KNKSSFPDKFRAPDKKRTMFYRLSELFPIVPRKD-NELAVCGDSMDSKVNGK 392
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RE:	Qу Дъ	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Оу	Qy Db	Qy Db	Qy Db	Qy Db	Qу Дъ	Qy Db	Qy Db
SULT 32 :-09-572-191 Sequence 2, Patent No. GENERAL INF APPLICANT: APPLICANT:	1587 1311	1532 1251	1475 1195	1433 1135	1377	1330 1020	1291 960	1234 901	1175 851	1118 806	1058 762	1001 705	946 648	903 591	843 539	790 488
191-2 2, Application US/ 0. 6355466 INFORMATION: NT: Beraud, Christ	CTEEDSGSNGKKIT :::: :: ERQQNTGLKNTPSEGQQNT	CVKKQCPQNSGCFRH : TGLKNTPSKGQQNTGLKNT	-KNNNFVGIADLSTDYNHNNLLTKFL	DLFVIHLEAKVLNYTYEKSNVEVKIKEL- : : :	NFANDVLGYYKILSEK 	ESDLIPYKDL-TSSNYVVK	GYYRSLKKQLEN : : : GLKENAELKNKELRNKGSD	DDEVDDVIIVPIFGESEED : : : : TDLAKGKEVTNKARENLEE	NTDVNNALESYKKF-LPEG	SLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGL 	NESVFENKKKEAEIAETEN : :: NLEEYNETDLA	LQLSFDLYNKYKLKLERLF :: : LAKGKEVTNKARENLEEYN	KSSENFYEKILKDSDTFYN	DKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNI : : :	LNNSLSQLFMEIYEKEMYCNLYKLK : : :	KYILVSHSTMNE
09572191 Ophe	1600	QNSGCFRHLDEREECKCLLNYKQEGDKCVENPN-PTCNENNGGCDADAK 1586 :	IADLSTDYNHNŮLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQ 1531 	NVEVKIKELNYLKTIQDKLADFK- 1474	GYYKILSEKÝKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVND-KI 1432 	SDLIPYKDL-TSSNYVVKÖPYKFLNKEKRDKFLSSYNYIKDSIDTDI 1376	GVYRSLKKQLEN	DDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLA 1290 	LESYKKF-LPEGIDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNV 1233 : : : : : :	NLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSEN 1174 : : :	NFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYA 1117 	LQLSFDLYNKYKLKLERLFÖKKKTVGKYKMQIKKLTLLKEQLESKLNSLNNPKHVLQ 1057 	SENFYEKILKDSDTFYNĖSFTNFVKSKADDINSLNDESKRKKLEEDINKLKKT- 1000 	NNSLKLFENILSLGKNKNIYQELIGQ 945 : : :	NLYKLKDNDKIKNILEEAKKVSTSVKTLSSSSMQPLSLTPQ 902	SHSTMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMEDS 842

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SEQ ID NO 2
LENGTH: 13
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CURRENT APPLICATION NUMBER: US/09/572,191
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
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hes 292;
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                                KQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLY
                                                                                                     PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL
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Pred. No. 9e-08;
10; Mismatches 5
                                                                                                                                       ---WTKQQEELLSQL--NVLEKQLQE-----
-VKLEYSSF---KTNQEKEFNKLSERHMHVQL-
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RESULT 33
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                                       SEQ ID NO 2
LENGTH: 13
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application Patent No. 6379912 GENERAL INFORMATION:
                                                                                                                                                                                                                               APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kennen
TITLE OF INVENTION: No. 6379912el motor proteins and methods
TITLE OF INVENTION: their use
FILE REFERENCE: 1017
                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/723,262
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/572,191
PRIOR FILING DATE: 2000-05-17
-09-723-262-2
                                                                                                       SOFTWARE:
                                                                                                                             NUMBER OF SEQ ID NOS:
                 ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATV 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKEQLESKLNSLNNPKHVLQNFSVFFN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDTDINFANDVLGYYKILSE--KYKSDLDSIKKYINDKQGENEKYLPFLNNIETL-YKTV 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---REMENLR--LES-----QQLIEKNWLLQGQ---LDDIKRQKENSDQNHPDNQQLKNE 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSESGSDTLEQSQPKKPA--STHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDL 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKHYKGLVKYYNGESSPLKTLSEE---SIQTEDNYASLENFKVL---SKLEGKLKDNLNL 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QQMAKVQKLEESLLATEKVIS------SLEKSRDSDKKVVADLMNQIQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDK-KKTVGKYKMQIKKLTL 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QLDNLRLENEKLLESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GRASKTS-LEHLVTKLNEDREVKNAEIL----RMKEQL-----
                                                             1388
                                                                                                    FastSEQ
                                                                                                       for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LRILSEDIERDMLCEDLAHATEQLNMLTEASKKHSGLLQSAQE 1091
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Que	47	ch 3.5%; Score 294; DB 4; Length 1388; l Similarity 19.4%; Pred. No. 9e-08;
γ		VASGGSVASGGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKEL-KY
В	207	SAAEAYQVLSGGWRNRRVASTSMNRESSRSHAVFTITIESMEKSNEIVNIR 257
Qγ	152
뮹	258	TSLLNLVD-LAGSERQKDTHAEGMRLKEAGNINRSLSCLGQVITALVDVGNGKQRHVCYR 316
VΩ	199	KIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYII
B	317	DGNAKTAIIANVHPGS 344
Qy	250	ENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKOLEE 294
Ъ	345	RCFGETLSTLNFAQRAKLIKNKAVVNEDTQGNVSQLQAEVKRLKEQLAELASGQTPPESF 404
Qy	295	AHNLISVLEKRIDTIKKNENIKE-LLDKINEIKNPPPANSGNTPNTLLDKNKKI 347
В	405	LTRDKKKTNYMEYFQEAMLFFKKSEQEKKSLIEKVTQLEDLTLKKEKF 452
VΩ	348	EIAKT
용	453	IQSNKMIVKFREDQIIRLEKLHKESRGGFLPEEQDRLLSELRNEIQTLREQIE- 505
VΩ	401	NEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKI 460
8	506	-HHPRVAKYAMENHSLREENRRLRLLEPVKRAQEMDAQTIAKLEKAFSEISGME 558
3 8	461	KIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK 520
VΩ	521	VEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYK 568
문	613	QLELESELQSLQKANLNLENLLEATKACKRQEVSQLNKIHAETLKIITTPTKAYQLHŞ 670
Qy	569	NLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLL 624
₽	671	RPVPKLSPEMGSF-GSLYTQNSSILDNDILNEPVPPEMNEQAFEAISEELRTVQEQMSAL 729
Qγ	625	MNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDXLKVFMPKVESL 684
₽	730	QAKLDE
Qγ	685	EKKNIKTEGQSDNSEPSTEG : :
В	761	FSSERID 788
VΩ	745	PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL 804
₽	789	
VΩ	805	MEI
문	811	DKELSSVKLEYSSFKTNQEKEFNKLSERHMHVQL- 844
Qγ	865	SVKTLSSSSMQPLSLTPQDKPEVSANDDTSHST
용	845	QLDNLRLENEKLLESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSD 898
Qγ	919	
B	899	LNNLMELLEAEKERNNKLSLQFEEDKENSSKEILKVLEAVRQEKQKETAKCE 950
Qy	979	DINKLKKTLQLSFDLYNKYKLKLERLFDK-KKTVGK
뮹	951	ESLLATEKVISSLEKSRDSDKKVV
Qy	1038	LKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKIL 1084

Query Best Match Qy Db 20 Oy 11 Db 21 Oy 11	US-09-V Sequel Gener Apprix Apprix Apprix TIT: TIT: FIL: CURR CURR PRIC VENTER NUM SOF SEQ SEQ TIY TIY TIY TIY TIY TIY TIY TIY TIY TIY	
	7234	994 1085 1049 1139 1199 11199 11131 11257 11166 1317 11199 11372 1199 11372 11346
Match J.58; Score Jocal Similarity J.48; Pred. S 292; Conservative J.40; Mis S VASGGSVASGGSGNSRRTNPSDNSSDSDA J. J. J. J. J. J. J. J. J. J. J. J. J. J	219-2 2, Application US/09723 2, Application US/09723 5, 6391613 INFORMATION: WIT: BARGWICZ, ROMAN NT: WOOD, KENNETH NT: WOOD, KENNETH NT: WOOD, KENNETH INFORMATION: their use FERENCE: 1017 APPLICATION NUMBER: US PPLICATION RSSVCEKTETIDTLKQELKDINCKYNSALVDRE LKHYKGLVKYYNGESSPLKTI.SEESIQTEDN LKHYKGLVKYNGESSPLKTI.SEESIQTEDN LEKKKLSYLSSGLHHLIAELKEVIKNKNTGNSPS	
294; DB 4; Length 1388; NO. 9e-08; NO. 9e-08; NO. 9e-08; NO. 9e-08; KSYADLKHRVRNYLLTIKEL-KYPQLFDLT : : : : : : : : : : : : : : : :	1219 Wel motor proteins and methods for 109/723,219 17572,191 Wersion 4.0	SALVDREESRVLIKKQEVDILDLKETLR SALVDREESRVLIKKQEVDILDLKETLR SALVDREESRVLIKKQEVDILDLKETLR SIQTEDNYASLENFKYLSKLEGKLKOLINI
ps 70; 151 257 198 316 249		1048 11138 11091 11198 11130 11256 11165 11165 11198 11198 11198 11371 11428 11345

1256 1165	99 VSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDL: 	Oy 11:	п О
1198 1130	39 EKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSDSENNTDVNNALESYKKFLPEGTDVATV	Qy 11: Db 10:	п О
1138 1091	5 LKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNL	Qy 108 Db 104	п о
1084	LREQUESKINSKINPKH VQNESVFFN	90 ad	
993			
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898	SQLDNLRLENEKLLESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSD	0 00	
844 618	OO NQINIINEEESNISSUUPUULENIQNII SYSSMODISITEDONKURVSUUSUULENIIIKKMYCKUX	Db 63	0 11 10
810			
744 788	85 INEEKKNIKTEGQSDNSEPSTEGEITGQATTROGOAGSALEGDSVQAQAQEKQAQPPV	Qy 60 Db 70	
684 760	MNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESL :	7 6	п о
624 729		Qy 5:	п о
568 670	VEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYK : :	Qy 5:	п о
520 612	61 KIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYK	Qy 41 Db 5	п о
460 558	.01 NEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKI .	Qy 4.	п о
400 505	EBHEKEIKEIAKTIKFNIDSLF-TDPLELEYYLREKNKNIDISAKVET-KESTEP :		- 0
347 452	295AHNLISVLEKRIDTLKKNENIKE-LLDKINEIKNPPANSGNTPNTLLDKNKKI : : : : : : : : : : :	Qy 2:	- 0
294 404	150ENINELIEESKRITDKNKNATKEEEKKKLYQAQYDLSIYNKQLEE	Фу . 2: 3.	п о
344	DGNAKTAIIANVHPGS	Db 3:	п

92	540 LEKLTKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQL 5	Qγ
300	256 AKNKITKELDDLNHKYKVNVELSENTKKLKAEKIKFDDLKKEQNY 3	Ъ
539	RYSYKVEKLTHHNTFASYENSKHN	Qy
255	422 ELNSGULLNPFDYTKEPSKALYTDNEKKE" - INELKEKIKLESDKKSYEDRSK 4 :::: : : :: :	₽ Q
421 211	KNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALN : :	Qy Db
361 175	LDKINEIKNPPPANSGNTPNTLL	Qy Db
318 116	267 KNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIKEL 3	Qy Db
6	226 KPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKN 2	Оy
s 56;	Query Match 3.5%; Score 293.5; DB 4; Length 1010; Best Local Similarity 20.0%; Pred. No. 6.5e-08; Matches 240; Conservative 201; Mismatches 417; Indels 341; Gaps	M B O
STAPHYLOCOCC	RESULT 35 US-09-134-001C-5178 US-09-134-001C-5178, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 SEQ ID NO 5178 SEQ ID NO 5178 LENGTH: 1010 TYPE: PRT GORGANISM: Staphylococcus epidermidis US-09-134-001C-5178	RESUUS
	1489 YNHNULLTK 1497 	ОУ
1488 1345	1429 NDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTD 1	Qу
1428 1302	1372 IDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKOGENEKYLPFLNNIETL-YKTV 1 :	Qy
1371 1245	1317 SRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDS 1 : : : : :	Qy Db
1316 1198	1257 GQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILN 1	Дb

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RESULT 36
US-08-446-855A-2
                                                                                                                                                                                                                            Sequence 2, Application US/08446855A
Patent No. 5849573
GENERAL IMPORMATION:
APPLICANT: Stewart, Thomas S
                                                                                                                                   APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                          NUMBER OF SEQUENCES:
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                                                             STREET:
                                                                                  ADDRESSEE:
                       STATE:
                                            CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKSSE--NFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQ 1002
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                                                                                                                                                                                                                                                                                                                                                                                               FGTL-DQETLETAIDTLINLKSSGR------MVGIISHVSELKQRIPLILEVTSNQYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEQQSINKLVENFEKQEKEIVNKIHQFD-----LDLSRKNTQKEKLEIQINDFERHSQ
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                   Arlington
E: Virginia
                                                             E: Nixon & Vanderhye PC 1100 No. 5849573th Glebe
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                                                               Road,
                                                               8th
                                                               Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0:
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
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REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47
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STRANDEDNESS: single
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ILVNPNIATVQTSKGLADKV-YFLPVNCEFVEKIIKKEKPDFILCTFG
                                                                                                                                                                   ILKRKELAISYINANDKSIEGISHKNGRFYSVQFHP----EGNNGPEDTSFLFKNFLL--
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                                                                                --DIFNKKKQYREYLGYNIIYIKKKVLLLGSGGLCIGQAGEFDYSGTQAIKSLKECGIYV
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19.1%; Pre
vative 252;
                                        ----DKLKVFMPK----VESLINEEKKN--IKTEGQSDNSEPSTEGE 708
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                                                                                                                 CSNYNNASAFVNGKDRNDNLENDCIEKNMDHTYKHYNRLNNRRSTNERMMLMVNN-----
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                                                                                                                                                                                                                                       TYKKNKYKDM-----GLNNNIVDELSNGTSHSTNDHLYLDNFNTSDEEIGNNKNMDMYL 1553
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                                                                                     KTVNDKIDLFVIHLEAKVLNYT--YEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIA 1483
                                                                                                                                              -----FANDVLGYYKILSEKYKSDLDSIKKY---INDKQGENEKYLPFLNNIETLY
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US-09-150-741-2
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SEQ ID NO 2
LENGTH: 2391
TYPE: PRT
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TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.5%; Score 293.5; DB 4; Best Local Similarity 19.1%; Pred. No. 1.9e-07; Matches 323; Conservative 252; Mismatches 543;
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APPLICANT: Stewart et al.
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CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DAYE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DAYE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DAYE: 1993-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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--DIFNKKKQYREYLGYNIIYIKKKVLLLGSGGLCIGQAGEFDYSGTQAIKSLKECGIYV 727
                                  NIHVPNSYKQENKQEPYYLIVLKKEI---
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                                                                    ILKRKELAISYINANDKSIEGISHKNGRFYSVQFHP----EGNNGPEDTSFLFKNFLL--
                                                                                                                                          IIFGICLGNQLLGISLGCDTYKMKYGNR----GVNQPVIQLVDNICYITSQNHGYCLKKKS
                                                                                                                                                                                                                  IIKNLIRHGMDLPLTYIIVPYYYNFNHIDYDAVLLSNGPGDPKKCDFLIKNLKDSLTKNK
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                                                                                                        NKPDEKILEVSD----IVKVQVQKVLLMNKIDELKKTQLILKNVELKH
                                                                                                                                                                              --EKELKYYKNLISKIENEIETLVENIKKDEEQ-----LFEKK
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ILVNPNIATVQTSKGLADKV-YFLPVNCEFVEKIIKKEKPDFILCTFG

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SKEKSISN-----KNPGNSYYVVDSVYNNEYKINKMKELIDNENLNDEYNNNVNMN 1604
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                                                                   KTVNDKIDLFVIHLEAKVLNYT--YEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIA
                                                                                                                            CSNYNNASAFVNGKDRNDNLENDCIEKNMDHTYKHYNRLNNRRSTNERMMLMVNN-----
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                                           -EKESNHEKGHRRNGLNKKNKEKNMEKN-KGKNKD-KKNYHYVN-H
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US-08-755-587-44
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Matches 382;
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FILING DATE: 23-NOV-1
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials a
TITLE OF INVENTION: identificat
TITLE OF INVENTION: susceptibil
NUMBER OF SEQUENCES: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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228
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kenneth D Sibley REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9 FILING DATE: 28-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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LDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSI
                                                                 VFPHDTTANVKSYFSNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN--
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                                           KTRKKIFHEAN-----
                                                                                                                            -SCKDHIGKSMPNV---
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Plaza, 3605 Glenwood
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18.6%; Pred. No. 3.3e
ative 288; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
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                                           - - ADECEKSKNOVKEKYSFVSEVEPNDTDPLDSNV-AHQKP
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nes 717;
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----SLTPQDK-----

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	Qy 1171 PSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQS 1210	ø
	Qy ,1111 QTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNS 1170	<u> </u>
	Qy 1072 AETENTLENTKILLKHYKGLVKYNGESSPLKTLSEESI 1110 :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	<u> </u>
		<u> </u>
	Qy 986 KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT 1036	<u> </u>
RESUI US-08 ; Seq ; Pat	Qy 943 IGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLN-DES 985 : : : : :	ō ö
D	Qy 887 KTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL 942	<u>Б</u> 0
O D !	Qy 827 FNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEBAKKVSTSV 886	<u> </u>
O D :	Qy 767 ENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKLSSCDPLDLL 826	<u> </u>
O D K	OY 708 EITGOATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPTPPAPVN-NKT 766	<u> </u>
Ov Db 43	Qy 648 HVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEG 707	<u> </u>
0 D X	Qy 597 ITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNI 647	<u> </u>
מ מ	Oy 547 LKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK 596	<u> </u>
Ov Db 4	Qy 498 SKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKA 546 :: :: : : : : : : : :	<u> </u>
	Qy 438 EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYD 497 : :: :	g o
Ov Db 12	Qy 379 LREKNKNIDISAKVETKE-STEPNEYPNGYTYPLSYNDINNALNELNSFGDLINPFDYTK 437 :	g ø
0v Db	Qy 347 IEEHEKEIKEIAKTIKFNIDSLFTDPLELEYY 378 :	g ø
Ov Ov	Qy 288 YNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEI-KNPPPANSGNTPNTLLDKNKK 346	<u> </u>
D D		<u>o</u>

RES S	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db		Qy Db	Qy	ρφ	Db
SULT 39 3-08-603-753D-4 5-08-603-753D-4 5-08-603-753D-4 5-08-603-753D-4 Fatent No. 5891857 GENERAL INFORMATION: APPLICANT: HOLT, JEFFREY T. APPLICANT: JENSEN, ROY A. APPLICANT: LINGEN, ROY A. APPLICANT: SING, MARY-CLAIRE APPLICANT: SZABO, CSILLA I. APPLICANT: TOBINSON-BENION, CHERYL L. APPLICANT: ROBINSON-BENION, CHERYL L. APPLICANT: THOMPSON, MARILYN E. TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PORRESPONDENCE ADDRESS: ADDRESSE: ARLES A. TAYLOR, JR. STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER CITY: DURHAM	1611 LFDGIFCSSS 1620 :: 1973 NTCGIFSTAS 1982	1567 VENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP 1610 : : :	1531 QCVKK	1519 GNLQGMLNISQH 1530 	1470 -LADFKKNNNFVGIADLSTDYNHNNLLTK-FLSTGMVFENLAKTVLSNLLD 1518 	1439LEAKVLNYTYE-KSNVEVKIKELNYLKTIQDK 1469 	1437	1413KYLPFLNNIETLYKTVNDKIDLEV 1436	1360 KFLSSYNYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDK-QGENE 1412 : :	1309 VNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRD 1359:	1258 QVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTF 1308 : : : : : : : : : :	1211 QPKKPASTHYGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDL	1283 VSEKNNKCQLILQNNIEMTTGTFVEEITENYKR-NTENEDNKYTAASRNSHNLEFDGSDS 1341

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; PAGES: 789-792
; DATE: 1995
; RELEVANT RESIDUES IN S
; RELEVANT RESIDUES IN S
US-08-603-753D-4
                                                                                                                                                                                                                                                                                                                                                           Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 0
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: r
ANTI-SENSE: nc
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REFERENCE/DOCKET NUMBER: 124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOSTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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   278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: .BRCA2 protein
LOCATION: 1 to 3418; Genbank locus HSU43746
IDENTIFICATION METHOD:
OTHER INFORMATION: BRCA2 protein has a negation of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the information of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens sapiens INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult TISSUE TYPE: female breast CELL TYPE: normal breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 20 FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                   DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNH-MLTLCDNIHGFKYL--IDGY 171
                                                                                                                VFPHDTTANVKSYFSNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN--
                                                                                                                                                                       AVTTSTPGSKGSVASGGSGSVASGGSVASG----SGNSRRTNPS
                                                                                                                                                                                                                                       VCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASET
-SCKDHIGKSMPNV---
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                                                                                                                                                                                                                                                                                                                                                     3.4%; Score 288.5; DB 2;
18.6%; Pred. No. 5.4e-07;
vative 287; Mismatches 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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-LEDEVYETVVDTSEEDSFSLCFSKCRTKNLQKVRTS
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GENERAL INFORMATION:
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TITLE OF
                                                       APPLICANT:
APPLICANT:
                                                                                                     APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PACE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
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                     INVENTION:
                                                                                                                                                                                                                             Application US/09099753
     INVENTION:
JETTON, THOMAS L.

ROBINSON-BENION, CHERYL L.

THOMPSON, MARILYN E.

THOMPSON, MARILYN E.

VENTION: CHARACTERIZED BRCA1 AND BRCA2

VENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS

VENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
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; RELEVANT RESIDUES
; RELEVANT RESIDUES
US-09-099-753-4
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                                                            Matches
                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: ARLES A. TAYLOR, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
160 VCGSLFHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASET 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER,
STREET: BOULEVARD
CITY: DURHAM
                                                                                                                                                                           VOLUME: 3/2
789-792
                                                                                                                                                                                                                             AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                        NAME/KEY: BRCA2 prote LOCATION: 1 to 3418; IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: adult TISSUE TYPE: female breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/61 FILING DATE: 20 FEB 1996 APPLICATION NUMBER: U.S. FILING DATE: 17 JAN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                     PAGES: 789
DATE: 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens sapiens INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 27707
                                                                                                                                                                                                                JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                              7
                         LCSFLF----FIINTQCVTH--ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (919) 419-0383
                                                                                                                                                                                                                  Nature
                                                           Conservative 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WORD PERFECT 6.1 and ASCII
                                                                                                                                                                                                                                                                                                                                       1 to 3418; Genbank locus HSU43746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC/XT/AT compatible SYSTEM: Windows 3.1
                                                                                                                                                                                                                                                                                                                                                       BRCA2 protein
                                                                                                                                                                                                                                                                                                                                                                                                    normal breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. TAYLOR,
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                                                                      3.4%;
                                                                                                                                      HZ
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                                                                                                                                      SEQ
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                                                                         Score 288.5; DB 4; Length Pred. No. 5.4e-07;
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                                                                                                                                      NO:
                                                           Mismatches
                                                                                                                                     4: granin box domain at amino
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                                                           Indels
                                                                                                                                                                                                                                                                                             of human mammary cells.
                                                                                                                                      acids 3334-3344
                                                                                         3418;
                                                           663;
                                                         Gaps
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1036 1115	KRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKMQIKKLT :	986 1057	Оy
1056	IGPISNHSFGGSFRTASNKEIKLSEHNIKKSKMFFKDIEBQYPTSLACV	997	Db .
985	IGQKSSENFYEKILKDSDTFYNESFTN	943	δ 8
942	KTLSSSSMOPLSLTPQDKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELSTKKDIVVVI AFENKNSVXOHIKAMIGODIK GOTGIDITDEKNNDVANKWAGI	887	를 ⁵
941	SDNENNEVEQVANERNNLALGNTKELHETDLTCVNEPIFKNSTMVLYGDTGDKQATQV	884	Db
886	SLNNSLSQLFMEIYEKEMVCNLYKLI	827	Q V
826 883	ENVSKLDYLEKLYEFLNYSYICHKYILVSHSYMNEKILKQYKITKEESKLSSCDPLDLL 	855	Db Qy
854	ELTKNIPMEKNODVCALNENYKNVELLPPEKYMRVASPSRKVQFNON	808	В
766	EITGQATTKFGQQAGSALEGDSVQAQAQEQKQAQPFVFVFVFEAKAQVFTFPAFVN-NKT	708	Qγ
807	YDHENASTLILTPTSKDVLSNLVMISRGKESYKMSDKLKGNNYESDV	761	Db
707	PKVE	648	Ωy
760	EGQCENDPKSKKVSDIKEEVLAAACHPVQHSKVEYSDTDFQSQKSLL	714	Db
647	ITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNI	597	Qy
713	 ILRKCSRNETCSN	659	D d
596	MEDYSLRNIVVEKELKYY	547	Qγ
658	AQFEANAFEAPL	618	Дb
546	NNIDLTNFEKMMGKRYSYKVEKLTHHN	498	Qy
617	KKKTNKFIYAIHDETFYKGKKIPKDQKSELINCS	584	В
497	EPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYD	438	Qγ
583	TEASESGLEIHTVCSQKEDSLCPNLIDNG-SWPATTTQNSVALKNAGLISTL	533	Ф
437	LREKNKNIDISAKVETKE-STEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTK	379	Qy
532	: :: :: :: :: :: :: :	474	Db
378	EKEIKEIAKTIKFNIDSLFTDF	347	Qγ
473	SEXDILDTENKRKKDFLTSENSLPRISSLPKSEKPLNEETVVNK-RDEEQH	424	뮹
346	쫎	288	Qy
423	ESGSDKISKEVVPSLACEWSQLTLSGLNGAQMEKIPLLHISSCDQNI	376	Db
287	MEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDL	228	Qy
375	KTRKKIFHEANADECEKSKNQVKEKYSFVSEVEPNDTDPLDSNV-AHQKP	327	DЪ
227	EEINELLYKLNFYFOLLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKP	172	Qy
326	- SCKDHIGKSMPNV	278	DЬ
171	KHRVRNYLL	115	Qy
277	VFPHDTTANVKSYESNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN	220	DЬ
114	AVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSGNSRRINDS	61	Qy

RESULT 41
US-08-986-106-4
US-08-986-106-4
Sequence 4, Application US/08986106
Patent NO. 6177410
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: KING, MARY-CLAIRE

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; PAGES: 789-792; DATE: 1995; RELEVANT RESIDUES IN SEQ ID; RELEVANT RESIDUES IN SEQ ID US-08-986-106-4
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APPLICATION UNMBER: 08/603,753

FILING DATE: 20 FEB 1996

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION UNMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 49-8000

TELEPAX: (919) 49-8000

TELEFAX: (919) 49-8000

TELEFAX: (919) 49-8000

TELEFAX: (919) 49-8000

TELEFAX: (919) 49-8000

TELEFAX: (919) 49-8000

TELEFAX: (919) 419-0383

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 3418
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4%; Score 288.5; DB 4; Length 3418; Best Local Similarity 18.6%; Pred. No. 5.4e-07; Matches 382; Conservative 287; Mismatches 718; Indels 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptability gene BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage COMPUTER: IBM PC/XT/AT compatible OPERATING SYSTEM: Windows 3.1 SOFTWARE: WORD PERFECT 6.1 and ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: THERAPBUTIC METHODS
TITLE OF INVENTION: PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                    115
327 KTRKKIFHEAN------ADECEKSKNQVKEKYSFVSEVEPNDTDPLDSNV-AHQKP 375
                                             172 EEINELLYKLNFYFDLLRAKLNDVCANDYCOI----PFNLKIRANELDVLKKLVFGYRKP 227
                                                                                                                                                                                                 220 VFPHDTTANVKSYFSNHDESLKKNDRFIASVTDSENTNQREAASHGFGKTSGNSFKVN-- 277
                                                                                                                                                                                                                                                                                                     160 VCGSLEHTPKFVKGRQTPKHISESLGAEVDPDMSWSSSLATPPTLSSTVLIVRNEEASET 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sind
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                61 AVTTSTPGSKGSVASGGSGSVASGGSVAS--GGSVASGGSVASGG----SGNSRRTNPS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: Nature VOLUME: 379
                                                                                                                                                                                                                                                                                                                                                        7 LCSFLF----FIINTQCVTH--ESYQELVKKLEALEDAVLTGYSLFQKEKMVLNEGTSGT 60
                                                                                                                                              DNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLEDLINH-MLTLCDNIHGFKYL--IDGY 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                               -LEDEVYETVVDTSEEDSFSLCFSKCRTKNLQKVRTS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N 0
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·· Db 1176 VDSSKQFEGTVEIKRKFAGLLKNDCNKSASGYLTDENEVGFRGFYSAHGTKL-NVSTEAL
1037 1037 1116 1072
Qy 887 KTLSSSSMQPLSLTPODKPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQEL
QY 648 HVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEPSTEG
498 SKFNNNID :: 618 AQFEANA- 547 LKYMEDYS 659 LTSSFGTI 597 ITKDENKP :: 714 EGQCENDP
Qy 228 LDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDLSI :: : : : : : : : : :

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US-08-290-919-4
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                                                                                                                                                                                                                                                                             Sequence 4, Application US/08290919 Patent No. 5720959
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HOLDER
                                                                                                                                                                                                              APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1797
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                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                 COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                  STATE:
                                                                                                                 STREET:
                                                                                                                                  ADDRESSEE:
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                                                                                                   WASHINGTON
                                                                                D.C.
                                                                                                                                                                                                            BLACKMAN, MICHAEL J.
CHAPPEL, JONATHAN A.
                                                                                                                CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                               HOLDER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12,
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                       APPLICANT: CHAPPEL, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1570 PNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-FEB-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                              STREET: 110.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 04-OCCCLASSIFICATION: 43
                APPLICATION NUMBER:
                                                            APPLICATION NUMBER: FILING DATE: 04-OC
                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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                                                                                                                                                                                                                                                                               ADDRESSEE:
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5720959
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DATE:
                                                                                                                                                                                                                                                             E: CUSHMAN DARBY & CUSHMAN, L.L.P. 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                            BLACKMAN, MICHAEL J. CHAPPEL, JONATHAN A.
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                                                               04-OCT-1994
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JMBER: GB 9203821.5
22-FEB-1992
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Pred. No. 7.1e-09;
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                                                                                                                Version
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; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-4
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US-09-356-952-4
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                                                                                                                                                                                                                                                                                                                                   Query Match 3.3%; Score 279.5; DB 3; Best Local Similarity 19.8%; Pred. No. 6.3e-07; Matches 323; Conservative 234; Mismatches 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 1589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%; Score 280; DB 1; Length 48; Best Local Similarity 100.0%; Pred. No. 8e-09; Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: Mor-Sogi, Dafina
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION UMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                     226 KPLDNIKDNVGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEKKKLYQAQYDL 285
                                                                                                                              188
                                                                                     127
187 AETSSGHNNT-----VSMNNSPFSAPNDASHITPQSSNFNSNASLSQDMTKSADGSSEM 240
                                                                                                                                                                                                         140 KELKYPQLFDLTNHMLT------LCDNIHGF---KYLIDGYEEINELLYKLNFYFDL 187
                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                          81 SVASGGSVASGGSVASGGSGASGGSGNSRRTNPSDNSSDSDAKSYADLKH-RVRNYLLTI 139
                                                                                                                                                                                                                                                  RDSHLRKHSHPMKKYSSSKSSRRSSLNSLGNSAYLHVPRNPSKSRRGSSTLSASLSNAHN 186
                                                                                                                                                                    YDFNYPIKKDSSSQLLSVQQGETIYILNKNSSGWWDGLVIDDSNGKVNRGWFPQNFGRPL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                            -- LRAKLNDVCANDYCQIPFN-LKIRANELDVLKKLVFGYR 225
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                                                                                                                                                                                                                                                                                                                                                                             Length 1589;
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1272 1100	ABSNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDN	1222 1050	Оу
1221	KNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVG :	1164	Qy
1049		999	Db
1163	QTEDNYASLENFKYLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKN	1111	Оу
998		939	
938	AELAETENTLENTKIL-LAHTKOLVAKTINGESSPLKTLSEESINLIKTPSILLDLESEEFLVHAMSSVSSVLTEFFDIKQAFHDIVIRLIMTTQQT	988	Db 49
885	INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INTEGRAL INT	832	db dy
831	ET RESET IN YASAHULINGENULANESAKAKEELINALAKI IQUES LULINA IRIGEREEKEEN ET I	782	Db 09
781	TISNEVTASSSKNSSISRIPPKMADAIASASGYSANSETNSQIDLKASSA	732	2 B &
907 731 961	TYEKEMYCNLYKCKDNÖKIKNLLEBAKKYSTSVKTLSSSKØDISLTPODKPEV VQLLYFVLOSSVFSDDNTLPOLLPRFFKGSFSGGSWTNPFSTFITDEFGNATKNKA SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUSTKIEENII SI-GENKUITGGEI IGGKSGENEVEKII KDSDRE SANDDREHSTEIN NUST	854 676	5 P 04
853	KQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFME : : :	805	Qy
675		619	Db
804	PVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKIL :	745	Qy
618		586	Db
744 585	8 EKKNIKTEGOSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPV	688 549	Оу
687	KKTQLILKNVELKHNIHVPNSYKQENKQÉPYYLIVLKKEIDKLKVFMPKVESLINE	632	Qy
548		498	Db
631 497	SKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDEL	572 457	Оу
571 456	MMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKYYKNLI	512 415	Qу
511	IKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFUNNIDLTNF-EK	456	Qy
414		355	Db
455	YPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINE	403	Qу
354		320	Дъ
402	KNKKIEEHEKEIKEIAKTIKFNIDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNE	343	Qy
319		301	Db
342	SIYNKQLEEAHNLISVLEKRIDTLKKNENIKEL-LDKINEIKNDPPANSGNTPNTLLD::	286	Qy
300		241	Db

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US-08-755-587-16
US-08-755-587-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Futreal
APPLICANT: Wooster
APPLICANT: Ashwort
APPLICANT: Stratto
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                                                                                                                                                                                  APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION DATA: GB 9617961.9
FILING DATE: GB 9617961.9
APPLICATION NUMBER: GB 9617961.9
APPLICATION NUMBER: GB 9617961.9
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APPLICATION NUMBER: GB 9617961.9
APPLICATION NUMBER: GB 9617961.9
APPLICATION NUMBER: GB 9617961.9
APPLICATION NUMBER: GB 9617961.9
                                                         REFERENCE/DOCKET NUMBER: 5.
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials and methods relating to the TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer TITLE OF INVENTION: susceptibility gene and uses thereof.
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                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: N
COUNTRY:
                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RITMFECLDRAWGTKYCNMGGSPNITKFIANANTLTNFVSHTIVKQADVKT-RSKL----
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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Stratton, Michael R
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GOSTY MRICH 20.9%; SCORE 279.5; DB 3; LENGTH 2329; BBSET LOCAL SIRILITITY 20.9%; PROTECTION TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLOGY TOOLogy Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Toology Tool	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Dъ	Qy	DЬ	Qy	рb	Qy	Db	Qy	Dъ	Qy	рb	Qy	Db	ОУ	Db	Qy	Db	Qγ	Db	Qy	рь	Qy	Db	Qy	Db	Qy	Ma Ma
20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, NO. 100-06; 20.9%, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, PECED, P	1040		1003	1181	963	1144	904	1101	845	1041	815	989	Cī.	934	704	874	5	822	603	764	550	714	490	656	433	605	380	557	321	506	265	4	229	386	187	ery Ma st Loc tches
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RESULT 46
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer,
STREET: 1201 New York Avenue
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer TITLE OF INVENTION: Susceptibility Gene
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APPLICANT: Weber, Barbara
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                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                FILING DATE: 2:
CLASSIFICATION:
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                                                                                                                                                                                                                         COUNTRY:
                                                                                 APPLICATION NUMBER:
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Couch, Fergus
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                                                                   29-APR-1996
11-JAN-1996
                                                                                                                 Release #1.0, Version
                 US 08/585,391
                                                                                 US/08/639,501
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N.W., Suite 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATE: 18-DEC ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Innen, Jeffrey L.
NAME: Z8,957
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 LLRAKLNDVCAN------DYCQIPFNLK----IRANELDVLKKLVFGY------RKPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                         GFRGFYSAHGTKLNVSTEALQKAVKLFSDIENISEETSAEVH-----PISLSSSKCHDSV 1269
                                                                                                                                                                                                                   LTPSQKAEITELSTILEESGSQF----EFTQFRKPSYILQ----KSTFEVPENQMTILKT 1154
                                                                                                                                                                                                                                                                                                           VE--IVNTLALDNOKKLSKPOSINTVSAHLOSSVVVSDCKNSHITPOMLFSKODFNSNHN 1102
                                                                                                                                                                                                                                                                                                                                                    MEDYSLRNIVVEKELKYYK-NLISKIENEIETLV----ENIKKDEEQLFEKK-ITKDEN 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDYTKEPSKN-IYTDNERKKFINEIKEKIKIE-KKKIESDKKSYEDR-SKSLNDITKEYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK--ELL--D
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PTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYK-ITKEEE 814
                                                                              STEGEITGOAT-----TKPGQQA----GSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQV 755
                                                                                                                              TSEECRDADLHVIMNAPSIGQVDSSKQFEGTVEIKRKFAGLLKNDCNKSASGYLTDENEV 1214
                                                                                                                                                                        -KQENKQEPYYLIVLKK---EIDKLKVFMPKVE----SLINEEKKNIKTEGQSDNSEP 703
                                                                                                                                                                                                                                                             -KPDEK--ILEVSDIVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSY-----
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18-DEC-1995
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RESULT 47
US-09-044-946-2
                                                                            Sequence 2, Application US/09044946 Patent No. 6033857 GENERAL INFORMATION:
    APPLICANT:
APPLICANT:
                                         APPLICANT: *
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                                                                                                                                                                                                                            1964 KLHKSVSSAN-TC
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                                                                                                                                                                                                                                                                                                         HKVFADIQSEEI-----LQHNQNMSGLEKVSKISP----CDVSLETSDICKCSIG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDINFANDVLGYY
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' Tavtigian, Sean '
Kamb, Alexander
Simard, Jacques
Couch, Fergus
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Best Local Similarity
Matches 330; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08
FILING DATE: 18-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3418 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
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APPLICANT: Weber, Barbara
TITLE OF INVENTION: Chromosome 13-Linked
TITLE OF INVENTION: Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   787
                                                                                                                                                                                                                                                              727
                                                                                                                                                                                                                                                                                                                                    667 LRKCSRNETCSNNTVISQDLDYKEAKCNKEKLQLFITPEADSLSCLQEGQCENDPKSKKV
                                                                                                                                                                                                                                                                                                                                                                         187 LLRAKLNDVCAN-----
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 21-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                           SDIKEEVLAAACHPVQHSKVEYSDTDFQSQKSLLYDHENASTLILTPTSKDVLSNLVMIS
                                                                                                          KYMRVASPSRKVQFN-QNTNL---RVIQKNQEETTSISKITVNPDSEELFSD------
                                                                                                                               KINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAK-TIKFNIDSLFTDPLELEYYL
                                                                                                                                                                                                                                                                                             DNIKDNV-----GKME--DYIKKNKKTI----ENINELI--EESKKT-----ID
FDYTKEPSKN-IYTDNERKKFINEIKEKIKIE-KKKIESDKKSYEDR-SKSLNDITKEYE
                                    NENNFYFQV-----ANERNNLALGNTKELHETDL-TCVNEPIFKNSTMYLYGDTGDK
                                                                   REKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNALNE---LNS----FGDLINP
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1201 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3418 amino acids
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; MOLECULE TYPE: US-09-044-908-2
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                                                                                                   TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                      TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     FILING DATE: 20-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-DEC-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                               TOPOLOGY:
                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/573,779 FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 22204
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                                                                                                                                  TELEPHONE:
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                        NAME:
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                                                                  LENGTH:
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                                                amino acid
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Ihnen, Jeffrey L.
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1201 New York Avenue N.W., Suite 1001
                                                                    3418 amino acids
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Weber, Barbara
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Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version
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Query Match

3.38;

Score 279.5;

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Length 3418;

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1322 NKYTAASRNSHNLEFDGSDSSKNDTVCIHKDETDLLFTDQHNICLKLSGQFMKEGNTQIK 1381 845 NSLSQL-FMEIKEKEMVCNLYKLKDNDKIKNLLEEAKKYSTSVKTLSSSSMQPLSLTPQD 903 1382 EDLSDLTFLEVAKAQEACHGNTSNKEQL-TATKTEQNIKDFETS 1424 904 KPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSBNFYEKILKDSDTF- 962 1	-KQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSDNSEP	265 KNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRIDTLKKNENIK-ELL-D 320	Cal Similarity 21.0%; Pred. No. 1.6e-06; 330; Conservative 225; Mismatches 569; Indels 449; Gaps LLRAKLNDVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPL 228
ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA 2IP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: FIRM PC compatible COMPUTER: PSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/480,604A FILING DATE: 07-UN-1995 CLASSIFICATION ADATA: APPLICATION NUMBER: US 08/422,711 FILING DATE: 14-APR-1995 PRIOR APPLICATION NUMBER: US 08/405,496	RESULT 49 US-08-480-604A-10 (Sequence 10, Application US/08480604A) ; Sequence 10, Ty36130 ; Patent No. 5736130 ; Patent No. 5736130 ; Patent No. 5736130 ; Patent No. 5736130 ; Patent No. 5736130 ; Patent No. 5736130 ; APPLICANT: THALLEY, BRUCE S. APPLICANT: PADHYE, NISHA V. APPLICANT: FIRCA, JOSEPH R. ; APPLICANT: STAFFORD, DOUGLAS C. TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE ; NUMBER OF SEQUENCES: 32 ; CORRESPONDENCE ADDRESS:	Qy 1207 LEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIVPIFGESEEDYDDLGQVVTGEAVT 1266	81; Qy 1091 LVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYL 1146 1

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FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INCOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2366 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 278.5; DB 1; Length 2366; Best Local Similarity 18.5%; Pred. No. 1.2e-06; Matches 347; Conservative 292; Mismatches 595; Indels 643;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-CCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907

FILING DATE: 02-DEC-1993

PRIOR APPLICATION NUMBER: US 07/985,321

APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                        555 IVVDKE--YLLEKISSLARSSERGYIHYIVQLQGDKISYEAACNLFAKTPYDSVLFQKNI 612
                                                                                                                                        510 QSTEQEMASLWSFDDARAK-----AQFEEYKRN-----YFEGSLGEDDNLDFS-QN 554
                                                                                                                                                                                                                                                                                                                                                                403 YPNGV--TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKE-- 458
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598 TKDE----NKPDEKILE-----VSDIVKVQVQKV-------LLM 625
                                                                                                                                                                                                                                                                                                                                       399 IVKQIENRYKILNNSLNPAISEDNDFNTTTNTFIDSIMAEAN--ADNGR--FMMELGKYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENI---KELL-----DKINEIKNPPPANSGNTPNTLLDKNKKIBEH------EK 352
                                                                                                                                                                                          ---EKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYME-----DYSLRN 557
                                                                                                                                                                                                                                                                      -----KIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNF- 509
                                                                                          IVVEKELKYYKNLISKIENEIET----LVENIKKD------EEQLFEKKI 597
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Gaps

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,	Qy	Db	Qy	В	Qy	В	Qy	Db	Qy	дь	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	рь	Qy	Db	Qy.	Дb	Qy	Db	Qy	ДĎ	Qy	Db .	γO	В
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	달	ISGELKILMLNSNHIQQKIDYIGFNSELQKNIPYSFVDSEGKENGFINGSTKEGL	TSPYKFLNKEKRDKFLSSYNYIKDSIDTDI	EINFSGEVNGSNGFVSLTFSILEGINAIIEVDLLSKSYKLL	FNKRENFK	ELSESDVWIIDVDNVVRDVTIESDKIKKGDLIEGILSTLSIEENKIILNSH	VPIFGES	RINLDSNTRSFIVPIITTEYIREKLSYSFYGSGGTYALSLSQYNMGINI	NNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQ	VFAWETGWTPGLRSLENDGTKLLDRIRD-NYEGEFYWRYFAFIADALITTLKPRYEDTNI	KLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV	IWRMEGGSGHTVTDDIDHFFSAPSITYREPHLSIYDVLEVQKEELDLSKDLMVLPNAPNR	YYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKK	VLRDKATKVVDYFKHVSLVETEGVFTLLDDKIMMPQDDLVISEIDFNNNSIVLGKCE	VLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVK	SDPLLRQEIEAKIGIMAVNLTTATTAIITSSLGIASGFSILLVPLAGISAGIPSLVNNEL	LLKEQLESKLNSLNNPKH	:: :	K-YKLKLERLEDKKKTVG	KGTIFDTYNGKLVKKVNLDTTHEVNTLNAAFFIQSLIE-YNSSKESLSNLSVAMKVQVYA	SDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYN	LEDSHFISFEDISETDEGFSIRFINKETGESIFVETEKTIFSEYANHITEEISKI	PEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKD	KVMLTECEINVISNIDTQIVEERIEEAKNLTSDSINYIKDEFKLIESISDALCDLKQQNE	KEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDK	KENKITVKSKNLPELSTLLQEIRNNSNSSDIELEE	STMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE	INKEESIIK-DISSKEYISFNPINKEESIIK-DISSKEYISFNP	QKQAQPPVPVPVPEAKAQVPTPPAAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSH	SQDSIIVSANQYEVRINSEGRRELLDHSGEW	ESLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQE	➣	NKIDELKKTQLILKNVELKHNIHVPNSYKQE-NKQEPYYLIVLKKEIDKLKVFMPKV	
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Query Match Best Local Matches 34 Qy 121 DAK	TELEFAX: INFORMATION FO SEQUENCE CHA SET TYPE: and TOPOLOGY: MOLECULE TYP US-08-405-496A-10	APPLIA FILII ATTORNI REGILI REGILI REFEI REFEI REFEI REFEI RECON	PRIOR / PRIOR / PRIOR / PRIOR / PRIOR / APPLI	OPERATING OPERATION SOFTWARE: CURRENT APP APPLICATION CLASSIFIC PRIOR APPLICATION APPLICATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OP	ADDRESSE STREET: CITY: STATE: COUNTRY: ZIP: 94 COMPUTER R MEDIUM T	RESULT 50 US-08-405-496A- ; Sequence 10, ; Patent No. 59 ; GENERAL INFO ; APPLICANT: ; TITLE OF I ; TITLE OF I ; UIMBER OF ; CORRESPOND	Qy 1566 CV Qy 1687 CV	1539	Db 1525 N- Qy 1486 Db 1570 NR
atch 3.3%; Score 278.5; DB 2; Length 2366; al Similarity 18.5%; Pred. No. 1.2e-06; 347; Conservative 292; Mismatches 595; Indels 643; Gaps 92; DAKSYADLKHRVRNYLL-TIKELKYPOLEDLTNHMLTLCD-NIHGFKYL 167	(415) 397 R SEQ ID RACTERIST 366 amino no acid linear E: prote	APPLICATION NUMBER: US 07/429,791 FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION: NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: 0PHD-01308 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	199 199 199	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMBER: US.08/405,496A FILING DATE: 16-MAR-1995 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION UNMBER: US.08/329,154	EE: MED 220 MO SAN FRAN CALIFOR USA 1104 1104 12ADABLE CYPE: F	10 Application US/084054: 19665 RMATION: WILLIAMS, JAMES A. NVENTION: VACCINE FOI NVENTION: NUCOTION: NEUROTOXIN SEQUENCES: 30 ENCE ADDRESS:	ENDNIQPYEIRENTLETNYTLYVGNRQNMIVEFNYDLDDSGDISSTVINFSQKYLYGLDS 1080 CVENPNPTCNENN 1578		NILTGYYLKDDIKISLSLTLQDE-KTIKLNSVHLDESGVAEILKFM 1569STDYNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCP 1538
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RESULT 51
US-08-915-136-10
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Patent No. 6
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                                                                                                                        APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
                                                                                                          CORRESPONDENCE ADDRESS:
    COUNTRY:
                                                                                        ADDRESSEE:
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                                             SAN FRANCISCO
                           CALIFORNIA
    UNITED STATES OF AMERICA
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                                                                                        MEDLEN & CARROLL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 02-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                      403
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CLASSIFICATION:
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YPNGV--TYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKE--
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                                                               EVQSSFESVLASKSDKSEIFSSLGDMEASPLEVK--IAFNSKGIINQGLISVKDSYCSNL
                                                                                                                                                     GGMYLDVDMLPGIQPDLFESIEKPSSVTVDFWEMTKLEAIMKYKEYIPEYTSEHFDMLDE
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,/957,310)/329,154)/161,907 //985,321 //429,791 OPHD-01121	C S Dz	OTAMIV	FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FFSIL FF
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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2366 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-310-10
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                               797 STMNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 IVKQIENRYKILNNSLNPAISEDNDFNTTTNTFIDSIMAEAN--ADNGR--FMMELGKYL 454
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                                                                                                                                                                                                            TEIEAAIDLAKEDISPKSIEI--NLLGCNMFSYSINVEETYPGKLLLKVKDKISELMPSI 730
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                                                                                                                                                                 --ESLI---NEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQE
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                                                                                                                                           SQDSIIVSANQYEVRINSEGRRELLDHSGEW------
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-----KENKITVKSK-------NLPELSTLLQEIRNNSNSSDIELEE
                                                                    ---INKEESIIK-DISSKEYISFNP------
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Оу	Qу Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qу Db	Qу Db	Qy Db	Oy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qу
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CVENPNPTCNENN 1578 : : CVNKVVISPNIYTDEIN 1703	QNSGCFRHL		DLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADL 1485 :	NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKI 1432	TSSNYVVKDPYKFLNKEKRDKFLSSYNYIKDSIDTDI 1376	EVLYLKPLAGVYRSLKKOLENNVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDL 1339	NVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEY 1281 : :	NNALESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQ 1231	KLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDV 1178 ::	YYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKK 1141	VLQNFSVFFNKKKEAEIAETENTLENTKILLKHYKGLVK 1093	LLKEQLESKLNSLNNPKH 1054 ::: : : SDPLLRQEIEAKIGIMAVNLTTATTAIITSSLGIASGFSILLVPLAGISAGIPSLVNNEL 1111	K-YKLKLERLFDKKKTVG	SDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYN 1009	PEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENPYEKILKD 958	KEMVCULYKLKDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDK 904

RESULT 53 US-09-336-447A-76 ; Sequence 76, Application US/09336447A

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; FEATURE:
; NAME/KEY: MOD_RES;
; LOCATION: (1036)..(3786)
; OTHER INFORMATION: Xaa = any
US-09-336-447A-76
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SEQ ID NO 76
LENGTH: 3788
TYPE: PRT
ORGANISM: Moraxella catarrhalis
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FEDENBURG, ROSS A.
TITLE OF INVENTION: USDA1 AND USDA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLYQAQYDLSIYNKQLE----EAHN--LISVLEKRIDTLKKNENIKELLDKINEIKNPP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRKPLDNIKDNYGKMEDYIKKNKKTIENINELIEESK---KTIDKNKNATKEE----EKK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDLGTIVDGFXXXSEQIDNPRTEINLINEARNAXANYATPSITINSSITDLGTIVDSEQI 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDNPRTEINLINEARNASITDLGXKVSEQIDNPRTEINLINEARNAXANYATPSITINSI 1376
IVKVQVQKVLLMNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDK 673
                                                  TEINLINEARNAFAATAIAKDKSE---QIDNPRTEINLINEARNAKASSENTQNIAKSEQ 1861
                                                                                                                                                  PRTEINLINEARNANSSDSEQIDNPRTEINLINEARNANKADADASFETLTKSEQIDNPR 1804
                                                                                                                                                                                                                                                                                   KK--FINEIK---EKIKIEK-KKIESDKKSY----EDRSKSLNDITKEYEKLLNEIYDSK 499
                                                                                                                                                                                                                                                                                                                                                                                                AKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNER 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMDSEQID----NPRTEINLINEARNAALESNVEEGLLDLSGSEQIDNPRTEINLINEAR 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YATPSITINSLLAEQQ-----LNGKTLTPVSEQIDNPRTEINLINEARNAAKHDAASTEKG 1551
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                                                                                                SLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSD
                                                                                                                                                                                                FNNNIDLTNFEKMMGKRYSYKVE-----KLTHHNTFASYENSKHNLEKLTKALKYMEDY
                                                                                                                                                                                                                                                TEINLINEARNANQNTLIEKSEQIDNPRTEINLINEARNAALHE--QQLETLTKSEQIDN 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EINELLYKLNFYFDLLRAKLN----DVCANDYCQIPFNLKIRANELDVLKKLVFG 223
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	1582 DADAKCTEEDSGSNGKKIT	Qy
9C 1581 9C 2710	1560 KQEGDCVENPNPTCNENNGGC :	Qy Db
W 1559	1534 KKQCPQNSGCFRHLDE;REECKCLLNY	p 09
		B &
SI 2533	₽-	g p
1475	1419 NNIETLYKTVNDKIDLFVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADEKK	Qy
PL 1418 PA 2483	1363 SSYNYIKDSIDTDINFANDYLGYYKILSEKYKSD-LDSIKKYINDKQGENEKYLPFL : : : : : : : : : : : : : : : : : :	Db Qy
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	3 NVMTFNVNVKDILNSRFNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKE	γQ
2395	1243 VPIFGESEEDYDDLGQVYTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLEN :	Qу Db
		; pb
	ESYKKFLPEGTDVATVVSESGSDTLEQSQPKKPASTHVGAESNTITTSQNVD	Q
L 1182	1127 KLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTDVNNAL	p Qq
N 2279	2225 QDQKSEQIDNPRTEINLINEARNAXANYATPSTTINNQA-DIAQNQTDIODLAAYN	Дb
.S 1126	1067 KEAEIAETENTKELLKHYKGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLS	Qy
)Q 2224	: : ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	Db -
K 1066	1014 KLERLFDKKKTVGKYKMQTKKLTLLKEQLESKLNSLNNPKHVLQNESVFFNKK	Qy
TL 1013	954 KILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKL 	Qy Db
Æ 2136	2081 NPRTEINLINEARNAILGDTAIVSNSQDSEQIDNPRTEINLINEARNAKALESNVE	Db
E 953	904 KPEVSANDDTSHSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYE	Qy
-	NNIYELAQQQDQSEQIDNPRTEI	망
)D 903	845 NSLSQLEMEIYEKEMVCNLYKLKDNDKIK-NLLEEAKKVSTSVKTLSSSSMQPLSLTPQD	ον
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84 6		
784 2025	728 DSVQAQ-AQEQKQAQPPVPVPVPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNT	P 64
	EQIDNPRTEINLINEARNAAKAXAANXDRSEQIDNPRT	Дb
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US-09-315-793-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Roberts, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEI
TITLE OF INVENTION: ACENTS, HERBICIDES, II
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT FILLING DATE: 1999-05-21
RUMBER OF SEQ ID NOS: 62
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DNDKIKNLLEEAKKVST---SVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLK 924
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                                                                                                                       KAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILV----SHSTMNEKILKQY
                                                                                                                                                                                                                                                                                                         IENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKK 633
                                            KVNLRELSSADTTPP-------VPA-----ETVRDLGFEGYLSDFITG----
                                                                        KITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLK
                                                                                                                                                                  RQAESKTKSLTTTDKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSVE------SLRDFQNKKGEIELHSQLL-PY-----
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                                                                                                      KDKILEPPI-MTVSAINAQFAAYLAQCVDY-NTS----KALTVVDSDSYKLFANPILDKF
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18.0%; Pred. No. 6.5e-07;
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US-08-290-919-1
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS
TITLE OF INVENTION: VACCINE
NUMBER OF SECTION:
                                                      APPLICATION NUMBER: PCT/
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                    APPLICATION NUMBER: GB 9: FILING DATE: 22-FEB-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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             NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1 REFERENCE/DOCKET NUMBER
                                                                                                                                                             FILING DATE: 04 CLASSIFICATION:
                                                                                                                                                                          APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW CITY: WASHINGTON
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                                                                       JMBER: PCT/GB93/00367
22-FEB-1993
             NUMBER:
                          16,773
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KPKDYAEWKIEIMVKFRDNAPLKKLDSHTQSGGERAVSTVLY--MIALQEFTSAPFRVVD
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INFORMATION:
                       212242/HCM/MJL/6BC8/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
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3.38

Score 274;

DB 3;

Length 1354;

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; MOLECULE TYPE: US-08-685-871-2
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US-08-685-871-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08685871
Patent No. 6013499
GENERAL INFORMATION:
APPLICANT: NAROWIYA, Shuh
APPLICANT: NAROWIYA, Shuh
APPLICANT: INAMATSU, Akihiro
TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.3%;
Best Local Similarity 100.0%;
Matches 47; Conservative (
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/685,871
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-262553
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1527 ISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT 1573
                                                                                                                                                    NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                    TELLEFAX: (2)
TELEFAX: 904136
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LOCATION: 1
OTHER INFORMATION: /label= X
OTHER INFORMATION: /note= "X = M and N, or N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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20007-5109
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3000 K Street, N.W., Suite 500
                                                                           1354 amino acids
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(02) 822-0944
                     protein
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Pred. No. 1.7e-08;
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Qy	Db	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	рь	Qy	Ф	Qy	Db	Qy	Db	Qy	Best 1 Matche
1384 GYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFVIHLEAKV 1	960EELTEKMKKAEEEKKLEKEEEISNLKAAFEKNINTERTLKTQAVNKLAEIM 1	ΞĘ	935 DHTVSRLEE	SKIENEYEVLYLKPLAGVYRSLKKQLENNVMTFNVNVKDILNSRFNKRENFKNVLE	919 ESKKAASRNROEITDK9	1211 QPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVVTGEAVTPSVI 1	866 EIEEKNRENLKKIQELQNEKETLATQLDLAETKAESEQLARGLLEEQYFELTQ 9	NKNYTGNSPSENNTDVNNALESYKKFLPEGTDVATVVSESGSDTLEQS	837 GOMRYFSTLYKTQVKELKE 8		778 QESNKRLLLQNELKT-QAFEADNLKGLEKQMKQEINTLLEAKRLLEFELAQLTKQYRGNE 8		722 EEREAREKAENRVVQIEKQCSMLDVDL-KQSQQKLEHLTGNKERMEDEVKNLTLQLE 7		671 IDLNYKLKSLQQRL-EQEVNEHKVTKARLTDKHQSIEE-AKSVAMCEMEKKLK 7		617 RGHDSEMIGDLQARITSLQEEVKHLKHNLEKVEGERKEAQDMLNHSEKEKNNLE 6	867KDNDKIKNLLEEAKKVSTSVKTLSSSSMQPLSLTPQDKPEVSANDDTSHSTNLNNSLK 9	580 SINRELQERNRILENSKSQTDKDYYQLQAILEAERRD 6	808 KITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKL- 8	530SQNSQLANEKLSQLQKQLEEANDLLRTESDTAVRLRKSHTEMSKSISQLE 5	748 VPEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQV 8	508 KRRNV	688 EKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVP 7	495 INEYQRKAEQENE 5	YYLIVLKKEIDKLKVFMPKVESLINE	443 MQLKDEMEQKCRTSNIKLDKIMKELDEEGNQRRNLE-STVSQIEKEKMLLQHR 4	570 LISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNK 6	384 PKAFYGNOLPFYGFTYYSNRRYLSSANPNDNRTSSNADKSLOE-SLQKTIYKLEEQLHNE 4	DYSLRNIVVEKELKYYKN	337 -FFKNDQWAWETLRDTVAPVVPDLSSDIDTSNFDDLEEDKGEEETFPI 3	CINEEKMMGKRYSYKV	: :	DYTKEPSKNIYTDNERKKFINEIKEKIKIEK	Hotel Fraction (1958) Pred. No. 1e-06; Best Local Similarity 19.6%; Pred. No. 1e-06; Matches 239; Conservative 195; Mismatches 389; Indels 394; Gaps
1443	1010	1383	959	1330	934	1270	918	1210	65	1159	836	1099	777	1040	721	982	670	924	616	866	79	807	529	47	507	687	494	627	442	569	383	521	336	464	s 56;

OGY: 13 7-185 h Similar Similar 58; Cor 1 : : ATKEEEKH : AKCNKEKI PPANSGNI	APPLICATION NUMBER: GB 9617961.9 APPLICATION NUMBER: GB 9617961.9 FILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION: NAME: Kenneth D Sibley REGISTRATION NUMBER: 31,665 REFERENCE/DOCKET NUMBER: 5405-135 INFORMATION FOR SEQ ID NO: 185: SEQUENCE CHARACTERISTICS: LENGTH: 1355 amino acids TYPE: amino acid	; APPLICATION NUMBER: US/08/755,587 ; FILING DATE: 25-NOV-1996 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: GB 9523959.6 ; FILING DATE: 23-NOV-1995 ; PRIOR APPLICATION NUMBER: GB 9525555.0 ; FILING DATE: 14-DEC-1995 ; PRIOR APPLICATION NUMBER: GB 9525555.0	STATE: NC COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM OPERATING SYSTEM: PC SOFTWARE: Patentin FC CURRENT APPLICATION DAT	; TITLE OF INVENTION: Materials and methods relating to the TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer; TITLE OF INVENTION: susceptibility gene and uses thereof. NUMBER OF SEQUENCES: 222 CORRESPONDENCE ADDRESS: ADDRESSEE: Bell Seltzer Park & Gibson STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107 CITY: Raleigh	TESULT 57 S-08-755-587-185 Sequence 185, Application US/08755587 PATENT NO. 6045997 GENERAL INFORMATION: APPLICANT: Futreal, Phillip A APPLICANT: Wooster, Richard F APPLICANT: Ashworth, Alan APPLICANT: Stratton, Michael R	Db 1011 NRKDFKIDRKKANTQDLRKKEKENRK
OY 1092 VKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLULEKKKLSYLS 1147 OY 1092 VKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLULEKKKLSYLS 1147 II :	Qy 943 IGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLNDESKRKKLEEDINKLKKTLQ 1002 ; ; ;	840 FDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLEEAKKVSTSVKTLSSS	Qy 752 KAQVPTPPAPVNNKTENVSKLD-YLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKI- 809	Qy 651NSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQSD 699	Db 303 ILNIDKIPDKIDDCMDKWAGPLDPISNHSFGGSFRTASNKEIKVSEHNIKKSKMFFKDIE 362 Qy 552 DYSLRNIVVEKELKYYKNLISKIENEIETLVENIKKDEEQLFEKK- 596	Qy 369 FTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNAL 420

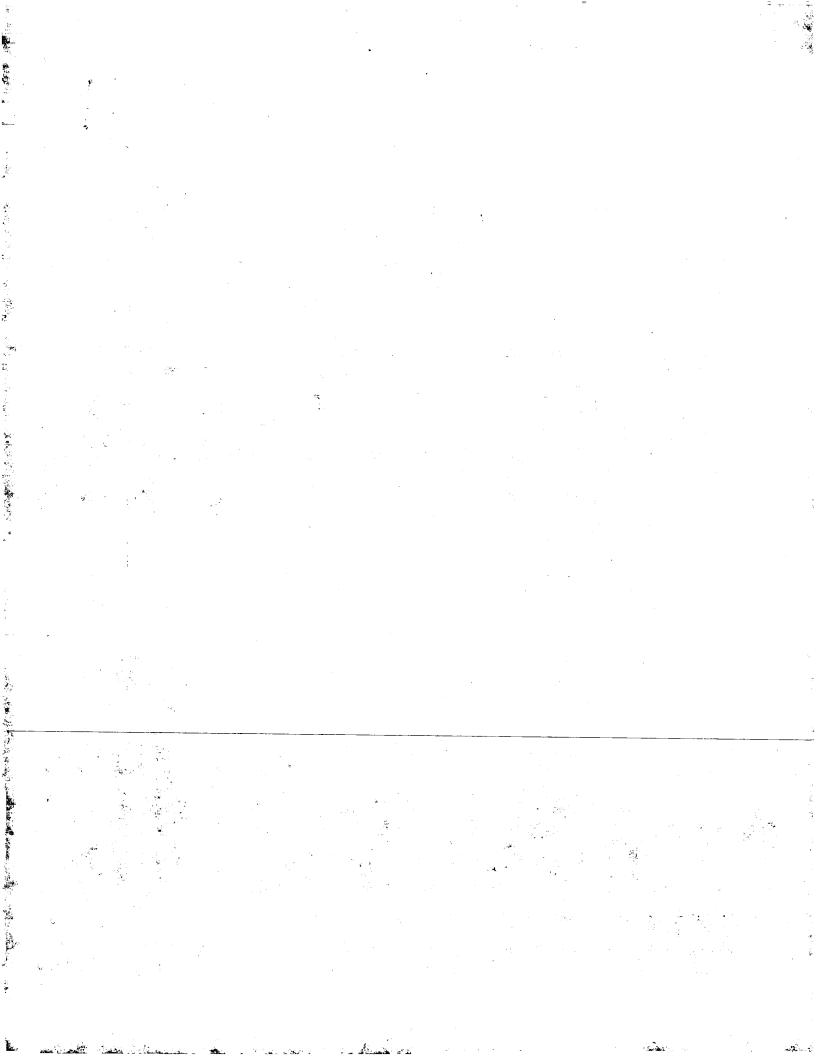
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US-08-290-919-2
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                                                               US-08-290-919-2
                              Query Match
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                   TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BLACKMAN, APPLICANT: CHAPPEL, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1203
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                 Local Similarity
                                                                          LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                           NAME: KOKULIS; PAUL N
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                         NAME/KEY:
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQTKIVAGCYEALDDSEDIFNSLDS 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND--VLGYYKIL--SEKYKSDLDS 1399
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5. 5720959
   46;
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20005-3918
                                                                                                                                                                                                : 48 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: CUSHMAN DARBY & CUSHMAN, L.L.P.
1100 NEW YORK AVENUE, N.W.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLACKMAN, MICHAEL J.
CHAPPEL, JONATHAN A.
VENTION: IMPROVEMENTS IN OR RELATING TO MALARIA
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOLDER, ANTHONY A.
                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                 (202)
                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1993
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                                                                                                                                                      protein
                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                 861-3000
              3.28;
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                                                                          /label= X
/note= "X = M and N, or N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                          16,773
Score 271; DB 1;
Pred. No. 2.4e-08;
1; Mismatches (
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   0;
                          Length 48
   Indels
 0;
 Gaps
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US-08-923-992A-10
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08923992A Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                       Matches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms
TITLE OF INVENTION: Streptococcal Beta Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1527 ISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENPNPT 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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 212
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                                                                                                                                                     141
                                                                                                                                                                                          187
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                91 PLEKTAGETSATDTGKREKQLQQWKNN---LKNDVHN---TILSHEQKNEFKTKID---- 140
                                                                                                                                                                                                                                                                                                            32 GSVAHASELVKHDSVKT-TEVAAKPYPSMAQTDQGNNSSSSELETTKIEIPTTDIKKAVE 90
                                                                                                                                                                                                                                                                                                                                                80 GSVASGGSVASGGSVASGGSVASGGSGNSRRTNPSDNSSDSDAKS-----YADLKHRVR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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                                                                      NQFNETNRLLHIKQHEEVEKDKKA-KQQKTLKQSDTKVDLSNIDKELNHQKSQVETMAEQ
                                                                                                          KTIENINELIE-ESKKTIDKNKNATKEEEKKKLYQAQYDLSIYNKQLEEAHNLISVLEKR 305
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18.2%; Pred. No. 1.
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: AHKTGGGTVR	972TDADKLHLKELTTKELADKIAHKTGGGTVRV	_	
DVKFT.NKFKR-	932 PDVPKLPDAPKLPDGLNKVGQAVFTSTDGNTKVTVVFDKP	Db 9	
LAGVYRSLKKQL	1241 IIVPIFGESEEDYDDLGQVVTGEAVTPSVIDNILSKIENEYEVLYLKPLAGVYRS	Qy 12	
DDEVDDV : : PDVPKLPDVPKL	1203 GSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDV : :	Qy 12 Db 8	
LPEGTDVATVVSES	TPQAPDTPHVPESPK	Qy 11 Db 8	
IDNLVHDAFSKMNAT	EGALADNLALEKAKLSY::::::::::::::::::::::::::::::::::::	Db 7	
KGLVKYYNGESS : : MSKVLDG			
KMQIKKLTLLKE : : : LTPFNKIKQIVD	983 DESKRKKL-EEDINKLKKTLQLSFDLYNKYKL-KLERLFDKKKTVGKYKMQIKKLTLLKE	Оу 9 ОБ 6	
VKSKADDINSLN : TRKVVQYINKYP	936 KNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVKSKADDINSLN :::: :::	Оу 9 Db 6	
-LFENILSLGKN : PIQEAITS	78 EAKKVSTSVKTLSSSSMOPLSLTPODKPEVSANDDTSHSTNLNNSLK- : : : : :: : : : : 78 QLEKLEKAIKEL	Оу 8 Db 5	
LKDNDKIKNLLE : : QELIKSAQQ	818 SSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYEKEMVCNLYKLKDNDKIKNLLE	Оу 8 5	
QYKITKEEESKL :: : KVPQEPKS	758 PPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHSTMNEKILKQYKITKEEESKL : : : : : 544 TPEQKDSKTEEKVPQEPKS	Qy 7 Db 5	
VPVPEAKAQVPT QVPK	698 SDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQAQPPVPVPVPEAKAQVPT	Оу 6 рь 5	
NEEKKNIKTEGQ : : : : LNESQTVTLKAK	638 LKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVESLINEEKKNIKTEGQ ::	Оу 6 рь 4	
NKIDELKKTQLI 	587 KDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLLMNKIDELKKTQLI	Qу 5 рь 4	
IETLVENIK:::: :::: LKQVVEDFRKKF	537 KHNLEKL-TKALKYMEDYSLRNIVVEKELKYYKNLISKIENEIETLVENIK : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	Оу 5 Db 3	
(LTHHNTFASYENS	477 RSKSLNDITKEYEKLLNEIYDSKFNNNIDLTNFEKMMGKRYSYKVEKLTHHNTFASYENS	Оу 4 Db 3	
KKIESDKKSYED :: : ETNVKLYKA	420 LNELNSFGDLINPFDYTKEPSKNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYED	Оу 4 Db 2	
TYPLSYNDINNA : CALAQKS	365 IDSLFTDPLELEYYLREKNKNIDISAKVETKESTEPNEYPNGVTYPLSYNDINNA 	Qy 3	

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Search completed: March 31, 2003, 07:28:27 Job time : 136 secs



AF062348 Plasmodiu AF218248 Plasmodiu

P.falciparu P.falciparu Plasmodium A92451 Sequence Description

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Perfect score:
Sequence:
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2160	ATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCC	2101	Db
2160	CAGATAACTCCGAGCCTTCCACAGAAGGAGAGAGATAACCGGACAGGCTACCAACCA	2101	Qy
2100	CCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAACATTAAAACTGAAGGACAG	2041	Ф
2100	GACAG	2041	Qy
2040	AGCAGGAACCATACTCATCGTACTCAAGAAGAGATAGACAAACTGAAAGTGTTC	1981	Db
2040	CAGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTT	1981	Qy
1980	CTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAAT	1921	Db
1980	TGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAC	1921	Qy
1920	CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATT	1861	Дb
1920	AAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTC	1861	Qy
1860	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801	Db
1860	raaagacgaaaataaaccagatgagaagatcctggaggtctccgatattgttaaagt	1801	Qy
1800	ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	1741	Db
1800	rgacgcttgttgagaacattaagaaggatgaagaacagttgtttgagaagaagat	1741	Qy
1740	ATTGTTGTGGAGAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1681	Db
1740	ttgtggagaaagaactaaagtattacaagaatctcataagtaag	1681	Qy
1680	CATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC	1621	Db
1680	ATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGG	1621	Qy
1620	TCTTACAAAGTGGAGAAACTGACACCATAATACCTTTGCATCCTATGAGAATTCTAAG	1561	Db
1620	CTTACAAAGTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCT	1561	Qy
1560	TCCAAATTCAACATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAACGGTAC	1501	DЬ
1560	CCAAATTC	1501	Qy
1500	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGAT	1441	Db
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1440	GAGAAGATCAAAATTGAGAAGAAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	1381	Db
1440	AGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCG	1381	Оу
1380	GAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	1321	Db
1380	aaccctctaagaatatctacacagacaatgagagaaagaa	1321	Оу
1320	ACCCTCTCAACGACCTCAATACCTTCGGTGACTTGATTAACCCCCTTCGATTATACGAAA	1261	Db
1320	TCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCCTTCGATTATACGAAA	1261	Qy
1260	ACCGAACCTAATGATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201	Db
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1200	TACTTGAGAGAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAAATCA	1141	Db
1200	ACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1141	Qy
1140	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTAC	1081	DЬ
1140	TACTGATCCCCTTGAGCTGGAGT	1081	Qy

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Submitted (14-DEC-1998) Bujard H.,
Biologie, Universitaet Heidelberg,
heidelberg, BW, GERMANY
2 (bases 1 to 4940)
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Cloning vector pBSK*-MSP-1s/FCB.
Cloning vector pBSK*-MSP-1s/FCB
                                                                                                                  Vaccine candidate MSP-1 from Plasmodium falciparum: a redesigned
                                                                                                                                                                                                                        artificial sequences; vectors 1 (bases 1 to 4940)
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                                                                                     4917 bp polynucleotide enables synthesis and isolation of full-length protein from Escherichia coli and mammalian Nucleic Acids Res. 27 (4), 1094-1103 (1999)
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1440 1440	31 GAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	138 138
1380 1380	21 GAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	132 132
1320 1320	31 AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA 	126 126
1260 1260	11 ACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC 	120 120
1200 1200	TACTTGAGAGAGAATAAGAATATAGACATCTCCGGCAAAGTCGAGACAAAGGAATCA 	114 114
1140 1140	I GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGATCCCCTTGAGCTGGAGTAC	108
1080	1 AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGGAGCACGAGAAAGAGATCAAAGAGATC	102
1020 1020	I CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	96 96
960	11 CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA	90
900	1 TTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAACA	84
840	11 GAATCCAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAGAAGAAAGA	78 78
780 780	1 ATGGAAGATTATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAA 	72 72
720 720	AAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAG	66
660	1 AATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTG	60
600	11 CTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC	54
540 540	1 TGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTC 	48
480 480	1 ACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTG	42
420 420	i AGCGATTCCGACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTC	36 36
360	1 GGCTCAGTGGCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCT	301

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л 4	TATGAACGAGAAGATTCTTAAACAGTACAAGATAACCAAGGAGAGAGA	4 0) Db
	ACTATGAACGAGAAGATTCTTAAACAGTACAAGATAACCCAAGGAAGAGGAGGAGAGTAAACTG	4	. Qy
40	CTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAG	34	Db
40	CTCTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGC	4	Qy
2340	CACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGA		DЪ
2340	CCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAG	Ν	Qy
2280	iΩ −		Db
2280	AGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTAC	2221	Qy
22	GGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAC	2161	DP 63
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16	TCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCC		Qy
2100	TGCCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAACATTAAAACTGAAGGACA	2041	b Db
2100	GAAGAGAAGAAGAACATTAAAACTGAA	2041	Qy
2040	TCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTT	981	Db
2040	AGCAGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGAC	981	Qy
1980	AGTTATAAGCAGGAG	9	Db
1980	TGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAA	9	Qy
1920		1861	Db .
1920	AAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCAT	1861	γQ
1860	Ď-	80	Db
1860	CAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGT	8	γQ
1800	ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	1741	Db
1800	TCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGAT	1741	Qy
1740	ATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	6	Db
1740	TTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1681	Qy
1680	CATAATCTTGAGAAGCTCACGAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC	1621	Db
1680	ATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAA	1621	Оу
1620	TCTTACAAAGTGGAGAAACTGACACCATAATACCTTTGCATCCTATGAGAATTCTAAG	1561	Db
1620	CTTACAAAGTGGAGAAACTGACACACACATAATACCTTTGCATCCTATGAGAATTCTAA		Qy
1560	TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAACGGTAC	Ċn	Db
1560	CCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTA		Qy
1500		44	Db
1500	GCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATG	1441	Qy

3660	GTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCT	3601	Qy
3600		3541	В
3600	TGAATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACT	3541	Qy
3540	GGAAGTCATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGAC	3481	В
3540		3481	Qy
3480 3480	CTGGAGAAGAAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTC	3421 3421	Db Qq
3420	AGCCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAAC	3361	Дb
3420	CCTCGAGAACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAAC	3361	Qy
3360	GAGTCTTCTCCTGTGAAGACTCTCTCCGAGGAGAGCATCCAGACCGAGGATAACTACGCC	3301	DB 4
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0	CTGGAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGC		y Q
3240	TTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACT	3181	Db
3240	TCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACT	3181	Qy
3180	CTCAAGGAGCAGCTTGAAAGCAAACTCACCTCACCTGAACAATCCGAAACACGTACTGCAGC 	3121	문 5
12	TCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTG	90	8
3120	CTCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTG	0	Qy
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	aagacactgcaactgagcttcgacctgtacaacaagtacaaactgaaactggac	3001	Qy
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2880	. ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAA 	2821	P 29
2820	CTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAAC	2761	В
2820	AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAAC	2761	Qy
2760	TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACC	2701	밁
2760	CTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACC	2701	Qy
2700	GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTTCCAGCTCCATGCAACCACTG	2641	망
2700	GAAGCTAAGAAGGTCTCCACCTCTGTTAAAAACTCTCTCT	2641	Qy
2640 2640	GAGATGGTCTGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAG 	2581 2581	D Q
2580	TCTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAG	52	В
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Plasmodium falciparum.

Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 5917)

Holder, A.A., Lockyer, M.J., Odink, K.G., Sandhu, J.S.,

Riveros Moreno, V., Nicholls, S.C., Hillman, Y., Davey, L.S.,

Tizard, M.L.V., Schwarz, R.T. and Freeman, R.R.

Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites

anture 317 (6034), 270-273 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-MAR-1991) Holder A.A., National Institute Research, The Ridgeway, Mill Hill, London NW7 1AA, UK Update of published sequence Data kindly reviewed (06-MAR-1986) by R.R. Freeman.
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Direct Submission
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                                                                      MNKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVE
SLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKPGQQAGSALEGDSVQAQAQEQKQA
QPPVPVPVEAKAQVPTPPAPVNNKTENVSKLDYLEKLYEFLNTSYICHKYILVSHST
                                                                                                                                             KFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKLLNEIYDSKFNNNIDLTN
FEKMMGKRYSYKVEKLTHHNTFASYENSKHNLEKLTKALKYMEDYSLRNIVVEKELKY
YKNLISKIENEIETLVENIKKDEEQLFEKKITKDENKPDEKILEVSDIVKVQVQKVLL
                                                                                                                                                                                                                  KLVPGYRKPLDNIKONVGKMEDY IKKNKKTIENINELLEESKKTIDKNKNATKEEEKK
KLYQAQYDLSIYNKOLEEAHNLISVLEKRIDTLKKNENIKLLDKINELKNPPPANSG
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                                                MNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLFMEIYE
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                   GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC
                                                                                TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG
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GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA
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                                                                                                                                                                GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
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4750...4752
/note="pot
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1219. .1221
/note="pot. glycosylation site"
2707. .2709
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2764...
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/note="I
2947...
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SSGLHHILIAELKEVIKNKNYTGNSPSENNTDVNNALSYKFLPEGTDVATVVSESGS
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475. .5334
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CKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP
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QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHY
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73.28;
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1390 AAAATTGAGAAGAAGAAAA 1798 AAAATAGAAAAAAAAAAAAAA	Дb
1330 AAGAATATCTACACAGACA/ 1738 AAAAACATATATACTGATA/	Оγ
1270 AACGAGCTCAATAGCTTCGG 	ру
1210 AATGAATATCCCAATGGTGT 1618 AATGAATATCCAAATGGAGT	Дy
150 GAGAAGAAT 558 GAAAAAAAT	Оy
090 ATTAAGTTCAACATAGATT 	Оy
030 CTGGACAAGAACAAGAAGA 	Оy
970 AAGATTAAT 378 AAGATAAAT	Дy
10 GTACTGGAGAAG 18 GTTTTAGAAAAA	ρ Q
50 GCCCAGTAC 58 GCTCAATAT	Db Qy
90 AAGACC 98 AAAACA	Дy
30 TATATT	Фр
70 GTCTTC 78 GTGTTC	ОУ
10 TGTCAAATTCCATTO	Оy
50 TIGAATTICTACTICGAC 58 TIAAACTITTATTIGAT	p qq
490 ATTCATGGCTTCAAATATC: 898 ATTCATGGTTTCAAATATT'	DP 6A
430 GAGCTGAAGTACCCACAGT	P 40
370 GACGCCAAGTCCTACGCCG	D Qy
- 3-3 6-6 9-8 3-2 6-6 9 9 3-8 6-6 6-6 6-6 6-6 6-6 6-6 6-6 6-6 6-6 6	370 GACGCC 778 GATGCT 430 GAGGCC 430 GAGCTC 490 ATTCAT 550 TTGAAF 550 TTGAAF 550 TTGAAF 610 TGTCAT 611 TGTCAT 611 TGTCAT 611 TGTCAT 612 TGTCAT 613 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT 138 TACATT

2/30 TITITAMATACTICATATATA 2410 GAGAAGATTCTTAAACAGTAC	2290 2698 2350	Qy 2170 GCCGGTTCAGCTCTCG Db 2578 GCAGGATCTGCTTTAG Qy 2230 CAGCCTCCAGTGCCAG Db 2638 CAACCACCAGTACCAG	Qy 2050 GTCGAGAGCCTGATCA	Oy 1930 GTGGAGTTAAAACATA	Qy 1810 GAAAATAAACCAGATG	Db 2098 GAAAAGAATTAAAAT Qy 1750 CTTGTTGAGAACATTA	630 038 690	Oy 1510 ANCAGTANCATCGACC Db 1918 ANTAGTATAGATT Db 1918 ANTAGTATAGATT Oy 1570 GTGGAGAAACTGACAC
ANGATAACCAAGGAAGAGAGAGAGTAAACTGTCCTCTA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG	GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGAAGCAGGAGCAGAGCAGAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCACAAGCAGC	GTCGAGAGCCTGATCAACGAAGAGAAGAAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC	GTGGAGTTANAACATATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAA	GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG	GAAAAAGAATTAAAAATATTAATAAAAATTTAATAAGCAAAATTAGAAAATTAGAAAACA CTTGTTGAGAACATTAAGAAGGGATGAAGACAGTTGTTTGAGAAGAGATTACAAAAGAC CTTGTTGAGAACATTAAGAAGGGATGAAGAACAGACTTGTTTGAGAAGAGAGTTACAAAAGAC	GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG	AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGATGAAAACGGTACTCTTACAA

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3669	610 GAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTC	Qy
3609 4017	3550 GCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCT	рь
3549 3957	490 ATTARGANCANGANCTRCRCCGGCANTAGCCCANGCGNGANTANTRCAGNCGTGNATANC	Db
3489 3897	430 AAGAAGCTCAGCTACCTCTCAGCGGACTGCATCACCTGATGGCCGAGCTCAAGGAAGTC	Db Qy
8 4	370 AACTTCAAGGTCCTGTCTAAGCTCGAAGCTGAAGCTGAACCTGAACCTGAACCTGAGACAAGCTGAACCTGAACCTGAACCTGAACCTGAACCTGAACCTGAACCTGAACCTGAACAAGCAAACTAAAGGATAATTTAAATTTAGAAAAAGAAAATTAAAAGGATAATTTAAATTTAGAAAAAA	dg dy
36 77	310 CCTCTGAAGACTCTCCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAG 	D Qy
3309 3717	250 ACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCT	Дb
3249 3657	190 GTGTTCTTCAACAAGAAGAAGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAAC	Оу
3189 3597	130 CAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCA	Дb
3129 3537	070 AAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAG	Db
3069 3477	010 CTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGAC	Дb
3009	2950 CTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACA	Оу
2949 3357	890 ACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCT	Qy
2889 3297	830 GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGAC 	Qy
ων	770 ARTICACTGARACTGTTTGAGARCATCCTGTCTGTGGCARGAATARGARCATCTGCCAA 	Db Qy
76 17	710 CCTCAAGACAAGCCCGAAGTGAGGGCTAACGACGACACCTCTCACTCGACCAACCTTAAT	d dy
2709 3117	ACA ACA	Оу
2649 3057	2590 TGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAG 	Дb
2997		Db

4749 5157	4690 CAAGAAGGAGATAAGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGG	Qy Db
4689 5097	4630 AGCGGCTGTTTCAGGCATCTGGACCAGCGCGCAAGAGTGCCAAGTGTCTCCTGAACTACAAA 	Qy Db
4629 5037	CTGCAGGGCATGCT	Фр
4569 4977	CGCCAAAACAGTG TGCTAAAACCGTT	рь
4509 4917	GGAATTGCAGACCTGTCTACCGATTATAACCACAACA	Qy Db
4449 4857	AACTACCTCAAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCGAIIIIIIIIII	Qy Db
4389 4797	4330 GCCAAGGTCCTCAACTATACCTTACGAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTG	Qy Db
4329 4737	ATCGAAACCCTGTACAAG	р _р
4269 4677	AAAAAGTATATCAAC	Qy Db
4209 4617	GATGTGCTGGGGTATTAC	оу ор
4149 4557	TTTCTGTCTAGTTACAACTATATCAAGG	Фр
4089 4497	TCCTCTAACTACGTTGTCAAGGACCCATACA;	Qy Db
4029 4437	AAGAGAAAATTTCAAGAACGTCTTG	Qу
3969 4377	GAGAATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTT	Qy Db
3909 4317	TACGAAGTGCTCTATCTO	Qy Db
3849 4257	ACCGGTGAG	Qy Db
3789 4197	ATCATTGTGCCTATCTTCGG	. DP
3729 4137	GGAGCCGAGTCCAATAC	О У
4077	4018 GAAAGTGGATCCGACACATTAGAACAAAGTCAACCAAAGAAAACCAGCATCAACTCATGTA	DЬ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-APR-1989) Myler P.J., Seattle Biomedical Research Institute, 4 Nickerson Street, Seattle WA 98109-1651, U S A 2 (bases 1 to 7038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide and deduced amino acid sequence of the gp195 (MSA-1) gene from Plasmodium falciparum Palo Alto PLF-3/Bl1 Nucleic Acids Res. 17 (13), 5401 (1989)
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                                                                                    ETKESTEPNEYPNGYTYPLSYNDINNALNELNSFGDLINPFDYTKEPSKNIYTDNERK
KFINEIKEKIKIEKKKIESDKKSYEDBSKSLADITKEYEKLLEEIVDSKFNNNIDLTN
FEKMMGKRYSYKVEKLTHHNTFASYENSKHLEKLTKALKYMEDYSLRNIVVEKELKY
YKNLISKIENEIETLUNIKKOBEQLFEKKITKDENKEDEKILEVSDIVVOVQKVLL
MIKIDELKKTQLILKNVELKHNIHVPNSYKQENKQEPYYLIVLKKEIDKLKVFMPKVE
SLINEEKKNIKTEGQSDNSEPSTEGEITGQATTKFQQQAGSALEDSVQAQAQEQKQA
DPPVPVPBAKAQVETPPAFVNNTENVSKLDYLEKLYEFLNTSYICHKYILVSHST
MNEKILKQYKITKEEESKLSSCDPLDLLFNIQNNIPVMYSMFDSLNNSLSQLEMBIYE
KEMVCNLYKLKDNKIKNLLEBAKKYSTSVKTLSSSSMQFLSLTDGOKKPEVSANDDTS
KEMVCNLYKLKDNKIKNLLEBAKKYSTSVKTLSSCONPLEILTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="plasmodium falciparum"
/strain="Palo Alto PLF-3/Bl1"
/db_xref="taxon:5833"
/dev_stage="trophozoite/schizont.'
1592..6511
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QIKKLTLLKEQLESKLNSLNNPKHVLQNFSVFFNKKKEAEIAETENTLENTKILLKHY KGLVKYYNGESSPLKTLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYL
                                                                                                                                                                                                                                                                                                 HIGFRYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLK
KLVFGYRKPLNNIKDNVGKMEDIYIKNKKIIENINELLEESKKIDKNAKTKEEEKK
KLYQAQYDLSIYNKOLEEAHNLISVLEKRIDYLKKNENIKELLDKINEIKNPPPANSO
KLYQAQYDLSIYNKOLEEAHNLISVLEKRIDYLKKNENIKELLDKINEIKNPPPANSO
                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LFQKEKMVLNEGTSGTAVTTSTPGSKGSVASGGSVASGGSVASGGSVASGGSVAS
GGSGNSRRTNPSDNSSDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDN
                                             SKADDINSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFDKKKTVGKYKM
                                                                        HSTNLNNSLKLFENILSLGKNKNIYQELIGQKSSENFYEKILKDSDTFYNESFTNFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="gp195 surface antigen preprotein"
/protein_id="CAA33163.1"
/db_xref="GI:9897"
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                                                                                                    AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAAGAAGAAGTTGTACCAG
                                             TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA
                                                                                                                                                                               TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG
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ANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDLFV
IHLEAKYLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHNNL
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CKCLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYP
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1929 3511	1870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC 	Оy
1869 3451	810 GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG 	Qу
1809 3391	750 CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGAC 	Фр
1749 3331	690 GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG 	Qy Db
1689 3271	1630 GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG	Qy Db
1629 3211	70 GTGGAGAAACTGACACACATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT 	Qy Db
1569 3151	510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAA	Оy
1509 3091	1450 CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC	Qy Db
1449 3031	1390 AAAATTGAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGAACGCGCAGCAAAAGT	Оу
1389 2971	330 AAGAATATCTACACAGACAATGAGAGAGAAGAAGTTTATCAACGAAATCAAGGAGAAGATC	Оy
1329 2911	1270 AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT	Qy
1269 2851	210 AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC	Qy Db
1209 2791		Qy Db
1149 2731	1090 ATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGA	Db Qy
1089 2671	1030 CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACC 	ОУ
1029 2611	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTG 	Db Qy
969 2551	GAATGAAAATATCAAAGAACTGCTCGAC 	Db 04
909 2491	AAACAGCTTGAAGAAGCCCATAACCTCATCAGC 	ОУ

C 306	CTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGA	3010	Qy
7	TTGAATGATGAACAAAAAGGAAGAAATTAGAAGAAGATATTAATAAAATTAAAAAA	4532	DЬ
Þ	CTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAAGACATCAATAAGCTGAAGAAGAC	2950	γQ
A 4	ACATTUTALAACABAACETTACAAATTTTGTAAAATCTAAAGCTGATGATATTAATTC ACATTTTATAATGAATCTTTTACAAATTTTGTAAAATCTTAAAGCTGATGATATTAATTC	4472	Db
9 1-3	GAATTAATAGGTCAAAAAGTAGTGAAAACTTTTATGAAAAGATATTAAAAGATAGTGA	41	рь
i) i)	GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCG	œ	Qγ
∀−∀	ACTCACTGAAACTGTTTĞAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAA	2770 4352	P 29
11 —	CCTCAGGATAAACCCGAAGTAAGTGCAAATGATGATACATCACATTCTACAAATTTGAAT	N	Дb
. i.j.	CCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTT	2710	Qy
¥ - ¥	AAGGTCTCCACCTCTGT#ÀAAACTCTCTCTTCCAGCTCCATGCAACCACTGTCTCTCAC	2650 4232	Db dg
A 4	? TGTAATTTATATAAACTTAAGGATAATGACAAAATTAAAAATTTATTAGAGGAAGCGAAA	417:	Дb
G 2	TGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCT	2590	Qy
T 4	GATAGCCICANCANICICICICICICANCIGII CAISSASAINI I ISSONASSISSAISSIC 	4112	DB 42
	GATCCATTAGACTTATTGTTTAATATACAAAATAACATACCTGTAATGTATTCTATGT	7 C) DB
. 0	GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTTC	47	Qy
T - T	GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAGAGAGGAGAGTAAACTGTCCTCTTG	2410 3992	Db Db
	TTTTTAAATACTTCATATATATGTCACAAATATATTTTGGTTTCACACTCAACTATG	93	В
0 2	TCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGCACTATGAAC	2350	Qy
×ω	CCAGTAAATAATAAAACT	3872	Db
G 2	CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATG	2290	Qy
Σ	CAACCACCAGTACCAGTACCAGAAGCAAAAGCACAAGTCCCAACACCACCAGC	3812	Db
T 2	CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGC	2230	Qγ
.ω ω		3752	Дb
.≱	GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAC	2170	Qy
Α ω	TCGGAACCATCAACCGAAGGAGAAATAACAGGACAAGCAACTACAAAACCTGGACAACAA	3692	Дb
G 2	TCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCCGGACAAC	2110	Qy
ij	GTAGAATCATTGATAAAT	3632	Db
0 2	GTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACTGAAGGACAGTCAGAT	2050	Qy
G 3	CCTTAT	3572	Db
A 2	CONTACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCC	1990	ν
> -	GTAGAATTAAAACATAATATACATGTTCC	51	Dp :
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DEFINITION ACCESSION VERSION SOURCE ORGANISM RESULT A92450 LOCUS KEYWORDS ഗ

REFERENCE AUTHORS TITLE A92450 Sequence A92450 A92450.1 unclassified.

1 (bases 1 to 4920)
Pan,W. and Bujard,H.
METHOD FOR PRODUCING RECOMBINANTS
MALARIA ANTIGENE GP190/MSP1 unidentified unidentified GI:6741180 from Patent 4920 bp wo9814583. INTENDED DNA FOR linear USE Ä PAT Þ

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Š ΔÃ δõ DЪ Qγ Qy Qγ Qy VQ ρy QУ δÃ Db QΥ Дb рЬ Д В В Ъ В В 밁 QY Дb 뫄 Ωy B Qy В δÃ Дb νQ 뫄 δÃ DЬ QΥ 1801 1690 1501 1510 1390 1210 1141 1090 1870 1810 1030 GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG GTGGAGAAACTGACACACÇATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAACGGTACTCTTACAAA TTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGATAGCAAATTC AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTG GTTGAGAAACTTACACACCATAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTC AAGAATATCTACACAGACAATGAGAGAAAGAAGTTTTATCAACGAAATCAAGGAGAAGATC AATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAACAACGCTCTC GAAAAAATAAAATATTGATATAAGTGCAAAGGTTGAAACAAAGGAATCAACTGAACCC GAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCT CTTGATAAGAACAAAAAAATCGAGGAACACGAAAAAGAAATAAAAAATTGCCAAAACT CTGGACAAGAACAAGAAGATAGAGGAGGACAAGAGAAAGAGATCAAAAGAGATCGCCAAAACC CCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA **AATAATAATATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATAAA AATGAACTTAATTCTTTTGGTGATTTAATTAATCCATTTGATTATACAAAAGAACCAAGT** AATGAATATCCAAATGGAGTTACTTATCCTTTGTCATATAACGATATTAACAATGCTTTA 1260 1980 1989 1860 1800 1809 1740 1749 1680 1689 1629 1560 1569 1500 1440 1380 1389 1329 1269 1209 1140 1080 1929 1869 1620 1509 1200 1089 1029 1020

3129	3070 AAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAG :	Qy
3069	3010 CTGCAACTGAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGAC	рь
3009	2950 CTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACA :	Оy
2949 2940	2890 ACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCT :	Qу
2889 2880	2830 GAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGAC :	Ф
2829 · 2820	2770 AACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAA :	Qу
2769 2760	2710 CCTCAAGACAAGCCCGAAGTGAGGCGCTAACGACGACACCTCTCACTCGACCAACCTTAAT :	Оу
2709 2700	2650 AAGGTCTCCACCTCTGTTAAAACTCTCTCTCCAGCTCCATGCAACCACTGTCTCTCACA	ОУ
2649 2640	2590 TGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAG	ОУ
2589 2580	2530 GATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTC	pb Qy
2529 2520	2470 GATCCACTGGACCTGGTGTTCAATATCCAGAACACATTCCCGGTTATGTATTCTATGTTC	Оy
2469 2460	2410 GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAGAGAGGAGAGTAAACTGTCCTCTTGT	Qу
2409 2400	2350 TTCCTGAATACATCCTACATCTGCCACAATATATACCTCGTCTCTCACAGCACTATGAAC	Qу
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2289 2280	2230 CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCAGCT	Оу
2229 2220	2170 GCCGGTTCAGCTCTCGAAGGGGATAGCGTGCAAGCTCAAGGCAGAAGAGCAGAAGCAGGCA	Оу
2169 2160	2110 TCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAG :	Qу
2109 2100	2050 GTCGAGAGCCTGATCAACGAAGAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC	Оу
2040		Db

4209	GATGTGCTGGGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATT	4150	Оу
4200		4141	Дъ
4149	TTTCTGTCTAGTTACAACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAAT	4090	Qy
4140		4081	Db
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		4021	Db
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4020		. 3961	dd
3969	GAGAATAACGTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAAT	3910	Qy
3960		3901	da
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3849	ACCGGTGAGGCTGTCACTCCCTTCCGTGATTGATAACATTCTGTCCAAAATCGAGAACGAA	3790	Оу
3840		3781	Дъ
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3780		3721	дъ
3729	GGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTC	3670	Qy
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3660		3601	Db
3609	GCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCT	3550 3541	ду р
3549	ATTAAGAACAAGAACTACACCGGCAATAGCCCCAAGCGAGAATAATACAGACGTGAATAAC	3490	Qy
3540		3481	Db
3489	AAGAAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTC	3430	ду
3480		3421	рь
3429	AACTTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGCAGACCTGGAGCAGGGIIIII	3370	Qу
3420		3361	ДЪ
3369	CCTCTGAAGACTCTCCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAG	3310	Qу
3360		3301	Оъ
3309	ACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCT	3250	Qу
3300		3241	дь
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3240		3181	da
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3180		3121	Db
3120	AAAAAGAAAACAGTTGGTAAATATAAAAATGCAAATTAAAAAACTTACTT	3061	DЬ

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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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KFI NBIKEKI KIEKKI ESDKKSY BDDRSKSLNDITKEYEKLAKBIYDSKNIYTDNERK
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Best Local Similarity Matches 3587; Conserv 216 ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTATTATAAATACACAATGTGTA Conservative 54.88; 72.18; 0; Score 2706.2; Pred. No. 0; Mismatches 1343; DВ 9 Indels 45; Length 5760; Gaps 275 69

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GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC TCTGTGGGCTCTGGGGGTTCCCGTCGCCTCCGGGGGCAGCCTGGCATCAGGTGGCTCAGTG ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG GATGCTAAATCTTACGCTGATTTAAAACACAGAGTACGAAATTACTTGTTAACTATCAAA GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC TCAGTTGCTTCAGGTGGCTCAGTTGCTTCAGGTGGCTCAGTTGCTTCAGGTGGCTCAGTT ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA GAACTCAAATATCCTCAACTCTTTGATTTAACTAATCATATGTTAACTTTGTGTGATAAT 549 489 429 575 369 309 455 395 189 695 515 249

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1569 1775	1510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAACGGTACTCTTACAAA 	ф
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AAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTGTT 2	CTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGGTGGTCTGCAACCTGTATAAACTC 2	GATAGCCTCAACAATTCT 2	GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATCTATGTTC 2	GAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGGAGTAAACTGTCCTCTTGT 2 	TTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGCACTATGAAC 2	CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG 2	CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGCT 2	GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGCAGAAGCAGGCA 2	TCCGAGCCTTCCACAGAAGGAGAATAACCGGACAGGCTACCACCAAGCCCGGACACAG 2	GTCGAGAGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC 2 	CCATACTACCTCATCGTACTCAAGAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA 2	GTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAA 1 	AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC 1	GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG 1 	CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGAC 1 	GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG 1 	GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG 1 	GTTGAGAAACTTACACACCCTAATACTTTTGCATCCTATGAAAATTCTAAACATAATCTT 1
2667 2915	2607 2855	2547 2795	2529 2735	2469 2675	2409 2615	2349 2555	2289 2495	2229 2435	2169 2375	2109 2315	2049 2255	1989 2195	1929 2135	1869 2075	1809 2015	1749 1955	1689 1895	1835

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2668	TCCAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAAGCCCG	
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2728 2976	GTGAGGGCTAACGACGACACCTCTCACTCGACCACCTTAATAACTCACTGAAACTGTTT 2787 	
2788 3036	GAGAACATCCTGTCTCCGGCAAGAATAAGAACATCTACCAAGAACTTATTGGACAGAAA 2847 	
2848 3096	TCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTATAACGAGAGC 2907	
2908 3156	TTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGATGAATCTAAA 2967	
2968 3216	CGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGAC 3027	
3028 3276	CTGTACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGC 3087	
3088	AAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTC 3147	
3148 3396	AACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAG 3207	
3208 3456	ANGGANGCCGAGATCGCCGAGACAGAGACACACTCTGGAGAACACCAAGATTCTTCTCAAA 3267	
3268 3516	CACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAGACTCTCTCC 3327	
3328 3576	GAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGTCT 3387	
3388 3636	AAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGATCAGCTAGCT	
3448 3696	TCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTAC 3507	•
3508 3756	ACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAACGCACTGGAATCTTACAAG 3567 	
3568 3816	AAGTTCCTGCCTGAAGGAACAGATGTCGCCACTGTGGTGTCTGAATCTGGCTCCGACACA 3627	
3628 3876	CTGGAGCAGTCTCAACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACA 3687 	
3688 3936	ATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCATTGTGCCTATCTTC 3747	

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CCAGCTCTAATTTCCTGGGCATC 4884	CCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTC	4825	Qy
ACATGTGAATGTACTAAA 50	AATGTACCGAAGAAGATTCAGGTAGCAACGGAAAG	01	Db
CTAAG 4	ATGCACCGAGGAAGACAGCGGCTCTAACGGAAA(76	Qy
	TTGAAAATTCAAATCCTACTTGTAACGAAAAI	95	Db
SCGGGTGTGACGCCGATG	GCGTGGAGAACCCAAACCCTACCTGCAATGAAAAC	4705	Qγ
GTAAA 495	CATTTAGATGAAAGAAGAATGTAAATGTTTAATTAA	4896	Db V
AGITCIGGAIGIIICAGA 489	UACAAUACCAATGUGTAAAAAAACAATGA 	2) b
CCCCAGAATAGCGGCTGTTTCAGG 4644	\sim	5 8	r Oy
AACTTGCAAGGTATGTTAAA 48	TTGCTAAAATCCGTTTTATCTAATTTACTTC	77	Db
AACCTGCAGGGCATGCTGAA 458	AGTGCT	4528	Qy
TTAGTACAGGTATGGTTTTTGAA 4775	ACAGATTATAACCATAATAACTTATTGACAAAGTTCCTTAGTA	4716	Db
CTGGCATGGTGTTCG	CGATTATAACCACAACAATCTCCTGA	4468	Qy
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TAGAAGCAAAAGTTCTAAATTAT 4595	ACAGTTAATGATAAATTGATTTATTTGTAATTCATTTA	4536	Db
SAGGCCAAGGTCCT	CAGTGAACGACAAAATCGACCTCTTCGTAATT	æ	Qy
ACAATATTGAGACCTTATATAAA 4535	AAACAAGGTGAAAATGAGAAATACCTTCCCTTTTTAAACAAT	4476	Db
ATCGAAACCCTGTAC	AGCAAGGCGAGAATGAAA	4228	Qy
ATTCAATTAAAAAATATATCAACGAC 4475		4416	Db
AACG	AGATCCTGAGCGAAAAATACAAGTCTGACCTTG	4168	ОУ
CAAATGATGTTCTTGGATATTAT 4415	TATATTAAGGATTCAATAGATACGGATATAAATTTTGCA	4356	Db
AATGATGTGCTGGGGTATT	ATATCAAGGACTCCATCGACACCGATATCAATTTCG	₩.	Qy
	AAAGATCCATATAAATTTCTTAATAAAGAAAAAAAAGAGI	296	Db
CTAGTTAC	ACCCATACAAGTTCCTCAATAAAGAGAAGA	048	Qy
TAACATCAAGTAATTATGTTGTC 4295	AATGTTTTAGAATCAGATTTAATTCCATATAAAGATT	236	Дb
TGACCTCCTCTAACTACGTTG	PCTTGGAGAGCGACTTGATTCCCTATAAAGACC	886	Qy
CGATTTAATAAACGTGAAAATTTCAAA 4235	ATTCA	4176	Db
AAGAGAGAAATTTC	AATGTCAACGTGAAGGACATTCTGAACAGC	3928	Qy
ATTAGAAAATAACGTTATG	TAAAAAAA	116	Db
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TGGTCACCGGTGAGGCTGTCACT 3807	GGACTACGATG	3748	Qy

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JOSON APICOMPLEXA; Haemosporida; Plasmod.

JOSON JASABHARA, S.S., Barenteina, R...

JARCLONING FOR ANTIGEN OF PROTOZOA
PATENT: JP 1986019490-A 1 28-JAN-1986;

WELLCOME FOUND LTD:THE

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PN JP 1986019490-A/1

PD 28-JAN-1986

PF 22-FEB-1984 GB 84 8044692, 26-SEP-1984 GB 84 8424340 PI
ANSONII AASAA HORUDAA, MAIKURU JIEEMUSU KOTSUKUITAA, PI
JIYASUBLAA SHINGU SANDEYU, BARENTEINA RIBEROSU MORENO, PI KARERU
PC (12N1/20, A61K39/015,C07H21/04,C07K13/00,C12N1/20,C12P21/02,
PC (12N1/20)
CC Strandedness: Single;
CC hypothetical: No;
FT Key Location/Qualifi-
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                                     AACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCT
                                                                                                                    GAAAAAAATAAAATATTGATATAAGTGCAAAGGTTGAAACAAAGGAATCAACTGAACCC
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                        AATGAACTTAATTCTTTTGGTGATTTAATTAATCCATTTGATTATACAAAAGAACCAAGT
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	2110 TCCGAGCCTTCCACAGAAGGAGAGAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAG	P 29
	2050 GTCGAGAGCCTGATCAACGAAGAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC 	9 9
	1990 CCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA	B 5
	1930 GTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAAGAA 	B 5
<u>ن</u> د ز	1870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC	₽ 5
× ~	1810 GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG 	ρ γ
	1750 CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGAC 	9 24
≽ ດ	1690 GAGAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGAC 	₽ 2
	1630 GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGGGGAACATTGTTGTG	9 8
	1570 GTGGAGAAACTGACACACATAATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTT 	g 9
	1510 AACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGGTACTCTTACAAA 	B 5
$\alpha - \alpha$	1450 CTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATT 	₽ 24
H - H	1390 AAAATTGAGAAGAAGAAAATTGAGAGGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAG	B 5
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48 TCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTAC 3507 	Qy 34 Db 36
	36
8 AAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAC	w
28 GAGGAGAGCATCCAGACCGÁGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGTCT 3387 	Qy 33
ATAAAGGACTTGTTAAATATTATAATGGTGAATCATCTCCATTAAAAACTT	U)
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56 AAAGAAGCTGAAATAGCAGAAACTGAAAACACATTAGAAAACACAAAAATATTATTGAAA 3515	34
AAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCAAGATTCTTCTC	32
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76 TTATATAAATATAAATTAAAATTAAAATTAGAAAGATTATT	N
28 CTGTACAACAAGTACAAACTGAAACTGGAGAGAGAGACTCTTCGACAAGAAGAAGAACAA	0
16 AGGAAGAATTAGAAGAAGATATTAATAAATTAAAAAAACTTTACAGTTATCATTTG	32
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AAATTTTGTAAAAATCTAAAAGCTGATGATATTAATTCATTGAATGATGAATG	31
TCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTTAACGAT	29
96 AGTAGTGAAAACTTTTATGAAAAGATATTAAAAGATAGTGATACATTTTATAATG	0
AGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTA1	Qу 28
36 GAAAACATATTGAGTCTTGGAAAAAAAAAATATATATCCAAGAATTAATAGGTCAAAAA 3095	30
AGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAACTTATTGGACAC	7
76 GTAAGTGCAAATGATGATACATCACATTCTACAAATTTGAATAATAGTTTAAAATTATTT 3035	29
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16 AAAACTCTT	9
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56 AAGGATAATGACAAAATTAAAAAATTTATTAGAGGAAGCGAAAAAAGTATCCACATCTGTA 2915	00
08 AAAGACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTG	26
96 GTATTTATATTATGAAAATTTATGAAAAAAGAAATGGTTTGTAATTTATATAAAC	27
48 CTCTCTCAACTGTTCATGGAGATATATGAGAAG	25
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30 GATAGCCTCAACA	25
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Pan,W., Tolle,R. and Bujard,H.
A direct and rapid sequencing strategy
falciparum antigen gene gp190/MSA1
Mol. Biochem. Parasitol. 73 (1-2), 241-
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GAACTCAAATATCCTCAACTCTTTGATTTAACTAATCATATGTTAACTTTGTGTGATAAT
                              GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC
                                                                                                                                                                      GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG
                                                                                                                                                                                                                                                                                                          GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC
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                                                                                                                                                                                                                                                              ACTITACCTCGTTCAAATACTTCATCTGGTGCAAGCCCTCCAGCTGATGCAAGCGATTCA
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EXPONGTYPLSYNDINNALINELMSFEGDLINPPDYTKEPSKUTYTDNERKKEINEIKEK
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IKIEKKKIESDKKSYEDRSK SLINDITKEYEKLLETYDSKENNUTDLINFEKMIGKRY
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NEIETLVENITKOEEOLFEKKITKOENROEKILEVSDLYKVOVOKVLLIMNKIDEKK
TOLLIKNVELKHNIHVPNSYKOENROEKTLEVSDLYKVOVOKVLLIMNKIDEKK
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KITKEGESKLSSCDPLDLLENIONNIPVMYSMFDSLINSSOLEMEITYSETMUNEKILKOY
KITKEEESKLSSCDPLDLLENIONNIPVMYSMFDSLINSSOLEMEITYSESTMLNNSL
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NEDSKRKKLEEDINKLKKTLOLSSDLYNNYKLKEIELKTYLLKHYKGLYKYYN
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VYENLAKTVLSOHOOPNONTASOHOOVNKOOLONDSCEFRHLDEREECKCLLNYKO
SONFLOENENLOGONDAKCTEEDSGSNKKITCECTKPDSYPLFDGIFCSS
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OGENECVERRIPPORDAKCTEEDSGSNKKITCECTKPDSYPLFDGIFCSS
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OGENECVERRIPPORDANCTEEDSGSNKKITCECTKPDSYPLFDGIFCSS
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/db_xref="SHISS-PROT:P04932"
/db_xref="SHISS-PROT:P04932"
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SPPADASDSDAKSYADLKHRVRNYLLTIKELKYPQLFDLTNHMLTLCDNIHGFFKYLID
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SIYNKQLEEAHNLISVLEKRIDTLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDK
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AATAATAATATAGATTTAACTAATTTCGAAAAAATGATGGGTAAAAGATATTCATATAAA
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                                       TTAAATGATATAACAAAAGAATATGAAAAATTACTTAATGAAATTTATGATAGCAAATTC
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                                                                              AAAATAGAAAAAAAAAATTGAATCTGATAAAAAATCTTACGAAGACAGATCTAAGTCT
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2709	2650 AAGGTCTCCACCTCTGTTAAAACTCTCTCTTCCAGCTCCATGCAACCACTGTCTCTCACA 2	Qy
2684	25 TGTAATTTATATAAACTTAAGGATAATGACAAAATTAAAAAATTTATTATTAGAGGAAGCC	망
2649	90 TGCAA	Qy
2589 2624	2530 GATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTC 2	Дb
56	470 GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTC	р
2469 2504	O GAGAAGAT	Оy
2409 2444	2350 TTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGCACTATGAAC 2	Оy
2349 2384	2290 CCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAG 2	Qу
2289 2324	2230 CAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCCAAGTGCCTACACCACCACCT 2	Оу
2229	2170 GCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGGCACAAGAGCAGGAAGCAGGCA 2	Оy
2169 2204	2110 TCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAG 2	Оy
2109 2144	2050 GTCGAGAGCCTGATCAACGAAGAGAAGAAGAACATTAAAACTGAAGGACAGTCAGATAAC 2 	Оy
2049 2084	1990 CCATACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAA 2 	Оу Оъ
1989 2024	1930 GTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAA 1 	Оy
1929 1964	1870 AAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAAC 1 	Qу
1869 1904	1810 GAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAG 1 	Оy
1809 1844	1750 CTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGAAGTTACAAAAGAC 1	Ф
1749 1784	1690 GAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACG 1 	Оy
1689 1724	1630 GAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTG 1 	Оу
1629 1664	1570 GTGGAGAAACTGACACACCATAATACCTTTTGCATCCTATGAGAATTCTAAGCATAATCTT 1 	Qу

3670 3705 3730	3525 ATA 3550 GCA 3585 GCA 3610 GAA 3645 GAA	Db 3345 CCATTAL Qy 3370 AACTTCL Db 3405 AACTTTL Db 3405 AACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3165 3190 3225 3250 3285 3310	985 010 045 070 105	2685 2710 2745 2770 2805 2865 2865 2890
SATICUGACACHTRAGAACAAAGTCAACCAAAGAAACCAGCATCAGCTCAT	ATRAAAATTATACAGGTAATTCTCCAAGTGAAAATAATACGGATGTTAACAATTAAAATTATACAGGTAATTCTCCAAGTGAAAATAATACGGATGTTAACAAATTACAAGAAGTTCTCCAAGTGAACAGATGTCGCCACTGTGGTGAAGGAACAGATGTCGCCACCTGTGGTGAATCTTACAAAAAATTCTCCCAGAAGGAACAGATGTTGTACAACAGTTGTAAAAAATTTCTCCCAGAAGGAACAGAAGCTGCATCTACTACTACTACTACAACACACCAACAAACCAACAA	CCATTAAAAACTTTAAGTGAAGAATCAATCAAACAGAAGATAATTAAT	TCAAAATTGAATTCACTTAATAACCCAAAGCATGTATTACA AACAAGAAGAAGGAAGCCGAGAGAAGAACAC AACAAGAAGAAGGAAG	GACTCTA GATTATTA TATTATA TATTAAAA	
37	AAT 3584 AAT 3584 TCT 3609	IRA 3404 IAG 3429 II IRG 3464 IRG 3489 IR 3524 IRA 3524 IRA 3524	AC 3249	шшшшшш	H 2744 CA 2744 AT 2769 H 2804 AT 2829 AA 2829 H 2864 AA 2864 AA 2869 CT 2949 CT 2949 CT 2984

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TGTGAATGTACTAAACCTGATTCTTATCCACTTTTCGATGGTATTTTCTGCAGTTCCTCT
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/product="merozoite
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Query Match Best Local Similarity Matches 2944; Conserv COUNT 850 846 786 670 666 790 730 726 610 606 550 546 490 486 430 426 370 366 310 250 246 306 190 186 130 126 70 66 10 GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA 789 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT 729 TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT 609 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG GAACTCAAATATCCCGAACTCTTTGATTTAACCATATGTTAACTTTGTTGTGTAAT GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC 489 GATGCTAAATCTTACGCTGATTTAAAACATAGAGTTCAAAATTACTTGTTCACTATTAAA GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGATTGTACCAG 849 **GTGTTCGGATATAGAAAACCATTAGACAATATTAAAGATAATGTAGGAAAAATGGAAGAT** TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG TTAAACTTTATTATGATTTATTAAGAGCCAAATTAAATGATGCATGTGCCAATAGTTAT GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC TCAGGTGGTTCAGGTGGCTCAGTTGCTTCAGGTGGCTCAGTTGCTTCAGTT TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG GCCGTTACAACCAGCACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG ATGAAAATCATTTTCTTCCTCTGTTTCATTTCTTTTTTTATCATCAATACTCAGTGGGTG TGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAATTAGACGTACTTAAAAAAATT **GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA** GCTGTTACAACTAGTACACCTGGTTCAAAGGGTTCAGGTGGCTCAGTTGCTTCAGGTGGT 2313 Conservative Q) PTSGSLLTELQQVVQSQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAISVTMDNI
LSGFERIEYDVITUKPLAGVYRSLKKQLEKNIITFNLMILNDILKSRLKKRKYELDVLES
DLMQFKHISSKENEYIIEDSFKLLNSEGOKNTLLKSYKYLIKESVENDIKFADEGISYYEKV
LAKYKDDLESIKKVIKEEKEFPSSPTTPPSPAKTDEQKKESKFLFFLINIETLYNNL
VNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLKALDDKIDJFKNTMDFEAIKKLI
NDDTKKDMLGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFR
HLDEREECKCLLNYKQEGDKCVUNPNPTCNENNGGCDADAKCTEEDSGSNGKKITCEC
TKPDSYPLFDGIFCSSSNFLGISFLLLLMLILYSFI" 28.4%; 57.3%; O 0; Score 1400.6; DB 3; Length 5271 Pred. No. 6.7e-297; 0; Mismatches 1974; Indels 219; 690 g 1581 t 5271; Gaps 725 429 909 549 545 425 305 245 189 785 669 665 605 485 69 369 365 309 249 14;

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1971	CAACTCATTCTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAG	1912	Qу
2042		1983	Db
1911	GTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACT	1852	Qу
1982		1923	Db
1851 1922	AAGAAGATTACAAAAGACGAAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATT	1792 1866	Фр
1791	GAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAG	1732	Db
1865		1806	
1731 1805	CTGCGGAACATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1672 1746	Qу
1671 1745	AATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCT	1612 1686	Qу
1611 1685	AAACGGTACTCTTACAAAGTGGAGAAACTGACACCATAATACCTTTGCATCCTATGAG	1552 1626	Оу
1551 1625	ATCTATGATTCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGA	1492 1566	Qу
1491	GAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAG	1432	Qy
1565		1506	Db
1431	GAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTAC	1372	Db dg
1505		1446	
1371	TATACGAAAGAACCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	1312	Qy
1445		1386	Db
1311	AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGAT	1261	Qy
1385		1326	Db
1260	ACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201	Qy
1325		1266	Db
1200	GAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCA	1150	da
1265		1206	VQ
1149	ATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGA	1090	Qy
1205		1146	Db
1089 1145	CTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACC	1030	Qy Db
1029	AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGCTG	970	Qy
1085		1026	Db
969	GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATATGAAAATATCAAAGAACTGCTCGAC	910	Qy
1025		966	Db
965	GCTCAATATAATCTTTTTATTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC	906	DЪ

2958 3119	2899 AACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGAT	Qy
2898 3062	2839 GGACAGAAATCGTCCGAGAACTTCTACGAGAGATACTGAAAGACAGCGACACATTCTAT	Оy
2838 3002	2782 CTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAACTTATT	Оу
2781 2942	2722 CCCGAAGTGAGCGCTAACGACGACACCTCTCGACCAACCTTAATAACTCACTGAAA	Ωу
2721 2882	2688 CATGCAACCACTGTCTCTCACACCTCAAGACAAG	Оy
2687 2822	2658CACCTCTGTTAAAACTCTCTCTTCCAGCTC	Qу Дъ
2657 2762	2617 GACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTC	Qу Дъ
2616 2702	2557 CTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAAGACAC	Оy
2556 2642	2497 CAGAACAACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACAATTCTCTCTC	Оу
2496 2582	2437 ACCAAGGAAGAGGAGAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTCAATATC	ОУ
2436 2522	2377 AAATATATCCTCGTCTCCACAGCACTATGAACGAGAAGATTCTTAAACAGTACAAGATA	Оy
2376 2462	2317 AGCAAACTGGACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATCTGCCAC	D Qy
2316 2402	2257 GAGGCTAAAGCTCAAGTGCCTACACCACCACCACCTGTGAATAACAAGACCGAGAATGTC	Оy
2256 2342	2206 CAAGCACAAGAGCAGAAGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCA	Qу
2205 2282	2146 GCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCT	Qу Дъ
2145 2222	2092 GAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGAGAGTAACCGGACAG	Qу
2091 2162	2032 AAAGTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACT	Ф
2031 2102	1972 CAGGAGAATAAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGA	Qy

οy Вþ δÃ 밁 Qγ DЪ δÃ Ъ νQ Ъ Ş В Qy Вb δÃ 뫄 δÃ ₽ Qy 밁 γQ 뫄 Ω В Qy Ъ δÃ Вb QY В ν̈́ Вþ Q B Qy B Ş 4017 3648 3480 3319 3360 3840 3780 3597 3660 3600 3540 3079 3019 GAATCTAAACGTAAGAAGCTGGAAGAGAGACATCAATAAGCTGAAAGAAGAAGACTGCAACTG GTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTCTTGGAG GGAGTATATAGAAGCTTAAAAAAACAAATTGAAAAAAACATTATTACATTTAAATTTAAAT GGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTCAATGTCAAC GAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCCGTGATT CAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAA CAGAACGTCGACGATGAGGTCGATGACGTCATTGTGCCTATCTTCGGCGAGAGCGAG TCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC AAGAACTACACCGGCAATAGCCCAAGCGAGGAATAATACAGACGTGAATAACGCACTGGAA GTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGAAGCTC CTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAG GAACTTGGCCAAGACAAAATTAAAAAACTTACTTTATTAAAAGAACAATTAGAA GAAACACAAAAAAATGCATTAAAATGAAATTAAAAAATTAAAAAGATACTTTACAGTTA AGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGACCCATAC TTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTATTAGAA GATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATATCTGTCACAATG---GAAACACAAATACCAACTTCAGGCTCTTATTAACAGAATTACAACAAGTAGTACAATCA GATGTAACTCCATCTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAA -----CACTGTGGTGTCTGAATCTGGCTCCGACACTGGAGCAGTCTCAACCTAA AGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAAC AACAAGAAGAAGGAAGCCGAGATCGCCGAGACACAGAGAACACTCTGGAGAACACCAAGATT AGCAAACTCAACTGAACAATCCGAAACACGTACTGCAGAACTTCTCTTC ACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAA TCTTACGAAAATTTTCTCCCCAGAAGCAAAAGTTACAACAGTTGTAACTCCACCTCAACCA AAAAATTATACAGGTAATTCTCCCAAGTGAAAATAATAAGAAAGTTAACGAAGCTTTAAAA TCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAGTAATAAAAAAT **AACAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAACACATTAGAAAAACACAAAAAATA** TCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAACTTTTCTGTTTTCTTT -GCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCT 3647 3539 3479 4059 4196 4136 4076 4016 3959 3899 3839 3779 3558 3659 3599 3378 3419 3258 3359 3299 3138 3239 3179 3879 3699 3596 3318 3078 3018 3438

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AGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCCTATCCACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAACATCTCCCAGCACCAA 4602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAAAAGAAGGAA 4496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAAATATAAGGATGATTTAGAATCAATTAAAAAAAGTTATCAAAGAAGAAAAAGGAGTTC 4436
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                                                                                                                                                                                                                                                                                   TTCGATGGTATTTTCTGCAGTTCCTCTAACTTCTTAGGAATATCATTCTTAATAATACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATGTAAATGTTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAATCCAAAT
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                                                                                                                                                                                                         ATGCTGATCCTGTACAGCTTCATCTAATAGATCGATG
                                                                                                                                                                                                                                                                                                                                   ATTGACGATTACTTAATTAACTTAAAGGCAAAGATTAACGATTGTAATGTTGAAAAAGAT 4616
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JOURNAL
                             Query Match 26. Best Local Similarity 56. Matches 2919; Conservative
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Jiang, G., Liu, R.Z., Daubenberger, C.A. and Pluschke,
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DVDKKITSARYTYNVEKORYNNKESSSNNSVYNVOKLKKALSYLEDYSLRKGISEKDF
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DLYNKYKLKLDRLFNKKKELGODKMOIKKLTLLKEDLESKLKSULNUPHNVLOMESVFF
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LIDGYEEINELLYKLMFYYDLLRAKLMDACANSYCO.FFNLKTARNELDVLKKIVFGY
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YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLEDIDKIKTDAEKLTTGSKPNP
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                                                                                                                                                                                                                                                              LKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTNDFEAIKKLINDDTKKDMLG
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Pred. No. 1.26
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CH-4002, Switzerland
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                                  1978;
                                                                               DB 3;
                                                                                  Length 5243;
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RESULT 10 AF062348

LOCUS DEFINITION

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1143	4 AAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTAC	80
108 112	7 CTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCC :	1027
102 106	O AAGATTAATGAAATTAAGAATCCTCCGGCAGCCAACTCTGGGAACACCCCTAACACG	0 7
969 100	CACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC 	910 948
909 947	CATAACCTCATCAGC	ω υ
849 887	0 AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAAAAA	2 9
789 827	TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA 	σ ω
729 767	GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT 	
669 707	TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	610 648
609 647	TIGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	550 588
549 587	ATTCATGGCTTCAAATATCTGATTGACCGCTTACGAAGAGATCAATGAACTCCTGTACAAG	490 528
489 527	GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGAGACACTGTGTGAGTAAC	43C 468
429 467	GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG	7
369 407	GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCTGACAACTCTAGCGATTCC	310 348
309 347	TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG	250 306
249 305	GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG	
189 245	ACCGGATACAGCCTGTTCCAGAAGGAAGATGGTGCTGAATGAA	130 186
129 185	ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT	70 126
69 125	ATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTATCATCAGTACATACTCAGTGCGTG 	10

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AAAGTATATCAACGATAAG 4230	89 A	41	Qy
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AAATGAATACATTATTGAAGATTCATTTAAATTATTG 4235	76	41	Db
ATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTC 4068	009 ATTCCCTATAAAGACCTGACCTCCTCTAACTAC	4.	Оу
ATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTATTAGAATCTGATTTA 4175	116 ATCTTAAATTCACGTCTTAAGAAACGAAAATAT	4	DЪ
GAGAGAAAATTTCAAGAACGTCTTGGAGAGCGACTTG 4008	49	39	Qγ
AGAAGCTTAAAAAAACAAATTGAAAAAAAAACATTATTACATTTAAATTTAAATTTGAACGAT 4115	56	40	Db
GAATAACGTGATGACCTTCAATGTCAACGTGAAGGAC 3948	89	38	Qy
CTCTCAGGATTTGAAAATGAATATATATATATATATAAAACCTTTAGCTGGAGTATAT 4055	96	35	Db
CGAAGTGCTCTATCTGAAACCTCTGGCAGGCGTCTAT 3888	29	38	Qy
TGGAGAAGCAATATCTGTCACAATGGATAAT	39 GAATATTTAGATCAAGTAGT	39	DЬ
CGGTGAGGCTGTCACTCCTTCCGTGATTGATAA	69 GATGACCTCGGCCAGGTGGT	37	Qy
TGTATTACCCATTTTTGGAGAATCCGAAGATAATGAC 3938	79 GACGAAGAAGATGATTCCTTAGTTGTAT	38	Дb
CTATCTTCGGCGAGAGCGAGGAGGACT	09 GACGATGAGGTCGATGACGTCATCATTG	37	Qγ
AACAGAATTACAACAAGTAGTACAATCACAAAATTAT 3878	19 ATACCAACTTCAGGCTCTTTATTAACAGAATT	36	Db
AGCCGAGTCCAATACAATTACCACATCTCAGAACGTC 3708	51GCCTGCATCTACTCATGTCGGAGCCGAGTC	36	Qy
ATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAAGAAGAAACACAA 3818	59 CC	37	Db
CCGACACACTGGAGCAGTCTCAACCTAAGAA 3650	97 ÇA	ω	Qy
TACAACAGTTGTAACTCCACCTCAACCAGATGTAACT 3758		36	Db
TGTCGC 3596	8	ω Us	Qy
ACAGGTAATTCTCCAAGTGAAAATAATAAGAAAGTTAACGAAGCTTTAAAAATCTTACGAA 3698	39	36	ДD
>>	80	ω	Qy
TCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAGTAATAAAAAATTAAT 3638	79	35	Db
CGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTAC 3507	48	34	Qy
AAAATAGATGGAAAACTCAATGATAATTTACATTTAGGAAAGAAA	19	35	Db
CAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACCTC 3447	88	ω ω	Qy
HAGTATCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAATTTAGAGTATTAAGT 3518	59 G	34	ф
TAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGTCT 3387	28 G	ω	Qy
TTATAATGGTGAATCATCTCCATTAAAAACTTTAAGT 3458		ω	ф
TCTTCTC	68 CACTACAAAGGCCTCGTC	32	Qy
	39 AAAGAAGCTGAAATAGCAGAAAC	33	Db
AGAACACTCTGGAGAACACCAAGATTCTTCACA	3208 AAGGAAGCCGAGATCGCCGAGACAGAGAACACT		Qy

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Shan, Z.X., Yu, X.B., Li, X.R., Ma, C
Molecular cloning and sequence ar
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                                                                                                         ATGAAGATCATATTCTTTTATGTTCATTTCTTTTTTTTTATTATAAATACACAATGTGTA 60
 GCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGTTACTTCAGGTGGTTCAGGTGGT
          GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
                                  ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
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Guangdong 510089, P.R.China
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27.|0%;
Conservative
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1425	6 ATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAAATTGAGAGTGACAAGAAA	Qу 136	
1362	GATACTAAAGAAAAAATTAATGAAAAAATTATTACAGATAATAAGGAAAGAAA	Db 130	
1365	6 TTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAGAGAAGAAGTTT	Qy 130	
1302		-	
1305	5 ATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCC	Qy 125	
1242	3 GTTCAAATACCAAAAGTTCCTTATCCAAATGGTATTGTATATCCTTTACCACTCACT	11	
1254	ŢŖŖŖĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	Ov 119	
1182		_	
1194	4 TTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAG	Qy 114	
1122	AAAACTATTAAATTTAACATTGATAGTTATTTACTGATCCACTTGAATTAGAATATTAT	Db 106	
1143	4 AAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTAC	ОУ 108	
1062	THE TENTAL AND THE TENTAL THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL AND THE TENTAL	Db 100	
1083	7 CTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCGCC	Qу 102	
1002	3 GATATAGATAAAATTAAAACAGATGCCGAAAAACTCACTGCAGGAAGTAAACCAAATCCT	Db 94	
1026	0 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACG	Qy 97	
942	3 GTTTTAGAAAAACGTATTGACACTTTTAAAAAAAATGAAAACATAAAGAAATTACTTGAA	Db 88	
969		Qy 9j	
882	3 GCTCAATATAATCTTTTTATTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC	Db 82	
909	O GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCCATAACCTCATCAGC	Qу 85	
822	AAAACAATTGATCAAAATAAGAATGCAGATAATGAAGAAGGAAAAAAAA	Db 76	
849		Qy 79	
762	TACATTAAAAAAATAAAACAACCATAGCAAATATAAATGAATTAATT	Db 70	
789	0 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA	Оу 73	
702	3 GTGTTCGGATATAGAAAACCATTAGACAATATTAAAGATAATGTAGGAAAAATGGAAGAT	Db 64	
729	0 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT	0у 67	
642		ن. ن	
669	0 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	Qy 61	
582			
609	0 TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	Qу 55	
522		Db 46	
549	0 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG	Оу 49	
462	GAACTCAAATATCCCGAACTCTTTGATTTAACCAATCATATGTTAACTTTGTGTGATAAT	Db 40	
489	0 GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC	0у 43	
402		ω	
429	O GACGCCAAGTCCTACGCCGACCTCAAGCACCGACTGAGAAACTATCTCCTCACTATCAAG	w	
342	CAMPADE CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONT	Db 28	
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2505	2446 GAGGAGAGTAAACTGTGCTCTTGTGATCCACTGGACCTGCTGCTGTTCAATATCCAGAACAAC	Qy
2436	-	Db
2445	AACGAGAAGATTCTTAAACAGTACAAGATAACCAAGGAA	Qy
2385 2376	2326 GACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATC	Фр
2325	2266 GCTCAAGTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAGAAATGTCAGCAAACTG	Db 04
2256	CHRISTAN CHARGE AND AND CHRIST CHARGE CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTINUES IN CONTIN	Db dg
2196	137 TCCACACACATTATCCCAATCAGGAGAAACAGAAGAAGAAACAGAAGAACAGTAGGACAC	₽ }
2205	2146 GCTACCAGCCCGGACAAGCACGGCCGGTCAGCTCTCGAAGGCGATAGCGTGCAAGCT	Qy
2145 2136	2086 AAAACTGAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAG	Оу
2085	2026 AAACI'GAAAGI'GI'ICATGCCCAAAGI'CGACGCC'IGAI'CAACGAGGAGGAGGAAGAACATT 	Db
2019	60 TATAAACCACAAAATAAACCAGAACCATATTAATTTAAT) Db
2025	CATACTACCTCATCGTACT	Qy
1965 1959	1906 AAGACTCAACTCATTCTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGT	Db Oy
89		Db &
1839	TAGAAAAAAATTITAAAGGACTAACACATTCAGCAAATGCTTCCTTAGAAGTATCT btattcttaaa	8 8
1845	1786 TTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCC	Qy
1785 1782	1726 AAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTG	Оу
N	663 TATTCTTTAAGAAAAGGAATTTCTGAAAAAGGATTTTAATCATTATTATTACTTTGAAAACT	₽ :
1725	666 TATTCTCTGCGGAACATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGT	ΟV
1665 1662	1606 TATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGAC	Db Qy
1602	1546 ATGGAAAACGGTACTCTTACAAAGTGAAAACTGAACACCACCATAATACCTTTGCATCC 	Db Qy
54	483 GAAAAATTTTATGAAATGAAATTTAATAATAATTATTGACAAAGATGTCGTAGATAA	DЬ
1545	1486 AACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCTACTTCGAGAAAATG	Qy
1485 1482	1426 AGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTG	Db Oy
1422		Dъ

_		59	Db -
ATAACCACAACAATCTC 4491	AAA	4432	Qy
		4531	뮹 .
ARAMAGAIGAAGCACAI 4330		44/1	0
	TTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATACTTACGAGAAGAGCAATGTGGAA	4312	ş Q
TTAATAAATTGACGAT 4470		4411	Дb
ACGACAAAATCGACCTC 4311	CTGCCCTTCCTGAATAACATCGAAAACCCTGTACAAGACAGTGAACGACAAAATCGACCTC	4252	Qy
AGAAGGAAAGTAAGTTC 4410	CCACCAACAACACCTCCGTCACCAGCAAAAAACAGACGAA	4351	рь
CAAGGCGAGAATGAAAAATAT 4251		4231	Qy
AGGAGTTCCCATCATCA 4350	AAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAAGG	4291	рь
4230		4189	Qy
AGGTTTTAGCGAAATAT 4290	AATGATATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAGGTTTTAGCGAAATAT	4231	Вb
TCCTGAGCGAAAAATAC 4188		4129	Qy
TAAAAGAATCAGTAGAA 4230	AATTCAGAACAAAAAAACACACTTTTAAAAAAGTTACAAATATATAAAAGAATCAGTAGAA	4171	Db
TCAAGGACTCCATCGAC 4128	AATAAAGAGAAAGAGGGATAAATTTCTGTCTAGTTACAACTATAT	4069	Qy
SATTCATTTAAATTATTG 4170	ATGCAATTTAAACATATATCCTCAAATGAATACATTATTGAAC	4111	Db
ACCCATACAAGTTCCTC 4068	ATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAG	4009	Qy
TATTAGAATCTGATTTA 4110		4051	Db
TCTTGGAGAGCGACTTG 4008		3949	Qy
ATTTAAATTTGAACGAT 4050		3991	DЪ
ATGTCAACGTGAAGGAC 3948		3889	Qy
CTTTAGCTGGAGTATAT 3990	CTCTCAGGATTTGAAAATGAATATGATGTTATATATTTAAAACCTTTAGCTGGAGTATAT	3931	Db
CTCTGGCAGGCGTCTAT 3888		3829	Qy
CAATGGATAATATC 3930		3874	Db
-		3769	Qy
AATCCGAAGATAATGAC 3873	GACGAAGAAGATGATTCCTTAGTTGTATTACCCATTTTTGGAGAATCCGAAGATAATGAC	3814	Db
AGAGCGAGGAGGACTAC 3768		3709	Qy
AATTACAACAAGTAGTACAATCACAAAATTAT 3813	ATACCAACTTCAGGCTCTTTATTAACAG	3754	Db
CCACATCTCAGAACGTC 3708	GCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACCACATCTCAGAACGTC	3651	Qy
CAAAAGAAGAAACACAA 3753	CCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACAAAAGAAGAAGAAA	3694	В
CAACCTAAGAA 3650	CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCAACCTAAGAA	3597	Qy
CTCAACCAGATGTAACT 3693		3634	Db
3596		3568	Qy
		3574	Db
CACTGGAATCTTACAAG 3567	· >>	3508	Qy

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DEFINITION ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-JAN-1999) K. Tanabe, Osaka Biology, 5-16-1 Ohmiya, Asahi-ku, Osaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allelic dimorphism in a surface antigen parasite Plasmodium falciparum J. Mol. Biol. 195 (2), 273-287 (1987)
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189 315	ACCGGATACAGCCTGTTCCAGAAGGAGGAGAAGATGGTGCTGAATGAA	130 256	
129 255	ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT	70 196	

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2550 2694	2491 AATATCCAGAACAACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACAATTCTCTC	D 04
2490 2634	2431 AAGATAACCAAGGAAGAAGAAGAAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTC	Db Qy
2430 2574	2371 TGCCACAAATATATCCTCGTCTCCACAGCACTATGAACGAGAAGATTCTTAAACAGTAC	B 8
2370 2514	2311 AATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATC	υ
2310 2454	2256AGAGGCTAAAGCTCAAGTGCCTACACCACCACCTCTGTGAATAACAAGACCGAG	DP 6A
2394	2335 GAAACAGTAGGACACACAACAACGGTAACAATAACATTACCACCAAAAGAAGAATCAGCA	Db

o da Vo		AGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCAGTCTTCTCCT 3
Oy dd	3313	CTGAAGACTCTCTCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAAC 3372
Qy	3373 3592	TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGGAACCTGGAGAAGAAG 3432
Qy Db	3433	AAGCTCAGCTACCTCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT 3492
Qy Db	3493 3712	AAGAACAAGAACTACACCGGCAATAGCCCCAAGCGAGAATAATACAGACGTGAATAACGCA 3552
Db VQ	3553 3772	CTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC 3596
Qy	3597	
Db	3832	CAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCACA 3891
. Q	3642	ACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTACC 3693
Ş	3694	بد 7
Дb	3952	
Qγ	3754	AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCC 3813
DЬ	4012	TCCGAAGATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATATCTGTC 4068
Qy	3814	GTGATTGATAACATTCTGTCCAAAATCGAAGTACGAATACGAAGTGCTCTATCTGAAACCT 3873
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Qy	3934	TTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC 399
Db	4189	TTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTA 4248
Qy	3994	TIGGAGAGCGACTIGATICCCTATAAAGACCTGACCTCCTCTAACCTACGTTGTCAAGGAC 4053
ρb	4249	4
ν	4054	-
Db	4309	4
, Q	4114	AAGGACTCCATCGACACCGATAITCAATTTCGCTAATGATGTGTGCTGGGGTATTACAAGATC 4173
ρ	4174	CTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAAGTATATCAACGATAAG 4230
DЬ	4429	GTTTTAGCGAAATATAAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAAG 4488
Qy	4231	
마	4489	GAGAAGTTCCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAA 4548

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                                                                                                                                p.falciparum (isolate FC27 from Papua New Guinea), cDNA to mRNA, clone Ag75, gl.1, gl26, pEPG3.3.

plasmodium falciparum maid properties and semosporida; plasmodium.

Loses 1 to 5754)

Peterson, M.G., Coppel, R.L., McIntyre, P., Langford, C.J., Woodrow, G., Brown, G.V., Anders, R.F. and Kemp, D.J.

Variation in the precursor to the major merozoite surface antigens
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1. .5754
/organism="Plasmodium falciparum"
/isolate="FC27 (Papua, New Guinea)"
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TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                       GCTGTTACAACTAGTACACCTGGTTCAAGTGGTTCAGTTACTTCAGGTGGTTCAGTTGCT
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LVSNSSMDKLLEVYNLTPEERMELKSCOPLDLLFNIONNIPAWYSLYDSMNIDLQHL
FFELYOKEMIYYLHKLKEENHIKKLLEEQKOLTGTSSTSSSPONTTVNTAQSAYHSNSQ
NQQSNASSTNTQNGVAVSSGPAVVEESHDPLTVLSISNDLKGIVSLLNLGNKTKVPNP
LTISTTEMEKFYENILKNNDTYFNDDIKQFVKSNSKVTTGLTFYCKNALNDEIKKLKD
TLOLSFDLYNKYKKLLDLAFHNKKKELGODKNOIKKLTLLKEOLESKLMSLNNPHNYLC
NKFYVEALKSYENFLEAKVTTVVTPPOPDVTSSPLSVYYNGESSPLKTLSEVSIQTEDN
YANLEKFRALSKIDGKLMDNLHLGKKKLSFLSSGLHHLTELKEVIKNNTTCNSPSE
SLLTELQOVYQLQNYDEEDDSLVYLPIFGESEDNDEYLDQVTGEAISVTMDNILSGF
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178. .5223
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DVUDKIFSARTTYNVEKQRYNNKFSSSNNSVYNVQKLKKALSYLEDYSLEKGISEKDF
NHYYTLKTGLEADIKKLTEEIKSSENKILEKNFKGLTHSANASLEVSDIVKLQVQKVL
LIKKLEDLRKLELFLKNAQLKOSIHVPNIYKPQNKPEPYYLIVLKKEVDKLKEFIPKV
KDMLKKEQAVLSSITQPLVAASETTEDGGHSTHTLSQSGETEVTEETEVTEETVGHTT
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RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDONKNADNEEGKKKLYQAQ
YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTDAENPTTGSKPNP
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LFQKEKMVLNEGTSGTAVTTSTPGSSGSVTSGGSVASVASGASVASGGSGSVASGGSGNS
RRTNPSDNSSDSNTKTYADLKHRVQNYLFTIKELKYPELFDLTNHMLTLSKNVDGFKY
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709 c 708 g 1798
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121. .17/7
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EREECKCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECTKP
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IDDYLINLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNTNDFEAIKKLINDD
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EKHISSNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKY
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KSVQIPKYPYPNGIVYPLPLTDIHNSLAADNDKNSYGDLMNPDTKEKINEKIITDNKE
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1. .5754
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/db_xref="GI:160413"
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121. .5226
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TIT GATIATIA GAAAGAAKCCITCIAAGAATATCITACACAGACAATIGAGAGAAGAAGATTI 1355	TTCGATTATACGAAAGAACACTA 	1423	B 5
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CGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCC 13	ATCAACAACG	25	2 04
AAGTTCCTTATCCAAATGGTATTGTATATCCTTTTACCACTCACT	GTTCAAATACCAAAAGTTC	30	Db 42
_ ,	GAATCAACCGAACCTAATG	19	0
AGAGAAAAAAAAAAAAGTTGATGTAACACCTAAAGTCGAGACAAAG 1194	TTGAGAGAGAAGAATAAGA	1144 1243	QQ VQ
AAAACTATTAAATTTAACATTGATAGTTTATTTACTGATCCACTTGAATTAGAATATTAT 1242	AAAACTATTAAATTTAACA	1183	뫄
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3492	QY 3433 AAGCTCACCTACCTACCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT	Ø
3432 3636	Qy 3373 TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAG	ם ם
3372 3576	Qy 3313 CTGAAGACTCTCTCCGAGGAGAGCGATCCAGACCGAGGATAACTACGCCAGCCTCGAGAAC	9 0
3312 3516	Qy 3253 AAGATTCTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCT	U 0
3252 3456	Qy 3193 TTCTTCAACAAGAAGAAGGAAGCCGAGACTCGCCGAGACAGAGAACACTCTGGAGAACACCC	8 0
3192 3396	Qy 3133 CTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTG	U 0
3132 3336	Qy 3073 AAGAAGACAGTCGGCAAGTATAAGATGCAGAAGTAGAAGTTGACTCTGCTCAAGGAGCAG	0 0
3072 3276	QY 3013 CAACTGAGCTTCGACCTGTACAACAACTACAAACTGAAACTGGAGAGACTCTTCGACAAG	D 0
3012 3216	953 AACGATGAATCTAAACGTAAGAAGCTGGAAGAAGAACATCAATAAGCTGAAGAAGA 	0 0
2952 3159	1	0 .0
2892 3099	QY 2833 CTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACACA	U O
03	2776 CTGAAACTGTTTGAGAACATCCTGTCTCCGGCAAGAATAAGAACATCTACCAA	0 0
97	2721GCCGAAGTGAGCGCTAACGACGACCTCTCACTCGACCAACCTTAATAACTCA 2920 GGTCCTGCTGTAGTTGAAGAAAGTCATGATCCCTTAACAGTATTGTCTATTAGTAACGAT	ם ס
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2641 2799	QY 2611 GACAACGACAAGATTAAGAACCTTCTGGAGG	оo
2610 2739	AGATGGTCTGCAACC AAATGATTTATTATT	U 0
2550 2679	Qy 2491 AATATCCAGAACAACATTCCCGTTATGTATCTATGTTCGATAGCCTCAACAATTCTCTC	<u>а</u> .о
2619	Db 2560 AATCTTACTCCAGAAGAAGAAAATGAATTAAAATCATGTGATCCATTAGATTTATTT	D

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4 AACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCA	4294 4594 4354	Qy Db
34 GGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAGACA 	4234 4534	Фр
91	423 447	Qy Db
4 CTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAA 	417 441	Qy Db
4 AAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGJ	4114 4354	Qу Db
34 CCATACAAGTTCCTCAATÅAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTATATC 	405 429	Qy Db
94 TIGGAGAGCGACTIGATICCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCA 	3994 4234	Qy Db
34 GTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACG 	3934 4174	Qy
4 CTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTC:	387 411	Qy Db
.4 GTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACC 	381 405	Qy Db
34 AGCGAGGAGGACTACGATGÀCCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTC0	375 399	Оу
4 ACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCATTGTGCCTATCTTC	369 393	Qy Db
12 ACCTAAGAAGCCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATT	364 387	Qy Db
)7	3597 3817	Qy Db
S3 CTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC	355 375	Qy Db
33 AAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATAATACAGACGTGAATX 	349 369	Qy Db
37 AAATTATCTTTCTTATCAAGTGGATTACATCATTTAATTACTGAATTAAAAGAAGTAATA	363	Db

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                                                                                      Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. fur Molekulare Biologie (ZMBH), Univ. Heidelberg, Feld 282, 69120 Heidelberg, Germany On Aug 5, 1995 this sequence version replaced gi:5
                                                                                                                                                                                                                               merozoite surface antigen-1
Exp. Parasitol. 81 (1), 47-
                                                                                                                                                                                                                                                            Tolle,R., Bujard,H. and Cooper,J.A. Plasmodium falciparum: variations within
                                                                                                                                                                                                                                                                                                                            Mol. Biochem.
96123395
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GGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTGGCAAGCGGCGGTTCC
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YLKKLDEFLTKSYICHKYILVSNISMORKLEVYNLTPBEENELKSCOPLDLICHNION
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KRGIYSLLNLGNKTKYUPNLFITSTTEMEKFYENILKNNDTYFNDDIKOFVKSNSKVIT
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KEQLESKLUSLNNHNVLQNESVFENKKKEAEIAETENTENTKILKHYKGLVKYYN
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RVSGSSGSTKEDVLSSTLTELQQVVQLQNNDEEDDSLVVLPIFGESEDNDEYLD
QVVTGCBALSVYMDNLLSGFENSTDVIYLKELGKSTLTSLKKQIEKNIFTFNLNLNDILN
SRLKKRKYFLDVLESDLMOFKHISSNBYIIEDSFKLMSGCRNFTLKSVKYIKESVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELFDLTNHMLTLCDNIHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQI
FPINLKIRANELDVLKKLYFGYBKPLDNIKDNVCKMEDYIKKNKFTIANINELIEGSKK
TIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEBAHNLISVLEKRIDTLKKNENIKKL
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YLREKNKKVDVTPKSQDPTKSVQIPKVPYPNGIVYPLPLTDIHNSLAADNDKNSYGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIKRANGEGISYYEKYLAKYKODLESIKKVIKBEKEKPPSSPPTPPSTAKTDEOKKES
KELPFLTNIETLYNNLYNKIDDY LINLKAKINCONVEKDEAHVKITKLSDLKAIDDKI
DLFKRAPYDFEAIKKLINDDTKKDMLGKILSTGLVQNFPNTIISKLIEGKRODMLMISG
HOCYKKOCPENSGCERHLDBREECKCLLNYKOEGDKCYENPNTTCNENNGGCDADATC
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109. .5271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEEDSGSSRKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI"
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ANGSLEVSDIVKLQVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVPNIYKPQNKPEPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNPHTKEK I NEK I ITDNKERK I F I NNI KKK I DLEEKN I NHTKEQNKKLLEDYEKSKKD
YEELLEKFYEMKFNNNFDKDVVDK I FSARYTYNVEKQRYNNKFSSSNNSVYNVQKLKK
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/dev_stage="blood stage"
109. .5271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="gp190, MSA1,
703 c 705 g
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/db_xref="GI:929796"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 1.1e-268; 
0; Mismatches 2018;
                                                                                                                                                                                                                          -GGGACGAGTGGCACGGCCGTTACAACCAGC
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1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5312;
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                                                                                                                                                                              348
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NCAGACAATGAGAGAAAGATTTATCAACGAAATCAAGGAGAAG 1386 	AGACAATO	1327 1489
TCGGTGACTTGATTAACCCCTTCGATTATACGAAAGAACCC 132 	-CAACGAGCTCAATAGCTTCGGTGACT 	42
ACGTACCCTCTGTCTTATAACGATATCAACAACGCTCT 1268 	TATCCCAATGGTGTGACGTACCCTCTGT	1216 1369
CGAGACAAAGGAATCAACCGAACCTAATG	GA	1165 1309
TCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGAGAGA	GATTCTCTCTTTACTGATCCCCTTGAGC	1105 1249
ACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATA 1104 	AAGATAGAGGAGCACGAGAAAGAGATCA 	1045 1189
CCAACTCTGGGAACACCCCTAACACGCTGCTGGACAAGAACAAG 1044 	100 100	985 1129
AGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATT 984 	ATAGACACCTCAAGAAGAATGAAAATATCAAAG 	925 1069
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ACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAA 804 	AAGAAGACCATCGAGAACATTAACGAGC	745 889
TCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAGAAT 744 	AAGCCTCTCGACAACATCAAGGACAATG 	685 829
CCAACGAGTIGGACGTATTGAAGAAGTIGGTCTICGGATATCGC 684	AATTTGAAGATCAGAGCCAACGAGTTGG	625 769
AACTGAATGACGTTTGCGCCAATGACTATTGTCAAATTCCATTC 624 	GACTTGCTAAGGGCCAAACTGAATGACG	565 709
ACGAAGAGATCAATGAACTCCTGTACAAGTTGAATTTCTACTTC 564 	TATCTGATTGACGGTTACGAAGAGATCA 	505 649
CTAATCATATGCTGACACTGTGTGATAACATTCATGGCTTCAAA 504 	CAGTTGTTCGACCTCACTAATCATATGC	445 589
GAGTGAGAAACTATCTCCTCACTATCAAGGAGCTGAAGTACCCA 444 	GCCGACCTCAAGCACCGAGTGAGAAACT. 	385 529
CCAATCCATCTGACAACTCTAGCGATTCCGACGCCAAGTCCTAC 384	CCTCC	325 469
GGTCCAAGTGGTCCAAGTGGTACAAGTCCATCATCTCGTTCAAACACTTTACCTCGTTCA 468	GGTCCAAGTGGTCCAAGTGGTACAAGTC	409

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3513	3454 GGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATTAAGAACAAGAACTACACCGGC	Qy
3702	3643 GATGGAAAACTCAATGATAATTTACATTTAGGAAAGAAAAAATTATCTTTCTT	Db
3453	AAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACCTCTAGC	Qy
3642	3583 TCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAATTTAGAGTATTAAGTAAAATA	В
3393		γQ
3333 3582	3274 AAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCCTCTGAAGACTCTCTCCGAGGAG	Db 04
3522		당 :
3273	GCCGAGATCGCCGAGACAGAGAACACTCTCGGAGAACACCAAGATTCTTCTAAAACACTAC	Q V
3213 3462	3154 CTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAGAAGAAGGAA :	P 04
3402		Db
3153	C _A	Qy
3342	3283 AATAAATATAAAATTAGATAGATAGTTAATAAGAAAAAAGAACTTGGCCAAGAC	В
3093	ΑŢ	Qy
3033 3282	2974 AAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGTAC	DP QA
3222	6 CAATTCGTAAAATCTAATTCAAAAGTAATTACAGGTTTGACCGAAACACAAAAAAAAT	ф
2973	2914 AACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGATGAATCTAAAGGTAAG	Qy
2913 3165	2854 GAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACATTCTATAACGAGAGCTTCACT	Оу
3105	3046 TTAAATCTTGGAAATAAAACTAAAGTACCTAATCCATTAACCATTTCTACAACAGAGATG	Db
2853		Qy
3045	2/3/ AACGACGCTCTCACTCGACCAACCTTAATACTCACTGAAACTGTTTGAAAAAATC	B 5
	727	2 8
2736	2703 TCTCACACCTCAAGACAA	P 04
2925	. 2866 ACCGTAAATACTGCTCAATCCGCAACTCACAGTAATTCCCAAAACCAACAATCAAATGCA	Db
2702		Qy
2865		Db
2657		Qy
2631	25/2 TRIYAGAAGGAGATIGGTCTIGCAACCTGTATAAACTCAAAGACAACAACGACAAGATTAAGAAC	р 4
6/40	000 00101010111101010101010101010101010	2
2571	2512 GTTATGTATTCTATGTTCGAGATAGCCTCAACAATTCTCTCTC	P Q
2511 2685	2452 AGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCC	Фр

GAACAAAAAACACACTTTTAAAAAGTTACAAATATATAAAAGATCAGTAGAAAATGAT 419 ATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGTCCTGAGCGAAAAATACAAGTCT 4194 ATTAAATTTCGCTAATGAAAAGTTATAAAAAATATATATA		Db 4180 Oy 3955 Db 4240 Oy 4015 Oy 4075 Db 4360 Oy 4135 Db 4420 Oy 4195 Db 4480 Oy 4231 Db 4540 Oy 4255 Db 4560 Oy 4375 Oy 4375
		4 2 4 4 4 4 4
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AATAGCCCAAGCGAGAATAATACAGACGTGAATAACGCACTGGAATCTTACAAGAAGTTC 3573	14	Qу 351
		Db 3703

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KEYWORDS
SOURCE
ORGANISM
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PFAGP195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGACGAGGGGCGAAGAGTGCAAGTGT 4674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAAATTACTTAGTACAGGATTAG---TTCAAAATTTTCCTAATACAATAATATCAAAA 4896
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                                                                                                                                                                                                                                                                                                                                                                   Exp. Para
89005525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major merozoite surface antigen.
P.falciparum (strain Uganda-Palo Alto) DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 5276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siddiqui, W.A.
Plasmodium fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cds
M37213
M37213.1 GI:160315
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                                                                                                                                                                                                                                                                                                                                                                                                                               major merozoite
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falciparum major merozoite surface antigen (gp195) gene,
                                                                                                                                                                                                                                                                                                                                                                                        Parasitol.
TLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEEKIKEIAKTIKFNI
DSLFTDPLELEYYLREKNKKVDVTPKSQDPTKSVQIPKVPYPNGIVYPLPLTDIHNSL
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Nylftikelkypelfdltnimltlcdnihgfkylidgyeeinellyklnryfdllrak
                                         ANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRID
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/db_xref="GI:160316"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                               /organism="Plasmodium
/db_xref="taxon:5833"
                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                        /note="major merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                  falciparum:
                                                                                                                                                                                                                                              .5181
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                                                                                                                                                                                                                                                                                                                                                                                                                                 surface
                                                                                                                                                                                                                                                                                                                                                                                                                           gene structure and hydropathy profile of
e antigen (gp195) of the Uganda-Palo Alto
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                                                                                                                                                                                                                                                                                    falciparum'
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NISVYINVQKLKALSYLEDYSLEKGISENDFHIFYTILTGLEADIKLTEEIKSSENK
ILEKNERGIFHSANASLEVYDIVKLOVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVP
NIYKPQNKPEPYYLIVLKKEVDKLKEFIPKVKDMLKKEQAVLSSITQPLVAASETTED
GGHSTHTLSQSGETEVTEETEETEETVHTTTYTITLPPKEVKVVENSIEHKSNDNSQ
ALTKTYVLKKLDEFLTKSYICHKYILVSNSSMDQKLLEVNLTFEEENELKSCDPLDL
LENIQNNIPAMYSLYDSMNDDLOHLFFELYQKEMIYYLHKLKEENHIKKLLEEQKQIT
GTSSTSSPGNTTVNTAQSATHSNSQNQQSNASSTNTQNGVAVSSGPAVVEESHDPLTV DADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSNFLGISFLLILMLILYSFI " AIDDKIDLEKNHNDEDAIKKLINDDTKKDMLGKLLSTGLVQNEPNTIISKLIEGKEQD MLNISQHQÇVKKQCPENSGCERHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGC

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 ATTAATGAATTATTATATAAATTAAAACTTTTATTTTGATTTATTAAGAGCAAAATTAAAT
                 ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAAT 588
                                                                     ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG
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                                                         ATGTTAACTTTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAA
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D; Mismatches 1998;
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1710	1651 AAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTGGAGAAAGAA	Qy
1740	1681 AATAAATTTTCATCCTCTAATAATTCTGTATATAATGTTCAAAAATTAAAAAAGGCTCTT	B
1650		Qy
1680	1621 GTCGTAGATAAAATATTCAGTGCAAGATATACATATAATGTTGAAAAACAAAGATATAAT	DЪ
1590		Qy
1620		В
1530	C	Qy
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1470		Qy
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1410	GAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATT	Qy
1440		Db
1350	1291 GACTTGATTAACCCCTTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAAT	γQ
1380	AGCTGCAGATAATGATAAAAATTCATATGGT	Db
1290		Qy
1320	1261 GATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATTGTATATCCT	Db
1239		ρ
1260	1201 GAATTAGAATATTATTAAGAGAAAAAAATAAAAAAAGTTGATGTAACACCTAAATCACAA	DЪ
1187		Qy
1200		Db
1128		γ
1140	1081 GGAAATACACCAAATACTCTCCTTGATAAGAACAAAAAAATCGAGGAACACGAAGAAAAA	Db
1068		φ
1080	1021 AACATTAAGGAATTACTTGATAAGATAAATGAAATTAAAAATCCCCCACCGGCCAATTCT	В
1008		Ωу
1020	961 GAAGCACATAATTTAATAAGCGTTTTAGAAAAACGTATTGACACTTTAAAAAAAA	Дb
948		Qy
960		Вр
888		Qy
900	841 GAATTAATTGAAGGAAGTAAGAAAAAAATTGATCAAAATAAGAATGCAGATAATGAAGAA	Db
828		Qy
840	781 AATGTAGGAAAAATGGAAGATTACATTAAAAAAAATAAAACAACCATAGCAAATATAAAT	Db
768		Оу
780	049 TIOSHOUTATIONASANSTIGSTOTTOGSATATIOGAGGCOTOTOGACGACATCAAGGAO 	B 3
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648	589 GACGTTTGCGCCAATGACTATTGTCAAATTCCATTTTGAAGATCAGAGCCAACGAG	} &
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2720	2682 CAGCTCCATGCAACACTGTCTCTCACACCTCAAGACAA	Qy
TTCC 2814	2755 ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAATCCGCAACTCACAGTAAT	рь
CTTC 2681	2658CACCTCTGTTAAAACTCTCTCTTT	Qy
7	695 GAGGAAATCACATCAAAAAATTATTAGAGGAGGAAAAACAAATAACTGGAACATC	Db
2657	2611 GACAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTC	Оу
CAAA 2610 AAAA 2694	2551 TCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTCAAA	Db Qy
TTTA 2634	2575 AATATTCAAAATAACATACCTGCTATGTATTCATTATATGATAGTATGAACAATGATTTA	Db
TCTC 2550	AACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACAATTC	Qy
 ATTATTT 2574		Db
TGTTC 2490	raaccaaggaagaggagagtaaactgtcctcttgtgatccactggacci	Qy
 ATAT 2514		DЪ
TAC 2	371 TGCCACAAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAAC	Qy
ATA 2	2395 GCCTTGACAAAAACAGTTTATCTAAAGAAATTAGATGAATTTTTAACTAAATCATAT	₽ 5
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AGAA 2274	2216 AAGAT-GGGGTCACTCCACACACACATTATCCCAATCAGGAGAAACAGAAGTAACA	Db
AGGC 2190	VTAACCGGACAGGCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGA	Qy
AACTG 2215	2156 AAGAACAAGCTGTCTTATCAAGTATTACACAACCTTTAGTTGCAGCAAGCGAAACAA	Db .
CAGAAGGA 2130	argaagaacattaaaactgaaggacagtcagataactccgagccttccac	Qy
 GA 2155	NAGAAGTAGATAAATTAAAAGAATTTATACCAAAAGTAAAAGACATGTTAAA	Дb
≫ -	aaactgaaagtgttcatgcccaaagtcgagagcc	Qy
TA 2	2038 CATGTACCAAATATTTATAAACCACAAAATAAACCAGAACCATATTATTTAATTGTAT	Db
ACTC 2010	ATGTGCCGAATAGTTATAAGCA	Qy
TATT 2037	1978 ATAGAAGACTTAAGAAAGATAGATTTTTAAAAAATGCACAACTAAAAGATAGT	Db
TATA 1950	rtgaactcaagaagactcaactcattctgaagaacgtggagttaaaacat	Ωу
TAAAAAA 1977	1918 TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA	DЬ
CAAG 1890	AAGTGCAGAAGGTGCTCCTCATO	Qy
CT 1917	1861 AGTGAAAACAAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATG	Db
GAAG 1830	AGACGAAAATAAACCAG	Qy
GAGT 1860		Db
GAAG 1770	1711 AAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAG	Qγ
TTAT 1800	1741 TCATATCTTGAAGATTATTCTTTAAGAAAAGGAATTTCTGAAAAAGATTTTAATCATT	DЬ

3753 3951	ACATOTCAGAACGTOGAGGATGAGGTOGATGACCTCATTGTGCCTATCTTCGGCGAG 	3694 3892
69	ACCTAAGAAGCTGCATCTACTCATGTCGGAGCCGAGTCCAATACAATTA	83
3641 3831	CAACCAGATGTAACT	3597 3772
3596 3771	CTGGAATCTTA TTAAAATCTTA	3553 3712
3552 3711	AAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTGAAT	3493 3652
3492 3651	AAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATCGCCGAGCTCAAGGAAGTCATT	3433 3592
3432 3591	TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAG 	3373 3532
3372 3531	CTGAAGACTCTCCCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAAC	3313 3472
3312 3471	AAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCT	3253 3412
3252 3411	TTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCC	3193 3352
3192 3351	CTTGAAAGGAAACTCAACTCACTGAACAATCCGAAACAGTACTGCAGAACTTCTCAGTG	3133 3292
3132 3291	AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAG	3073 3232
3072 3231	CAACTGAGGTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGAGAGA	3013 3172
3012 3171	AACGATGAATCTAAACGTAAGAAGCTGGAAGAGGGACATCAATAAGCTGAAGAAGACACTG	2953 3115
2952 3114	TICTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTT	2893 3055
2892 3054	CTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAAGACAGCGACACACAC	2833 2995
2832 2994	CTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAA	2776 2935
2775 2934	GCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTTAATAACTCA	2721 2875
2874	CAAAACCAACAATCAAATGCATCCTCTACCAATACCCAAAAATGGTGTAGCTGTATCATCT	2815

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4714 AACCCAAACCTACCTGCAATGAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC 47/3	Qy Db
906 GAAAGAGAAGAATGTAAATGTTTAATTAAATTACAAACAA	ДΔ
AAGAGTGCAAGTGTCTCCTGAACTACAAACAAGAAGAAGAAGATAAGTGCGTGG	Qy
4594 CAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGAC 4653	Db Oy
	Дb
ATC	VQ
729 GATACGAAAAAGATATGCTTGGCAAATTACTTAGTACAGGATTAGTTCAAAATT	ДЬ
474 TATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGT	Qy
4414 AAGCTGGCAGATTCAAGAAAAATAACAATTCGTCGAATTGCAGCCCTCTCTACGAT 44/3 414	Db dy
609 GAAAAAGATGAAGCACATGTTAAAAGTAACTAAACTTAGTGATTTAAAAAGCAATTGATGAC 400) Db
354 GAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCAAGAC 44	Qy
AAGATTAACGATTG	рь
4294 AACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATACTTAC 4353	Qy
4489 AAGAAGGAAAGTTACCTTCCATTTTTAACAAACATTGAGACCTTATACAATAACTTA 4548	DЬ
TAACATCGAAACCCTGTAC	Qy
	рb
4231CAA 4233	Qy
4369 GTTTTAGCGAAATATAAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAG 4428	рь
CTGACCTTGACTCTATTAAAAAGTAT	Qy
4309 AAAGAATCAGTAGAAAATGATATAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAG 4368	В
4114 AAGGACTCCATCGACACCCATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAGATC 4173	Qy
4249 TCATTTAAATTATTGAATTCAGAACAAAAAAACACACTTTTAAAAAGTTACAAATATATA 4308	Db
4054 CCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTATATC 4113	Qy
4189 TTAGAATCTGATTTAAATGCAATTTAAACATATATCCTCAAATGAATACATTATTGAAGAT 4248	Db
3994 TTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAGGAC 4053	Qy
4129 TTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTCTTAGATGTA 4188	В
3934 GTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACGTC 3993	Qγ
	DЬ
AGCTGGAGAATAACGTGATGACCTTC	Qγ
3814 GTGATTGATGAGATTCTGTCCAAAATCGAAGAGGAGTAGGAAGGGCTCTATCTGAAACCT 30/3 11	Фр
932 TCCGARGATAATGACGAATATTTAGATCAAGTAGTAACTGGAAAAGCAATTTTAGATCAGT	מ
754 AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCCGGTGAGGCTGTCACTCCTTCC	, Q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-MAR-1987)
3 (bases 3594 to 5541)
Weber,J.L., Sim,B.K., Lyon,J.A. and Wolff,R. Merozoite surface protein sequence from the human malaria parasite Plasmodium falciparum Nucleic Acids Res. 16 (3), 1206 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variation in the gene encoding a major merozoite surface antigen of
the human malaria parasite Plasmodium falciparum
Nucleic Acids Res. 14 (8), 3311-3323 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 3593)
Weber, J.L., Leininger, W.M. and Lyon, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein; surface antigen; tandem repeat
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SGTSAQSGTSGTSGTSGTSGTSGTSGTSGTSAQSGTSGTSAQSGT
SGTSAQSGTSGTSGTSGTSGSSRSUTLPRSNTSSGASPPADASDSDAKSYADLKHRVR
NYLFI KELK VPELFDLTNHMLTLCDN1HGFKYLIDGVEENFLLYKLLNFYFDLLRAK
LNDVCANDYCQIPFNLK TRANELDVLKKLVFGYRKPLDNIKDNVGKMEDY IKNNKTTI
ANINELIEGSKKTIDQNKNADNEEGKKKLYQAQYDLSIYNKQLEEAHNLISVLEKRID
TLKKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEBHEEKIKEIAKTIKFNI
LFNIQNNIPAMYSLYDSMNNDLQHLFFELYQKEMIYYLHKLKEENHIKKLLEEQKQIT
GTSSTSSPGNTTVNTAQSATHSNSQNQQSNASSTNTQNGVAVSSGPAVVEESHDPLTV
                                          ILEKNFKGLTHSANASLEVYDIVKLQVQKVLLIKKIEDLRKIELFLKNAQLKDSIHVP
NIYKPQNKPEPYYLIVLKKEVDKLKEFIPKVKDMLKKEQAVLSSITQPLVAASETTED
GGHSTHTLSQSGETEVTEETEETEETEGTTTVTITLPPKEVKVVENSIEHKSNDNSQ
ALTKYVYLKKLDEFLTKSYICHKYILVSNSSMDQKLLEVYNLTPEEENELKSCDPLDL
                                                                                                                                      DSLFTDPLELEYYLREKNKKVDVTPXSQDPTKSVQIPKVPYPNGIVYPLPLTDIHNSL
AADNDKNSYGDLMNPDYKEKINEKIITDNKERKIFINIKKOIDLEEKKINHTKEQNK
KLLEDYEKSKKDYEBLLEKYYEMKFNNNFDKDVDKIFSARTYYNVEKGYNNKEYSS
NNSVYNVQKLKKALSYLEDYSLRKGISEKDFNHYYTLKTGLEADIKKLTEEIKSSENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="CAMP (Malaysia)"
/db_xref="taxon:5833"
283. .5463
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:P04934"
                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA27446
/db_xref="GI:9895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="pot. major merozoite
                                                                                                                                                                                                                                                                                                                                                                   translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Plasmodium falciparum"
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TTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC
                                                                GATGTATGTGCTAATGATTATTGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAA
                                                                                   GACGTTTGCGCCAATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAG 648
                                                                                                                                                                                                                                                     ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG
                                                                                                                                                                                                                                                                                                                                      AACTATCTCCTCACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAAATCATTTTCTTCCTCTGTTCATTTCTTTTTTTTATCATCAATACTCAGTGCGTG
                                                                                                                                                ATTAATGAATTATTATAAATTAAACTTTATTTTGATTTATTAAGAGCAAAATTAAAT
                                                                                                                                                                                    ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCCAAACTGAAT 588
                                                                                                                                                                                                                               ATGTTAACTTTGTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAA
                                                                                                                                                                                                                                                                                                                   AATTACTTGTTCACTATTAAAGAACTCAAATATCCCGAACTCTTTGATTTAACCAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                CCAGCTGATGCAAGCGATTCAGATGCTAAATCTTACGCTGATTTAAAAACACAGAGTACGA
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/note="19 imp. tandem repeats 1"

2542. .2586

/note="5 imp. tandem repeats 2"
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LNDILKSTLKRKYFLDVLESDLMGFKIISSNEYIIEDSFKLLNSEGKRYLKSYKYI
KESVENDIKFAQOEGISYYEKYLAKYKDDLESIKKVIKBEKERPSSPPTPPSPAKTO
EQKKESKFLPFLTNIETLYNNLVNKIDDYLINLKAKINDCNVEKDEAHVKITKLSDLK
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LVKYYKGESSPLKTLSEVSIQYEDNYANLEKFRVLSKIDGKLNUNLHLGKKKLSFLSS
GLHHLITELKVITKNKNYTGNEPSENNKKVNEALKSYENFLPEAKVTTVYTPPODDYT
PSPLSVRVSGSSGSTKEETQIPTSGSLLTELQQVVQLQNVDEEDDSLVVLPIFGESED
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MLNISQHQCVKKQCPENSGCFRHLDEREECKCLLNYKQEGDKCVENPNPTCNENNGGC
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	1003	TTAGACGTACTTAAAAAACTTGTGTTCGGATATAGAAAACCATTAGACAATATTAAAGAT 1	1062
	709 1063	– 7	122
	769 1123	L 6	128
	829 1183	TACGACCTGTCCATCTATAACAAACAGCTTGAA 8 	242
	889 1243	GAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGAACACCCTCAAGAAGAAGAATGAA 9)48 302
	949 1303	AATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	1008 1362
	1009 1363	GGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAG 1	.068
	ω φ	ATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTT 11	128
	1129 1483	AGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGA-	1187 1542
	ω α	GACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCT 1	.239
	240 603		290
	1291 1663	TGATTAACCCCTTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAAT 1 	350
	1351 1723	GAGAGAAAGAAGTTTATCAACGAAATCAAAGGAGAAGATCAAAATTGAGAAGAAGAAGAATT 1	782
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	1471 1843	TATGAAAAGCTGCTGAACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACC 1	530
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	1591 1963	AATACCTTTGCATCCTATGAGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTT 1	.650 .022
	1651 2023	TATATGGAGGACTATTCTCTGCGGAACATTGTTGTGGAGAAAGAA	710 082
-	1711 2083	AAGAATCTCATAAGTAAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAG 1	770 142

7 GGTCCTGCTGTAGTTGAAGAAAGTCATGATC	Db 315	
21GCCCGAAGTGAGCGCTAACGACCGACCCTCTCACTCGACCAACCTTAATAACTCA 2775	Qy 27:	
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20	Qy 268	
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60	Qy 265	
7	Db 297	
1 GACA	Qy 261	
17 CAACATCTCTTTTTGAATTATATCAAAAGGAAATGATTTATTT	Db 291	
51 TCTCAACTGTTCATGGAGATATATGAGAAGGAGGTGTCTGCAACCTGTATAAACTCAAA 2610	Qy 255	
AATA	Db 2857	
	Qy 2491	
97 AATCTTACTCCAGAAGAAAATGAATTAAAATCATGTGATCCATTAGATTTATTATTT 2856	Db 279	
1 AAGATAACCAAGGAAGAGGAGAGTAAACTGTCCTCTTGTGATCC	Qy 243	
37 TGTCATAAATATTTTAGTATCAAACTCTAGTATGGACCAAAAATTATTAGAGGTATAT 2796	Db 273	
1 TGCCAC	QY 237	
7	Db 267	
1 AATGTCAGCAAACTGGACTACCTTGAG	0у 231	
CCAAA	Db 2617	
1 GTTCCAGAGGCTAAAGCT¢AAGTGCCTACACCACCAGCTCCTGTGAA	Qy 225	
7 GAAACA	Db 255	
1 GATAGCGTGCAAGC	Qy 219	
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	Qy 2131	
	Db 2438	
	Qy 2071	
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1	Qy 201	
0 0	Db 232	
1 CATGTGCCGAATAGTTAT	QY 195	
0	Db 226	
<u> </u>	Оу 189	
00 TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAATTA	Db 2200	
-	Оу 183	
.43 AGTGAAAACAAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCT 2199	Db 214	
71 GATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAG 1830	Qy 1771	

3873	3814 GTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCT	Qy
4290	4234 TCCGAAGATAATGACGAATATTTAGATCAAGTAACTGGAGAAGCAATATCTGTC	Db
3813	3754 AGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTCACTCCTTCC	Qy
4233	1	Db &
3753	2 1	Ş
3693	3642 ACCTAAGAAGCCTGCATCTACTCATGTCGGAGGCCGAGTCCAATACAATTACC	} &
4113	054 CAACCAGATGTAACTCCCATCCCATTATCTGTAAGGGTAAGTGGTAGTTCAGGATCCAC	рь
3641	3597CACTGTGGTGTCTGAATCTGGCTCCGACACACTGGAGCAGTCTCA	Qy
4053	994	Db .5
3506	2	Q
3552 3993	3493 ARGARCARGARCEGOCARTRIGCCCARGCGAGARTARTRCAGACGTGARTRACGCA	p Qy
3933	874	В
3492	4	Qy
3873	3814 TTTAGAGTATTAAGTAAAATAGATGGAAAACTCAATGATAATTTACATTTAGGAAAGAAA	ф
3432	3373 TTCAAGGTCCTGTCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGGAAGCAGGAGAAGAAG	Qy
3813	3754 TTAAAAACTTTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAA	B 3
3700	31 4	2 5
ıω	5 2	P 09
3693	634	ф
3252	3193 TTCTTCAACAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCC	Qy
3633	3574 TTAGAATCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAACTTTTCTGTT	Db
3192	3133 CTTGAAAGCAAACTCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTG	Qy
3132 3573	3073 AAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAG	Qу
3513	3454 CAGTTATCATTTGATTTATATAATAAATTAAATTAAAATTAGATAGA	망
3072	3013 CAACTGAGCTTCGACCTGTACAACAAGTACAAACTGGAAACTGGAGAGACTCTTCGGACAAG	Qy
3453	3397 ACCGAAACACAAAAAAATGCATTAAATGATGAAATTAAAAAATTAAAAGATACTTTA	Db
3012	2953 AACGATGAATCTAAACGTAAGAAGCTGGAAGAGGGACATCAATAAGCTGAAGAAGACACTG	Qy
3396	3337 TATTTTAATGATGATATCAAACAATTCGTAAAAATCTAAATTCAAAAAGTTACAGGTTTG	B 3
) L	0 1	? ;
2892	2833 CTTATTGGACAGAAATCGTCCGAGAAACTTCTACGAGAAAGATACTGAAAAGACAGCGACACAC	P 69
2		gb
2832	2776 CTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAA	Q

4893	TATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCATCTCCTTCCT	4834	Qy
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4833	GAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAGCCCGACTCC	4774	Qy
4773 5307	AACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC	4714 5248	Qy Db
Ñ		18	Db .
4713	AGCGCGAAGAGTGCAAGTGTCTCCTGAACTACAAACAAGAAGGAGATAAGTGCGTGG	4654	γo
4653 5187	CAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGAC	4594 5128	Qy Db
5127	acaataatatcaaaattaattgaaggaaaattccaagatatgttaaacatt	5068	рь
4593	GCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGCATGCTGAACATCTCC	4534	Qy
5067	CTTGGCAAATTACTTAGTACAGGATTAGTTCAAAATT	5011	Ф
4533	AACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAA	4474	Qy
5010	AAAATAGATCTTTTTAAAAAACCATAACGACTTCGAAGCAATTAAAAAATTGATAAATGAT	4951	ου
4473	AGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTACCC	4414	Qy
4950	TAAAATAACTAAACTTAGTGATTTAAAAAGCAATTGATG	4891	Db
4413	AGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAA	4354	Оу
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4353	CGACCTCTTCGTAATTCACCTGGAGGCCAAGGTCCTCAACTATAC	4294	Qy
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4770	GAGAAGTTCCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGACGAACAA	4711	Db
4233	CAA	4231	Qy
4710	GTTTTAGCGAAATATAAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAAAG	4651	Db
4230	CAAGTCTGACCTTGACTCTATTAAAAAGTATATCAACG	4174	Оу
4650	AAAGAATCAGTAGAAAATGATATTAAATTTGCACAGGAAGGTATAAGTTATTATGAAAAG	4591	Db
4173	ACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTA	4114	Qy
4590	TCATTTAAATTATTGAATTCAGAACAAAAAAACACACTTTTAAAAAAGTTACAAATATATA	4531	рь
4113	ATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACI	4054	Qy
4530	GAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATTA	4471	В
4053	TGGAGAGCGACTTGATTCCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAAG	3994	Qy
4470	AAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATT	4411	Дb
3993	GAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTCAAGAACG	3934	Qy
4410	TGGAGTATATAGAAGCTTAAAAAAACAATTGAAAAAAACATTTTTACAT	4351	Db
3933	GGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATGACCTTC	3874	Qy
4350		4291	DЪ

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                                                                          TTGACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGA
                                                                                                                                                      GTGACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTC
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ACAGCTGTTACAACTACTACACCTGGTTCAAAGGGTTCAGTTGCTTCAGGTGGTTCAGGT
                                                                                              ACGGCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1968)
Li,X.R., Liu,S.C., Chishti,A.H. and Oh,S.S.
Direct Submission
Submitted (04-FEB-2002) Section of Hematology/Oncology Research,
St. Elizabeth's Medical Center, Tuft's University School of
Medicine, 736 Cambridge Street, Boston, MA 02135, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum FCB-1 merozoite surface protein 1 (MSP-1) mRNA, partial cds.
AF480451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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TSTPGSKGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVAS
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/protein_id="AAL88455.l"
/db_xref="GI:19423279"
/francledia="GI:19423279"
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<1. .>1968
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/codon_start=1
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/db_xref="taxon:5833"
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Jongwutiwes,S.
Direct Submission
Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical
Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                              EGF-like domains; major merozoite surface protein Plasmodium falciparum (isolate 806) merozoite, DNJ Plasmodium falciparum
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Mol. Blochem. Parasitol. 59 (1), 95-100 (1993)

No. 15-2-1
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NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL
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GSDTLEQSQPKKPASTHVGAESNTITTSQNVDDEVDDVIIVPIFGESEEDYDDLGQVV
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/db_xref="taxon:5833"
/chromosome="9"
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EGF-like domains;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japan
Phone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4 Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747), Fax:0958-47-6607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate 808) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Direct Submission
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12-4 Sakamoto-machi
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Jongwutiwes, S., Tanabe, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute of Tropical Medicine
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EECKCLLNYKQDEGDKCVENPPGCNENNGGCDADAKCTEEDSGSNGKKITCECTKRDS
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/chromosome="9"
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JOURNAL MEDLINE REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM REFERENCE ACCESSION DEFINITION AUTHORS TITLE JOURNAL P. falciparum DNA for the precursor to the major merozoite proteins, C-terminal.
D13360
D13360.1 GI:391798
EGF-11ke domains; major merozoite surface protein precursor.
Plasmodium falciparum (isolate 828) merozoite, DNA.
Plasmodium falciparum (isolate 828) merozoite, DNA.
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Plasmodium falciparum (isolate 828) merozoite, DNA. Direct Submitsion
Direct Submitsion
Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical
Medicine, Nagasaki Univ., Dept. of Protozoology: 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
Fax:0958-47-6607)
Submitted (05-OCT-1992) to DDBJ by:
Somchai Jongwutiwes Jongwutiwes, S., Tanabe, K. and Kanbara, H. Sequence conservation in the C-terminal part of the the major merozoite surface proteins (MSP1) of Plasm falciparum from field isolates
Mol. Biochem. Parasitol. 59 (1), 95-100 (1993) Institute of Tropical Nagasaki University 12-4 Sakamoto-machi Department of Protozoology Jongwutiwes,S. (bases 1 to Plasmodium precursor INV 29-MAY-2002

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Mol. Blochem. Parasitol. 59 (1), 95-100 (1993)
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D13362
D13362.1 GI:391806
EGF-like domains; major merozoite surface protein
Plasmodium falciparum (isolate 837) merozoite, DNP
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93295445
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Submitted (05-OCT-1992) to DDBJ by:
Somchai Jongwutiwes
Department of Protozoology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
Eukaryota; Alveolara; Apicomplexa; Haemosporida; Plasmodium
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0958-47-6607.
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FVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHN
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/db_xref="taxon:5833"
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No. 7.5e-189;
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Plasmodium falciparum (isolate T9/94) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                             Somchai Jongwutiwes
Department of Protozoology
                                                                                                                                                                               Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4 Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                the major merozoite surface proteins (MSPI) of Plasmodium falciparum from field isolates
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Jongwutiwes, S., Tanabe, K. and Kanbara, H.
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                                                                                                                                                        Submitted (05-OCT-1992) to DDBJ by:
                                                                                                                                                                       Fax:0958-47-6607;
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                                         TAGAAAATAACGTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTA
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NLITKELSTGKVFENLAKTVLSNLLDGNLQGMLNISQHQCVKKQCPQNSGCFRHLDER
EECKCLLNYKOLGDKCVENPNFTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDS
YPLFDGIFCSSSNFLGISFLLILMLILYSFI"
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/tsrclhhllaelkeyiknknytgnspsynnyddynnalesykklegctddeptddlgvs
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tgeavtpsyidnilskieneyevlylkplagvyrslkkqlennymtenuvkdilnsr
fnkrenfknylesdlipykdlyssnyvykdpykflnkekrdkflssynyikdsldtd
nfandvlgyykilsekyksdldsikkyindkqgenekylpflnnietlyktyndkidl
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/protein_id="BAA02617.1"
/db_xref="GI:391825"
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/chromosome="9"
/dev_stage="merozoite"
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7.5e-189;
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P. falciparum DNA for proteins, C-terminal.
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Matches 1179; Conserv
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  AGAAAAATTATCATACTTATCAAGTGGATTACATCATTTAATTGCTGAATTAAAAGAAG
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D13361.1 GI:391800
D13361.1 GI:391800
EGF-like domains; major merozoite surface protein precursor.
Plasmodium falciparum (isolate 834) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jongwutiwes, S.

Direct Submission

Direct Submission

Submitted (05-0CT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4

Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jongwutiwes,S., Tanabe,K. and Kanbara,H. Sequence conservation in the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-OCT-1992) to DDBJ Somchai Jongwutiwes
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NFANDYLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIETLYKTVNDKIDL
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/translation="plktlsbesiqtednynonaleynkkippgtpdngvyses
gsptleosopkkpasthygabsnttysonubbevdbyltyptgeseebydblcovy
Tgeavtpsvidnilskieneyevlylkplagvyrslkkolennvmtfnvnvkbilnsr
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/protein_id="BAA02622.1"
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/db_xref="taxon:5833"
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Pred. No. 1.7e-188;
0; Mismatches 453;
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                                      CCACTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCA
                                                                                        TCGGAATTGCAGACCTGTCTACCGATTATAACCACAACAATCTCCTGACCAAGTTTTCTGT
                                                                                                                                         TGAACTACCTCAAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCG
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                         GTACAGGTATGGTTTTTGAAAATCTTGCTAAAAACCGTTTTATCTAATTTACTTGATGGAA
                                                                          TTGGAATTGCTGATTTATCAACAGATTATAACCATAATAACTTATTGACAAAGTTCCTTA
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EGF-like domains; major merozoite surface protein precursor.
Plasmodium falciparum (isolate 844) merozoite, DNA.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1636)
Jongwutiwes,S., Tanabe,K. and Kanbara,H.
Sequence conservation in the C-terminal part of the precursof the major merozoite surface proteins (MSP1) of Plasmodium falciparum from field isolates
Mol. Biochem. Parasitol. 59 (1), 95-100 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins,
D13363
                                                                                                                                                                                                                                                                                                                             Submitted (05-OCT-1992) Somchai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                      Nagasaki 852
                                                                                                                                                                                                                     Nagasaki University
12-4 Sakamoto-machi
                                                                                                                                                                                                                                                                  Department of Protozoology
                                                                                                                                                                                                                                                                                   Somchai Jongwutiwes
                                                                                                                                                                                                                                                                                                 Fax:0958-47-6607)
Submitted (05-0CT-1992) to
                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                          Jongwutiwes, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P. falciparum DNA for the precursor
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              /gene="MSP1"
<1. .1622
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/db_xref="taxon:5833"
/chromosome="9"
/gene="MSP1"
                                                                                                                                       Location/Qualifiers
                                                           /dev_stage="merozoite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal.
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               CCTCCTCTAACTACGTTGTCAAGGACCCATACAAGTTCCTCAATAAAGAGAAGAAGAGGATA
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FNKRENFKNVLESDLLPYKDLTSSNYVVKDPYKFLNKEKDKFLSSYNVIKDSIDTDI
NFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENKYLPFLNNIFTLYKTVNDKIDL
FVIHLEAKVLNYTYEKSNVEVRIKELNYLKTIQDKLADFKNNNFVGIADLSTDYNHN
NLLTKELSTGNVFFENLAKTVLSNLLDGNLQGMLNISOHQCVKKQCPENSGCFRHLDER
EECKCLLNYKQDEGDKCVENPHTCNENNGGCDADAKCTBEDSGSNGKKITCECTKPDS
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ACCESSION VERSION KEYWORDS SOURCE

proteins, C-terminal.
D13359
D13359.1 GI:391796
EGF-like domains; major m
Plasmodium falciparum (is
Plasmodium falciparum
Eukaryota; Alveolata; Api
1 (bases 1 to 1636)

or merozoite surface (isolate 822/2 and 8

e protein 827) mero

merozoite,

Apicomplexa;

Haemosporida;

Plasmodium

REFERENCE

ORGANISM

RESULT 25 PFAMSP8222 LOCUS

DEFINITION

PFAMSP8222 P. falciparum DNA for

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linear major m

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Submitted (05-0CT-1992) Somehai Jongwutiwes, Institute of Tropical Medicine, Nagasaki Univ., Dept. of Protozoology; 12-4
Sakamoto-machi, Nagasaki 852, Japan (Tel:0958-47-2111(ex.3747),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jongwutiwes, S., Tanabe, K. and Kanbara, H. Sequence conservation in the C-terminal the major merozoite surface proteins (MS
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Department of Protozoology
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Submitted (05-OCT-1992)
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FNKRENFKNVLESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNVIKDSIDTDI
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FVIHLEAKVLNYTYEKSNVEVKIKELNYLKTIQDKLADFKKNNNFVGIADLSTDYNHN
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/db_xref="taxon:5833"
/chromosome="9"
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Olafsson,P., Matile,H. and Certa,U. Plasmodium falciparum: the repetitive MSA-1 surface protein RO-71 isolate is recognized by mouse antibody against the nonrepetitive repeat block of RO-33 Exp. Parasitol. 74 (4), 381-389 (1992)
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/product="major surface
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                                                                                                                                                      Certa,U., Rotmann,D., Matile,H. and Reber-Liske,R. A naturally occurring gene encoding the major surf precursor p190 of Plasmodium falciparum lacks trip EMBO J. 6 (13), 4137-4142 (1987)
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p190 gene; variable surface antigen.
Plasmodium falciparum (individual_isolate
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                                         /organism="Plasmodium
/isolate="RO-33 Ghana"
/db_xref="taxon:5833"
/product="p190 protein"
/note="RO-33 mRNA"
                                                                                                          Location/Qualifiers
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190 kD
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11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="D2 in MAD-20 mRNA"
3247. 3270
/note="results in a single point frame to KI; frameshift mutation a 430 c 437 g 1081 t
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337. .>351
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2496
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LFQKEKMVLKGGANTQVVAKPADAVSTGSAKNPFGATVPSGTASTKGAIRSFGANPS
DDSSDSDAKSYADLKREVQNYLFTIKELKYPELFDLTNHMLTLCDNIHGFKYLLIDYE
EINELLYKLNFYFDLLRAKLNIVCANDYCQIFFNLKIRANELDYLKKLVFGYRKFLDF
IKDNVGKMEDYIKKNKTTIANINELLEGSKKTIDQNKNADNEEGKKKLYQAQYDLFIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="p190 protein"
/note="MAD20 mRNA"
266. .>3518
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203. .>3518
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/protein_id="AAA29715.1"
/db_xref="GI:160550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="This frameshift results in 11 new amino acids present in MAD-20 or K1; frameshift mutation FS-1"
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1 mRNA"
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Pred. No. 1.6e-145;
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                                   ACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAAATTGAGAAGTGACAAGAAAAGTT
                                                                                                                                                                                                                                       CAACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCA 1258
                                                                                                                                                                                                                                                                                                          GAGAGAATAAGAATATAGACATCTCCGCCAAAGTCGA------GACAAAGGAAT 1198
                                                                                                                                                                                                                                                                                                                                                                                          CCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGA 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                TCCCTGAGATTAGAAAAAGAGTCGAG--ACACGAAGAAAAATAAAAGAAATTGCCAAAA
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                 ATAACATTAAAAAACAAATTGATTTAGAAGAAAAAAACATTAATCACACAAAAGAACAAA 1738
                                                                                   ATAATTCATTAGCTGCAGATAATGATAAAAAATTCATATGGTGATTTAATGAATCCTCATA 1618
                                                                                                                                                                                     ACAA-----CGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCCTTCG
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AGAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTC
                                                                                                                             TATCAAACTCTAGTATGGACCAAAAATTATTAGAGGTATATAATCTTAC---TCCAGAAG
                                                                                                                                                                                                                                      ACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATCCTCG
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                                            AAAATGAATTAAAATCATGTGATCGATTAGATTTATTTAATATTCAAAATAACATAC
                                                                                                                                                                                                                  ATCTAAAGAAATTAGATGAATTTTTAACTAAATCATATATGTCATAAATATATTTTAG
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TITLE
Query Match 14.
Best Local Similarity 56.
Matches 1511; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p190 gene; surface antigen
Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-NOV-1987) Ulrich 2FE, Grenzacher Str. 124, 4002 (bases 1 to 3518)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A naturally occuring gene encoding the m precursor P190 of plasmodium falciparum EMBO J. 6 (1987) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Certa, U., Rotmann, D., Matile, H. and Reber-Liske, R
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                                                                                                                                                                                                                                       /protein_id="CAA68280.1"
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//db_xref="GI:9925"
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DESSDSAKSYADLKHRVQNYLFTIKELKELYVLRENLELDVLKKLVFGYRRFLDF
IKDNYGKMEDYIKKLNFTIANINELLEGSKKTIDONNEADNEEGKKKLYGAQYDLFIY
NKQLQEAHNLISVLEKRIDTLKKLNEDIKLLEDYENEKILDAEKPTTGVNOILSLRLEK
ESRHEBEIKELAKTIKFNIDALFTDPLLELEYVLREKNIKXVDYTPKSQOPTKSVQIPKV
PYPNGIVPPLYTATIKHNIDALFTDPLKELYVLREKNIKXVDYTPKSQOPTKSVQIPKV
PYPNGIVPPLYTATIKHNIDALFTDPLLEKSKNDYELKKIITDNKERKIFINNI
KKQIOLEKNINHTKEONKKLLEDYEKSKKDYELLEKKYEMKRNINHFNUDVDKIFS
ARYTYNYEKGORTLAKRESSANSVYNOGKLKKALSYLEDYSLRGGISEKDPHNYTTLKT
GLEADIKKLTEEIKSSENKILEKNFKGLTHSANASLEVSDIVKLQVQKVLLIKKIEDL
RKIELFLKNAOLKDSHHVPNIYKPONKPEPYYLIVLKKEVDKLKEFIFXVKDMLKKEQ
AVLSSITOPLVAASETTEDGGHSTHTLSGGSTETTESTEETTGTTTTTTTTLEPKEV
KVVENSIEHKSSDNSQALTKTYVLKKLDEFLTKSYICHKYILVENSMOQKLLEVYNL
TPEENBELKSCORLDLLFNONNIPANYSLYDASSANDLQHLFFELLYKKERIYYLHKKE
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/strain="Ro-33"
/db_xref="taxon:5833"
/clone="RO-33/1"
                                                                                                                        MIPIFNDDIKQFVKSNSKVITGLTETQKNALNDEIKKLKDTLQLSFDLYNKYKLKLDR
LFNKKKELGQDKMQIKKLTLLKEQLESKLNS"
430 c 437 g 1081 t
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SGPAVVEËSHDPLTVLSISNDLKGIVSLLNLGNKTKVPNPLTISTTEMEKFYENILKI
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in codon)"
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Score 711.8; DB 3;
Pred. No. 1.6e-145;
0; Mismatches 1072;
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1147 1438	1088 CCATTAAGTTCAACATAGATTCTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGA 	B 8
1087 1378	1028 TGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGAGATCGCCAAAA	Db Qy
1027 1320	970 AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCTAACACGC	Оγ
969 1260	910 GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATATGAAAATATCAAAGAACTGCTCGAC 	Дb
909 1200	850 GCCCAGTACGACCTGTCCATCATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGC	DP QA
849 1140	790 AAGACCATAGACAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG 	Db Qy
789 1080	730 TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA 	D Qy
729 1020	670 GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT 	Дb
960	610 TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG	Db Qy
900	550 TTGAATTTCTACTTCGACTTGCGTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT	D Q
549 840	490 ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG 	DЬ
489 780	430 GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC	D Q
429 720	370 GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG	B 04
369	310 GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC	DB Q9
309	250 TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG	Оβ
249 576	190 GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG	Db Qy
189 516	130 ACCGGATACAGCCTGTTCCAGAAGGAGAAGATGGTGCTGAATGAA	D Oy
129 456	70 ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT	D Q
396	337 ATGAAGATCATATTCTTTTTATGTTCATTTCTTTTTTTTT	В

N	GTCACTCCACACACATTATCCCAATCAGGAGAAACAGAAGTAACAGAAGAAACAGAAAG	44	Db -
SCTCAAG 2209	CCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAG	2150	Οy
ATGGGG 2443	GTATTACACAACCTTTAGTTGCAGCAAGCGAAACAACTGAAG	2396	Db
CAGGCTA 2149	CTGAAGGACAGTCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTA	2090	Qy
TATCAA 2395	TAAAAGAATTTATACCAAAAGTAAAAGACATGTTAAAGAAAG	2336	Db
аттаааа 2089	TGAAAGTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACA	2030	Qy
SATAAAT 2335	AACCACAAATAAACCAGAACCATATTATTTAATTGTATTAAAAAAAA	2276	Db
GACAAAC 2029		1970	Оу
ATTTATA 2275	TAGAATTATTTTTAAAAAATGCACAACTAAAAGATAGTATTCATGTACCAAATATTTATA	2216	Db
AGTTATA 1969		1910	Qy
AGAAAGA 2215	TTGTAAAATTACAAGTACAAAAAGTTTTATTAATTAAAAAAATAGAAGACTTAAGAAAGA	2156	Db
AAGAAGA 1909		1850	Qy
CTGATA 2155		2099	Db
CCGATA 1849	AGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCT	1790	Qy
ATTCTAG 2098	TCGAAGCTGATATAAAAAATTAACAGAAGAAATAAAGAGTAGTGAAAACAAAATTC	2039	Db
TTGTTTG 1789	CGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATG	1730	Qy
ACTGGCC 2038	CTTTAAGAAAAGGAATTTCTGAAAAAGATTTTAATCATTATTATACTTTGAAAAACTGGCC	1979	DЪ
AGTAAGA 1729		1670	Оу
SATTATT 1978	ATAATTCTGTATATAATGTTCAAAAATTAAAAAAGGCTCTTTCATATCTTGAAGATTATT	1919	Дb
SACTATT 1669		1610	Qy
CCTCTA 1918	GTGCAAGATATACATATAATGTTGAAAAACAAAGATATAATAATAATATTTCATCCTCTA	1859	DЪ
rccrare 1609	GAAAACGGTACTCTTACAAAGTGGAGAAACTGACACACAC	1550	Qy
ATATTCA 1858	AATTTTATGAAATGAAATTTAATAATAATTTTAACAAAGATGTCGTAGATAAAATATTCA	1799	Db
ATGATGG 1549	AGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAA	1490	Qy
CTTGAAA 1798	ATAAAAAATTACTTGAAGATTATGAAAAGTCAAAAAAGGATTATGAAGAATTACTTGAAA	1739	DЪ
CTGAACG 1489	ACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGC	1430	Qy
II GAACAAA 1738	ATAACATTAAAAAACAAATTGATTTAGAAGAAAAAACATTAATCACACAAAAGAACAAA	1679	Db
AAAAGTT 1429		1370	Qy
TTCATTA 1678	CTAAAGAAAAATTAATGAAAAAATTATTACAGATAATAAGGAAAGAAA	1619	Db
TTATCA 1369		1310	Qy
CCTCATA 1618	ATAATTCATTAGCTGCAGATAATGATAAAAATTCATATGGTGATTTAATGAATCCTCATA	1559	Db
CCTTCG 1309	ACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACC	1259	Qy
GATATTC 1558	AAATACCAAAAGTTCCTTATCCAAATGGTATTGTATATCCTTTTACCACTCACT	1499	Db
SATATCA 1258		1199	Qy
 CTGTTC 1498	GAGAAAAAATAAAAAAGTTGATGTAACACCTAAATCACAAGATCCTACGAAATCTGTTC	1439	Db
AAGGAAT 1198		1148	ОУ

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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                          IKKYINDKOGENEKYLPFLNNIETLYKTVNDKIDLFYIHLEAKYLNYYYEKSNYEVKI
KELNYLKTIQDKLADFKKNNNFYGIADLSTDYNHNNLLTKFLSTGMYFENLAKTVLSN
LLDGNLOGMLNISQHOCVKKOCPONSGCFRHLDEREECKCLLMYKQEGDKCVEMPNPT
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/db_xref="taxon:5833"
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Query Match
Best Local Similarity
TCCACTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGC
                                                                                                                                               CTGAACTACCTCAAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTC
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859. .1200
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/note="19 kDa fragment"
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AF325919
AF325919.1 GI:1275139
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/protein_id="AAK07641.1"
/protein_id="AAK07641.1"
/db_xref=="Gi:12751399"
/translation="AVTPSVIDNILSKIENEYEVLYLKPLAGVYRSLKKQLENNVMTF
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NYIKDSIDTDINFANDVLGYYKILSEKYKSDLDSIKKYINDKQGENEKYLPFLNNIET
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/isolate="FCB-1"
                                                                                                /gene="MSP-1"
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 GATGCTAAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAAAAATCACATGCGAGTGT
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                                                                        GGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTAT
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                                                                                                                                                                                                                                                                                                                   GTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAA
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               ATCAACGATAAGCAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACC
                                                                                                                                  AGTTACAACTATATCAAGGACTCCATCGACACCCGATATCAATTTCGCTAATGATGTGCTG
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                                                          GGATATTATAAAATATTATCCGAAAAATATAAATCAGATTTAGATTCAATTAAAAAATAT
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                                                                                                                                                                             TATGTTGTCAAAGATCCATATAAATTTCTTAATAAAGAAAAAAGAGATAAATTCTTAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            merozoite surface protein.

Plasmodium falciparum (strain Vietnam Oak Knoll)

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida;

1 (bases 1 to 1065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primary amino acid sequence of the merozoite surface protein(MSP-1) Oak knoll (FVO) strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Conservative
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/db_xref="taxon:5833"
/dev <tacc-""
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Pred. No. 3.5e-126;
0; Mismatches 274;
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RESULT 32
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                                                                                                                                                                                        Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 999)
Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T.
Sequence variation in the tripeptide repeats and
P190 (MSA-1) of Plasmodium falciparum from field
Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
                                                                                                                                                                                                                                                                                                                                   999 bp
Plasmodium falciparum clone 808
(p190) gene, partial cds.
                                                                                                                                                                                                                                                                                                                               (p190) gene,
M77715
                                                                                                                                  2 (bases 1 to 999)
Jongwutiwes, S.
                                                                                                                                                                                                                                                                                      T-cell epitope; major merozoite Plasmodium falciparum.
                                                                              University, Rama4, Pathumwan, On May 21, 2002 this sequence
                                                                                                        Submitted (21-MAY-2002)
                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                   M77715.2 GI:2104|0168
                                                                                                                                                                1373473
           /organism="Plasmodium
/db_xref="taxon:5833"
/map="9"
/clone="808"
                                                                   Location/Qualifiers
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                                                                              Faculty of Medicine, Chulalongkorn
umwan, Bangkok 10330, Thailand
quence version replaced gi:309698.
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              GAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAAATAAGAATGCAACCAAGGAGGAA
                                                                                                                                       TTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC
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GAAAAAAAAAATTATACCAAGCTCAATATGATCTTTCTATTTACAATAAACAATTAGAA
                                                          GAATTAATTGAAGAAAGTAAGAAAACAATTGATAAAAATAAGAATGCAACTAAAGAAGAA
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LITKELKY POLFDTHMLTLCDN.HGFKYLLDGYEEINELLYKLAKFYDLLRAKLN
DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTIEN
DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKQLEBAHNLISVAKTIFNIT
INELIESSKKTIDKNKNATKEBEKKKLVGAQVULSIVKGLEBAHNLISVATAVTHENDIN
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<1. .>999
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Direct Submission
Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced gi:309705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 999)

Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanbara, H. Sequence variation in the tripeptide repeats and T cell epitopes Sequence variation in the tripeptide repeats and T cell epitopes Pl90 (MSA-1) of Plasmodium falciparum from field isolates Pl90 (MSA-1) of Plasmodium falciparum from field isolates
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KKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNID"
3 127 c 159 g 295 t
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                                                                                                                                                                      GAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAA
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Direct Submission
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Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanl Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanl Sequence variation in the tripeptide repeats and T cell ep 190 (MSA-1) of plasmodium falciparum from field isolates paragraphy. Biochem. Parasitol. 51 (1), 81-89 (1992)
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T-cell epitope; major
Plasmodium falciparum.
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/db_xref="taxon:5833"
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                                                  University, Rama4, Pathumwan, Sequence update by submitter On May 21, 2002 this sequence
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Plasmodium falciparum clone
                                                                    Submitted (21-MAY-2002) Faculty of Medicine, University, Rama4, Pathumwan, Bangkok 10330,
                                                                                           Jongwutiwes, S.
Direct Submission
                                                                                                                                              Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. Sequence variation in the tripeptide repeats and (Sequence variation lassmodium falciparum from field p190 (MSA-1) of Plasmodium falciparum from field Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
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                                                AATGTAGGAAAATGGAAGATTACATTAAAAAAAATAAAAAAACCATAGAAAATATAAAT
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                                                                                                                                                                                                                                            ATTAATGAATTATTATATAAATTAAACTTTTATTTGATTTATTAAGAGCAAAATTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="asexual"
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Pred. No. 4.3e-114;
0; Mismatches 269;
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PFAMSAIAF

PFAMSAIAF

ON

Plasmodium falciparum clone 822B major merozoite surface antigen

(pl90) gene, partial cds.

N M7718

M7718 2 GI:21040174

M7718.2 GI:21040174

M7718.3 F-cell epitope; major merozoite surface antigen; tripeptide repeat.

Plasmodium falciparum.

Plasmodium falciparum.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

E (bases 1 to 999)

I (bases 1 to 999)

S Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanbara, H.

Sequence variation in the tripeptide repeats and T cell epitopes in

P190 (MSA-1) of Plasmodium falciparum from field isolates

M01. Blochem. Parasitol. 51 (1), 81-89 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGAACACCCCTAACACGCTGCTGGACAAGAAGAACAAGAAGATAGAGGAGCACGAGAAAAGAG
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                730;
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92228018
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Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced g1:309703.
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                                Similarity
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                                                                                         418
                  Conservative
                                                                                    /codon_start=1
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<1. .>999
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                             11.5%;
73.1%;
               Score 568.6;
Pred. No. 4.3e
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No. 4.3e-114;
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GCCGTTACAACCAGCACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
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                                           GCTGTTACAACTAGTACACCTGGTTCAAAGGGTTCAGGTGGCTCAGTTGCTTCAGGTGGT
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Direct Submission
Submitted (22-APR-1998) Molecular Immunology,
Submitted (27-APR-1998) Molecular Immunology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
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/note="p190; surface
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66. .1133
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66. .>1133
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GGSGNSRTNPSDNSSDSDAKSYADLKHRVQNYLFTIKELKYPELFDLTNHMLTLCDN
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KLYQAQYNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLDKINEIKNPPPANSG
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66. .>1133
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/chromosome="9"
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                              CTGGACAAGAACAAGAAGATAGAGGAGGAGCACGAGAAAGAGATCAAAGA 1076
                                                                AAGATAAATGAAATTAAAAATCCCCCCACCGGCCAATTCTGGAAATACACCAAATACTCTC
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RESULT 38 AF286876 LOCUS REFERENCE AUTHORS REFERENCE AUTHORS TITLE SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION JOURNAL 38 kDa subfr falciparum Unpublished 2 (bases 1 to 1080)
Goel, V.K., Liu, S.-C., (msp-1) mRNA, AF286876 AF286876 Plasmodium Eukaryota; Plasmodium Plasmodium AF286876.1 lukaryota; Alveolata; A (bases 1 to 1080) loel, V.K., Liu, S.-C., C falciparum clone NA, partial cds. falciparum falciparum GI:9438194 MSP-1 Chisthi, A.H. Apicomplexa; Chisthi, A.H. 1080 FCB-1 gene of. and Oh,S...
of FCB-1 st merozoite and Haemosporida; mRNA Oh, S strain linear surface of Plasmodium Plasmodium. protein INV 25-JUL-2000

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CTGAAGACTCTCTCCGAGGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAAC
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747; Conser
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FFNKKKEAFLAETENFLENTKILKHKFKGLKKYYNGESSPLKTLSESSTQTEDNYKSL
ENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIAELKEVIKNKNYTGNSPSENNTD
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<1. .>1080
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/db_xref="taxon:5833"
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/note="38 kDa
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Pred. No. 1.6e-109;
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                                                                                                                          Exp. Para 95354793
                                                                                                                                           merozoite surface antigen-1 Exp. Parasitol. 81 (1), 47-
                                                                                                                                                                                                                          Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. I
fur Molekulare Biologie, (ZMBH), Univ. Heidelberg,
Feld 282, Heidelberg, 69120, Germany
4 (bases 1 to 1956)
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                                 GCAGTCTCAACCTAAGAA------GCCTGCATCTACTCATGTCGGAGCCGAGTCCAAT 3684
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GGATCCACAAAAGAAGAAACACAAATACCAACTTCAGGCTCTTTATTAACAGAATTACAA 660
                                                                   ACTCCACCTCAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCA 600
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CLLNYKQBGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLF
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/dev_stage="blood stage"
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Db	661	CAAGTAGTACAATTACAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCATT 720
Qy	3745	TTCGGCGAGAGCGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCCGGTGAGGCTGTC 3804
Д	721	TTTGGAGAATCCGAAGATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATA 780
Qy	3805	ACTCCTTCCGTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTAT 3864
Db	781	TCTGTCACAATGGATAATATCCTCTCAGGATTTGAAAATGAATATGATGTTATATAT 837
Qy	3865	CTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATG 3924
Db	838	TTAAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAAAA
Оу	3925	ACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAAATTTC 3984
Db	898	ACATTTAATTTAAATTTGAACGATATCTTAAATTCACGTCTTAAGAAACGAAAATATTTC 957
Qy	3985	AAGAACGTCTTGGAGAGCGACTTGATTTGCCTATAAAAGACCTCGCTCCTCTAACTACGTT 4044
Дb	958	TTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATT 1017
Qy	4045	GTCAAGGACCCATACAAGTTCCTCAATAAAGAGAGAGAGGGATAAATTTCTGTCTAGTTAC 4104
Db	1018	ATTGAAGATTCATATTAAATTATTGAATTCAGAACAAAAAAAA
Qy	4105	AACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGTGTGCTGGGGTAT 4164
Db	1078	AAATATATAAAAGAATCAGTAGAAAATGATATTAAATTTGCACAGGAAGGTATAAGTTAT 1137
Qy	4165	TACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAAC 4224
Db	1138	TATGAAAAGGTTTTAGCGAAATATAAGGATTAAGAATCAATTAAAAAAGTTATCAAA 1197
Qy	4225	GATAAG 4230
Db	1198	GAAGAAAAGGAGTTCCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAAACAGAC 1257
Qy	4231	CAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCCTGTACAAG 4287
Db	1258	GAACAAAAGAAGGAAAGTAAGTTCCTTCCATTTTAACAAACA
Qy	4288	ACAGTGAACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCCAAGGTCCTCAACTAT 4347
Db	1318	AACTTAGTTAATAAAATTGACGATTACTTAATTAACTTAAAGGCAAAGATTAACGATTGT 1377
Qy	4348	ACTTACGAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAATC 4407
Db	1378	AATGTTGAAAAGATGAAGCACATGTTAAAATAACTAAACTTAGTGATTTAAAAGCAATT 1437
Qy	4408	CAAGACAAGCTGGCAGATTTCAAGAAAATAACAATTTCGTCGGAATTGCAGACCTGTCT 4467
Db	1438	GATGACAAAATAGATCTTTTTAAAAAACCATAACGACTTCGAAGCAATTAAAAAATTGATA 1497
Qy	4468	ACCGATTATAACCACAACCAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAA 4527
ф	1498	ARTGATGATACGAAAAAAGATATGCTTGGCAAATTACTTAGTACAGGATTAGTTCAA 1554
Qy	4528	AACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAAC 4587
Db	1555	AATTTTCCTAATACAATAATCAAAATTAATTGAAGGAAAATTCCAAGATATGTTAAAC 1614
Qy	4588	ATCTCCCAGCACCAATGCGTGAAGAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCAT 4647
? 8		
Db Qy	1675	CTIGGACGAGCIGCAGAGAGGIGTCTICCTGAACTAACAAGGAGGAGATAAGTIGC 4/0/

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 GCTTTAGAAGATGCAGTATTGACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTA
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Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced gi:309707.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
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Plasmodium falciparum clone 828
(p190) gene, partial cds.
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T-cell epitope; major merozoite
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Jongwutiwes, S.
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Jongwutiwes, S., Tan
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                                                           Similarity
                                                                                                             421
                                                 Conservative
                                                                                                                                            /product="major merozoite surface antigen"
/protein_id="AAA29667.2"
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DVCANDYCOIFFNLKIRANELDVLKKLVFGYRRPLDNIKDNVCKMEDVIKKKKTIEN
                                                                                                            INELIEESKKTIDKNKNATKEEEKKKLYQAQYDLFIYNKQLEEAHNLISVLEKRIDTL
KKNENIKELLDKINEIKNPPPANSGNTPNTLLDKNKKIEEHEKEIKEIAKTIKFNID"
1 125 c 150 g 303 t
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                                                                                                                                                                                                                                                                                                   /dev_stage="erythrocytic"
                                                                                                                                                                                                                                                                                                              /sex="asexual"
                                                                                                                                                                                                                                                                                                                           /clone="828"
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/db_xref="taxon:5833"
                                                           11.18;
71.78;
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GAAGCCCATAACCTCATCAĠCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAA
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ATAAAAGAAATTGCCAAAACTATTAAATTTAATATTGAT
                 ATCAAAGAGATCGCCAAAA¢CATTAAGTTCAACATAGAT 1107
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                                                                                                                            GGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAG
                                                                                                                                                                      AACATTAAGGAATTACTTGATAAGATAAATGAAATTAAAAATCCCCCACCGGCCAATTCT
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                                                                                                        TCTTCTCCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCCAGC 3363
                                                                                                                                                   GAAAACACAAAAATATTATTGAAACATTATAAAGGACTTGTTAAATATTATAATGGTGAA
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                                                                TCATCTCCATTAAAAACTTTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAAT 300
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Direct Submission
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Submitted (18-JUL-1994) Ralf Tolle, Abt. Prof. H. Bujard, Zentrum fur Molekulare Biologie, (ZMBH), Univ. Heidelberg, Im Neuenheimer Feld 282, Heidelberg, 69120, Germany
Location/Qualifiers
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1956)
1 Tolle,R., Bujard,H. and Cooper,J.A.
Plasmodium falciparum: variations within the C-terminal region
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Exp. Parasitol. 81 (1), 47-54 (1995)
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LOOVVOLONYDEEDDSLVVLPIEGESEDNDEYLDQVVTGEAISYMDNILSGFENEYD
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SNEYIIEDSFKLLNSEQKUTLLKSYKYIKESVENDIKFAQEGISYYEKYLAKYKDDLE
SIKKVIKEEKEFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNNLVNKIDDYLI
NLKAKINDCNYEKDEAHYKITKLSDLKAIDDKIDLFKNPYDFEAIKKLINDDTKKDML
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CLLNYKQEGDKCVENPNPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="FNKKKELGODKMQIKKLTLLKEQLESKLNSLNNPHNVLQNFSVF
FNKKKEAEIAETENTLENTKILLKHYKGLVKYYNGESSPLKTLSEVSIQTEDNYANLE
KFRVLSKIDGKLNDNLHLGKKKLSFLSSGLHHLITELKEVIKNKNYTGNSPSENNKKV
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/chromosome="9"
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/isolate="RO-33"
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57.7%;
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	pb Qy	3424 GAGAAGAAGCTCAGCTACCTCTTAGCGGACTGCATCACCTGATCGCCGAGCTCAAG 3483
	Qy	GAAGTCATTAAGAACAAGAACTACACCGGCAATAGCCCAAGCGAGAATAATACAGACGTG
	ф	
	Py 09	3544 AATAACGCACTGGAATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC 3596
	Qy	GACTGTGGTGTGTGTGATCTGACTCCGACACACACTGGA
·	Ф	541 ACTCCACCTCAACCAGATGTAACTCCATCTCCATTATCTGTAAGGGTAAGTGGTAGTTCA 600
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	Db	601 GGATCCACAAAAGAAGAAACACAAATACCAACTTCAGGCTCTTTATTAACAGAATTACAA 660
	Qy	3685 ACAATTACCACATCTCAGAACGTCGACGATGAGGTCGATGACGTCATCATTGTGCCTATC 3744
	ДЬ	661 CAAGTAGTACAATTACAAAATTATGACGAAGAAGATGATTCCTTAGTTGTATTACCCATT 720
	Qy	3745 TTCGGCGAGAGGAGGAGGACTACGATGACCTCGGCCAGGTGGTCACCGGTGAGGCTGTC 3804
	Db	721 TTTGGAGAATCCGAAGATAATGACGAATATTTAGATCAAGTAGTAACTGGAGAAGCAATA 780
	Qy	3805 ACTCCTTCCGTGATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTAT 3864
	DЬ	781 TCTGTCACAATGGATAATATCCTCTCAGGATTTGAAAATGAATATGATGTTATATAT 837
	Qy	CTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAACGTGATG
	מט	TTAAAACCTTTAGCTGGAGTATATAGAAGCTTAAAAAAACAAATTGAAAAAAAA
	r Q	3925 ACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCGGCTTTAATAAGAGAGAAAAATTTC 3984
	Q _y	AAGAACGTCTTGGAGAGCGACTTGATTCCCCTATAAAGACCTGACCTCCTCTAACTACGTT
	Db	958 TTAGATGTATTAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATT 1017
	Qy	4045 GTCAAGGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTAC 4104
	рь	1018 ATTGAAGATTCATTTAAATTATTGAATTCAGAACAAAAAAAA
	Qy	AACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGTGTG
	Qy (4165 TACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAAC 4224
	Db	
	Qy	4225 GATAAG 4230
	Db	1198 GAAGAAAAGGAGTTCCCCATCATCACCACCAACAACACCTCCGTCACCAGCAAAAACAGAC 1257
	g 99	4231CAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAG 4287
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	В	1378 AATGTTGAAAAAGATGAAGCACATGTTAAAATAACTAAACTTAGTGATTTAAAAAGCAATT 1437

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REFERENCE
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Submitted (22-APR-1998) Molecular
Submitted (27-APR-1998) Molecular
                                                                                                                                                                                                                                                         Plasmodium falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1141)
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                                                                                                                                                Jiang, G., Daubenberger, C.A., Matile, H. and Pluschke, G
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71. .>1141
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                                             GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT
                                                                                         TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT
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71. .>1141
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0; Mismatches 321;
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/gene="mspl"
/product="merozoite s
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/72...1142
                                                                             /gene="msp1"
/note="p190; surface
activity"
         /translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LFQKEKMVLNEGTSGTAVTTSTPGSVASGGSVASGGSGGSVASGGSVASGGSVAS
GGSGNSRRTSPSDNSSDSDAKSYADLKHRVRNYLFTIKELKYPELFDLINHMLTLCDN
                                      /codon_start=1
/product="merozoite surface
/protein_id="AAC69739.1"
/db_xref="GI:3821973"
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72. .>1142
IHGFKYLIDGYEEINELLYKLNFYFDLLRAKLNDVCANDYCQIPFNLKIRANELDVLK
                                                                                                                                                                             /db_xref="taxon:5833"
/chromosome="9"
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/isolate="IFA12"
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GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG GTTTTAGAAAAACGTATTGACACTTTAAAAAAAAATGAAAACATAAAGAAATTACTAGAA GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC GCTCAATATGATCTTTCTATTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCCATAACCTCATCAGC AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA GTGTTCGGATATAGAAAACCATTAGACAATATTAAAGATAATGTAGGAAAAATGGAAGAT GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT TGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAATTAGACGTACTTAAAAAACTT TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTTGCGCCAATGACTAT ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG GAACTCAAATATCCCGAACTCTTTGATTTAACCAATCATATGTTAACTTTGTGTGATAAT GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC GCAAGCGGGGGTTCCGGGAACAGTCGAAGCAACCAATCTGACAACTCTAGCGATTCC TCAGGTGGCTCAGTTGCTTCAGGTGGTTCAGGTGGCTTCAGGTGGCTCAGTT TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTG GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG ACACATGAAAGTTATCAAGAACTTGTCAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT ATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTATCATCAATACTCAGTGCGTG TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG GCTGTTACAACTAGTACACCTGGTTCAGTTGCTTCAGGTGGTTCAGTTGCTTCAGGTGGT ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA Conservative 0, Score 538.8; DB 3; Pred. No. 1.5e-107; 0; Mismatches 322; Indels ω Gaps 1031 971 909 911 849 851 789 729 609 549 489 491 429 431 369 371 309 311 189 191 69 791 731 669 671 611 551 249 251 ۲

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Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 893)
Peterson, M.G., Coppel, R.L., McIntyre, P., Langford, C.J., Wood
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                                                          b
                                                                                                                                                                                                                                                    /product="merozoite surface antigen 1 gene, 3+-end"
/protein_id="CAA84557.1"
/protein_id="CAA84557.1"
/db_xref="c1:535252"
/db_xref="SPTREMBL:Q25923"
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                                                          EDGIFCSSSNFLGISFLLILMLILYSFI<sup>n</sup>
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                                                                                                                                   SIKKVIKEEKEKFPSSPPTTPPSPAKTDEQKKESKFLPFLTNIETLYNNLVNKIDDYL
INLKAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPYDFEAIKKLINDDTKKDM
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SNEYIIEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAKYKDDLE
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LQQVVQSQNYDEEDDSLVVLPIFGESEDNDEYLDQVVTGEAISVTMDNILSGFENEYD
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/isolate="FCH5/NF7"
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                                                                                                 KCLLNYKQEGDKCVENPNPTCNENNGGCDADATCTEKDSGSSRKKITCECTKPDSYPL
                                                                                                                   LGKLLSTGLVQNFPNTIISKLIEGKFQDMLNISQHQCVKKQCPENSGCFRHLDEREEC
                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                              /gene="gp190, MSA1, MSP1, PMMSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="9"
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Institute, Socinstrasse 57, Basel
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Sequence diversity of the merozoite
Falciparum in clinical isolates from
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Jiang,G., Daubenberger,C.A.,
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/db_xref=="G1:3821985"
/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
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           Ranford-Cartwright/L.C., Balfe,P., Carter,R. Direct sequencing of enzymatically amplified merozoite surface antigen MSA-1 gene from the Plasmodium falciparum
                                                                                         Submitted (10-MAY-1990) Ranford-Cartwright Animal and Population Genetics, University Road, Edinburgh, EH9 3JN, Scotland
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Plasmodium falciparum merozoite surface antigen (MSA-1) gene
fragment (clone HB3A).
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Location/Qualifiers
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Direct Submission |
Submitted (16-MAR-1994) Ranford-Cartwright L.C., Institute of Cell,
Animal and Population Genetics, University of Edinburgh, West Mains
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Ranford-Cartwright, L.C.
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/db_xref="G1:467604"
/db_xref="G1:467604"
/db_xref="S1:467604"
/db_xref="STPTEMBL:Q25865"
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/db_xref="taxon:5833"
/chromosome="9"
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Direct Submission
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/product="merozoite surface protein 1"
/product="merozoite surface protein 1"
/protein_id="AAC69735.1"
/db_xref="GI:3821965"
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VLKKLYPGYYKPLDNIKDNYGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEE
GKKKLYQAGYOLESIYNKOLEEAHNLISYLEKRIDTLKKENIKKLLEDIDKIKTDAEKP
TTESKPNTLLDKNKKIEEHEEKIKEI"
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/product="merozoite
71. >1150
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/chromosome="9"
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/isolate="IFA9.2"
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Pred. No. 5.5e-105;
0; Mismatches 328;
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                                                                                                                                                                 Acta
                                                                                                                                                                                                                                                                                 Plasmodium falciparum isolate (msp1) gene, partial cds. AF061139
                                                                                                     Submitted (22-APR-1998)
                                                                                                                 Jiang,G., Daubenberger,C.A., Matile,H. and Pluschke,G
Direct Submission
                                                                                                                                                                                   Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
                                                                                                                                                                                                       Pluschke, G
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Plasmodium falciparum
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                 /db_xref="taxon:5833"
/chromosome="9"
/note="wild isolate"
/0. .>1158
/gene="msp1"
70. .>1158
                                                         /organism-"Plasmodium
/isolate="IFAll"
                                                                                    Location/Qualifiers
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TTAACTTTGTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAAATT
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LFQKEKNYLNEGTSGTAVTTSTFGSKGSGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGAN
LTLCDNIHGFKYLIDGYEEINELLYKLNFYYDLLRAKLNDACANSYCQIPFNLKIRAN
ELDVLKKIVFGYRKFLDNIKDAVGKMEDYIKKNKTTLANINELLEGSKKTIDQNKNAD
NEEGKKKLYQAQYDLFYYNGOLGEHAILISVLEKRIDTLKKNENIKKLLEDIDKIKTD
AEKPTTESKPNTLDKNKKIEEHEEKIKE"
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/product="merozoite surface
/protein_id="AAC69738.1"
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/note="p190;
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Sequence diversity of the merozoite surface protein 1 of Plasmodium falciparum in clinical isolates from the Kilombero District,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 1102)
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Plasmodium falciparum isolate
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Jiang,G., Daubenberger,C.A., Matile,H. and Pluschke,
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                                                                                                                                             /organism="Plasmodium f
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71. .>1100
                                                                                                                          /note="wild isolate"
71. .>1102
                                         activity"
                                                                                           /gene="msp1"
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/translation="MKIIFFLCSFLFFIINTQCVTHESYQELVKKLEALEDAVLTGYS
LFQKEKMVLNBGTSGTAVTTSTPGSGGSVTSGGSGGSVASVASVASGGSGNSRATNPS
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EINELLYKLNBYYDLLFAKLNDACANSYCQIPPNLKIFANELDVLKKLYPGYERFPLDN
IKDNVGKMEDYIKKNKTTIANINELIEGSEKTIDQNKNADNEEGKKKLYQAQYNLFIY
NKQLQEANLTISVLEKRIDALKKNENIKKLLGKINEIKNPPPANSGNTPNTLLDKNKK
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TGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTG TTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGACTAT ATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAATGAACTCCTGTACAAG GAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTGTGTGATAAC GATGCTAAATCTTACGCTGATTTAAAACATAGAGTTCAAAATTACTTGTTCACTATTAAA GCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCTAGCGATTCC GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT ATGAAGATCATATTCTTTTATGTTCATTTCTTTTTTTTTATTATAAATACACAATGTGTA ATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTTATCATCAATACTCAGTGCGTG GCTCAATATAATCTTTTTATTTACAATAAACAATTACAAGAAGCACATAATTTAATAAGC GCCCAGTACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCCATAACCTCATCAGC AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG TATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAA GTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAT GAACTCAAATATCCCGAACTCTTTGATTTAACCAATCATATGTTAACTTTGTGTGATAAT GACGCCAAGTCCTACGCCGACCTCAAGCACCGAGTGAGAAACTATCTCCTCACTATCAAG GCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCAAGTGATTCA TCTGTGGCCTCTGGGGGTTCCGTCGCCTCCGGCGCAGCGTGGCATCAGGTGGCTCAGTG GCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGTTACTTCAGGTGGTTCAGGTGGT ACACATGAAAGTTATCAAGAACTTGTCAAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG TGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAATTAGACGTACTTAAAAAAATT TTAAACTTTATTATGATTTATTAAGAGCCAAATTAAATGATGCATGTGCCAATAGTTAT 11 Similarity 733; Conser 455 Conservative മ 10.3%; 68.7%; C 0; Score 508.2; 1 Pred. No. 8.2e 0; Mismatches 158 ρ -----AGTTGCTTCAGTTGCTTCAGTT 2; DB 3; 3.2e-101; nes 298; Indels Length 36; Gaps 609 454 429 310 934 909 874 849 814 789 729 694 669 634 574 549 514 489 394 369 309 250 189 190 129 69 754 334 249

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                 748;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1157)
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Acta Trop. 74 (1), 51-61 (2000)
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143 c 155 g 370 t
                                                                                                                                                /product="merozoite
72. .>1157
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                                                                                                                                                                                                                                                          /codon_start=1
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                            Score 508.2; DB 3; Pred. No. 8.2e-101;
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ATTAAGTTCAACATAGATTCTCTCTTTACTGAT
                                                                                          AAGATAAATGAAAATTAAAAATCCCCCCACCGGCCAATTCTGGAAATACACCAAATACTCTC
                                                                                                         AAGATTAATGAAATTAAGAATCCTCCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTG
                                                                                                                                                   GTTTTAGAAAAACGTATTGACACTTTAAAAAAAAATGAAAACATTAAGGAATTACTTGAT
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Plasmodium falciparum isolate HN5 merozoite surface protein
(msp1) gene, partial cds.
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Sequence diversity of the merozoite falciparum in clinical isolates from
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RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQ
YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTDAEKPTTGSKPNT
                                                                                                                                                                                                                                                                                 /db_xref="g1:3821983"
/translation="mkiiffloskcsggsggsggsyasvasggsvasvasggsgns
leokekmylimegtsctavytistpgskcsggsggsggsvasvasggsvasvasggsgns
rrtnpsdnssdsdaksyadlkhrvqnylftikelkypelfdltnhmltlcdnihgfky
                                                                                                                                                                                                                                                                                                                                                                               activity"
                                                                                                                                                                                                                                                                                                                                      /product="merozoite surface
/protein_id="AAC69744.1"
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/product="merozoite
                                                                                                                                                                                                                                                                                                                                                                                            /note="p190; surface protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wild isolate"
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                                                                  Plasmodium falciparum isolate (mspl) gene, partial cds.
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1 (bases 1 to 1124)
Jiang,G., Daubenberger,C., Huber,W., Matile,H., Tanner,M. an
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Jiang,G., Daubenberger,C.A.,
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LFQKEKMYLNEGTSGTAVTTSTPGSKGSGGSGGSGGSVASVASGGSCNS
RRTNSDNSSDSDAKSYADLKHRVQNYLFTIELKYPELDLTNHMLTJLCDNIHFGY
LIDGYEEINELLYKLNFYYDLLRAKLNDACANSYCQIPFNLKIRANELDYLKKIYGFY
RKPLDNIKDNVGKMEDYIKKNKTTIANINELIEGSKKTIDQNKNADNEEGKKKLYQAQ
YNLFIYNKQLQEAHNLISVLEKRIDTLKKNENIKKLLEDIDKIKTDAEKPTTGSKPNT
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/protein_id="AAC69743.1"
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/chromosome="9"
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Submitted
                Jiang,G., Daubenberger,C.A., Matile,H. and Pluschke,G. Direct Submission
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                                                                                                         Acta Trop. 74 (1),
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                                                                                  CTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATC
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                                                             TTAACTTTGTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAAATT
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LFHKEKMILNEGTSGTAVTTSTFCSGGSVTSGGSGGSVASGGSGGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGSVASGGSGGSVASGGSGGSVASGGSGGSVASGGSGGSVASGGSGGSVASGGSGGSVASGGSGGSVASGGSGSVASGGSGSVASGGSGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASGGSVASG
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/protein_id="AAC69737.1"
/db_xref="GI:3821969"
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/chromosome="9"
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/gene="mspl"
/product="merozoite
73. .>1167
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                                                                                                                                         /db_xref="taxon:5833"
/chromosome="9"
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/isolate="IFA9.10"
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/note="p190; surface
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/translation="mkiifflcsflffiinTqcvThesyqelvkklealedavlTgyg
LfhkekmilneeeitTkgasaqsgTsgTsgPsgTsgPsgTsgPsgtspssRsnTlprs
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                                                                                              activity
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71. .>1129
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                                                                                                           /gene="msp1"
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71. .>1129
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/chromosome="9"
                                                                               /codon_start=1
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                                                                                   AAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAG
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GTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGAC
                      GCTCAATATGATCTTTCTATTTACAATAAACAATTAGAAGAAGCACATAATTTAATAAGC
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              AATGAAGGGACGAGTGGCACGGCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTG
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 AATGAAGGAACAAGTGGAACAGCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGTT
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Direct Submission
Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn University, Rama4, Pathumwan, Bangkok 10330, Thailand On May 21, 2002 this sequence version replaced gi:309700.
Location/Qualifiers
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M77716
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Eukaryota; Alveolata;
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T-cell epitope; major
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                                                                                                                                                                                                                                                                   /product="major merozoite surface antigen"
/protein_id="AAA29663.2"
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/db_xref="Gi:21040171"
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SVTSGGSVTSVASVASVASVASVASGGSVSRXTNPSDNSSDSDAKSYADLKHRVQNY
LFTIKELKYPELFDLIPAKHLTLCDHIGFKYLLIGYEEINELLYKLNFYFDLLRAKUN
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DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNYGKMEDYIKKNKTTIAN
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<1. .>1002
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/codon_start=1
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/db_xref="taxon:5833"
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GI:21040184
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M Plasmodium falciparum
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              Haemosporida;
                                                                      merozoite
                                     antigen;
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                                                                             ATGTTAACTTTGTGATAATATTCATGGTTTCAAATATTTAATTGATGGATATGAAGAA
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Submitted (21-MAY-2002) Facult
University, Rama4 | Pathumwan,
On May 21, 2002 this sequence
Location Qualifiers
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DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTTIAN
DVCANDYCQIPFNLKIRANELDVLKKLVFGYRKPLDNIKDNVGKMEDYIKKNKTTIAN
INELIEGSKKTIDQNKNADNEGGKKKLYQAQYNLFIYNKGLQEAHHLISVLEKRIDTL
KKNENIKKLLDKINEIKNPPPANSGNTPNPLPENKKKEVEGHEEKIKEIAKTIKFNID
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umwan, Bangkok 10330, Thailand
quence version replaced gi:309712.
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                                                                                                                                                                                                                                                                                       (p190)
M77714
                                                                                                      Direct Submission
Submitted (21-MAY 2002) Faculty of Medicine, Chulalongkorn
University, Rama4, Pathumwan, Bangkok 10330, Thailand
On May 21, 2002 this sequence version replaced gi:309696.
                                                                                                                                                                                    Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Sequence variation in the tripeptide repeats and T cell P190 (MSA-1) of Plasmodium falciparum from field isola Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
                                                                                                                                                                                                                                               Plasmodium falciparum
Plasmodium falciparum
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                                                                                                                                                                                                                                                                   T-cell epitope;
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                                                                                                                                               Jongwutiwes, S.
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RASE COUNT
420 a 126 c 153 g 303 t

Query Match
9.8%; Score 485.2; DB 3; Length 1002;
Best Local Similarity 68.5%; Pred. No. 9.2e-96;
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T-cell epitope; major merozoite surface antigen;
Plasmodium falciparum
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 1002)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-MAY-2002) Faculty of Medicine, Chulalongkorn University, Rama4, Pathumwan, Bangkok 10330, Thailand On May 21, 2002 this sequence version replaced gi:309714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jongwutiwes, S., Tanabe, K., Nakazawa, S., Yanagi, T. and Kanbara, H. Sequence variation in the tripeptide repeats and T cell epitopes P190 (MSA-1) of Plasmodium falciparum from field isolates Mol. Biochem. Parasitol. 51 (1), 81-89 (1992)
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Merozoite Merozoite

surface surface surface

DNA sequence encod
Merozoite surface
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Plasmodium falcipa
PfMSP1.19 human C3
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Merozoite surface DNA encoding major

Merozoite surface Merozoite surface

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                                                  Recombinant production of complete gp190/MSP-1 Plasmodium surface protein - useful in anti-malaria vaccines, also stabilising genes reducing their AT content
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monoclonal antibody; passive immunisation; parasite; ss.
                                                                                                       WPI; 1998-240088/21.
P-PSDB; AAW54145.
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T 1980 T 1980	CTGAAGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAAAT 	1921 1921	Qy Db
T 19 T 19	CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCAT'	1861 1861	Db Qy
C 18	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801	Qy Db
T 18	ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	1741 1741	Qy Db
G 17 G 17	ATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	1681 1681	Оу
C 16	CATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC	1621 1621	Qy Db
91 9 	TCTTACAAAGTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAA 	1561 1561	Qy Db
C 15	TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAAACGGTA 	່ປາ ປາ	Db Oy
17 15	AGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGA: 	1441 1441	Оу
C 14	GAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGI 	1381 1381	Db Qy
6 13 6 13	GAACCCTCTAAGAATATCTACACAGACAATGAGAGAAAGAA	ω ω	Qy Db
A 13 A 13	AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA	1261 1261	Оу
C 12	ACCGAACCTAATGAATATCCCAATGGTGTGACGTACCCTCTGTCTTATAACGATATCAAC	1201 1201	Qy Db
A 12 A 12	TACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATC.	1141 1141	Qу
C 11	GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTAC	1081	Qy Db
C 10	AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATCIIIIIIIIII	1021	Qy Db
T 10	CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	961 961	Qy Db
A 96	CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA 	901 901	Qy Db

3120	1 CTCTTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTG	306	Qy
3060	AGAAGACACTGCAACTGAAGCTTCGACCTGTACAACAAGTACAAACTGAAACTGGAGA	300	밁
3060	CAACAAGTACAAACTGAAACTGGAGAG		Qy
3000	1 ATCAACTCTCTTAACGATGAATCTAAACGTAAGAAGCTGGAAGAGGACATCAATAAGCTG	294 294	ο Оу
2940 2940	1 GACAGCGACACATTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGAT	288 288	DP QA
2880 2880	1 ATCTACCAAGAACTTATTGGACAGAAATCGTCCGAGAACTTCTACGAGAAGATACTGAAA 	282 282	Дy
2820 2820	1 AACCTTAATAACTCACTGAAACTGTTTGAGAACATCCTGTCTCTCGGCAAGAATAAGAAC	276 276	Db Qy
2760 2760	1 TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACGACACCTCTCACTCGACC	270 270	B 63
2700 2700	1 GAAGCTAAGAAGGTCTCCACCTCTGTTAAAACTCTCTCTTCCAGCTCCATGCAACCACTG 	264 264	B 8
2640 2640	1 GAGATGGTCTGCAACCTGTATAAACTCAAAGACAACGACAAGATTAAGAACCTTCTGGAG 	258 258	Фр
2580 2580	ATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGA 	52	Ор
2520 2520	TCCTCTTGTGATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTAT	246 246	Db Oy
2460 2460	ACTATGAACGAGAAGATTCTTAAACAGTACAAGATAACCAAGGAAGAGGAGAGTAAACTG 	240 240	Db 04
2400 2400	CTCTATGAGTTCCTGAATACATCCTACATCTGCCACAAATATATCCTCGTCTCTCACAGC	234 234	dg VQ
2340 2340	CCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAG	228 228	B 6
2280 2280	AAGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCAAGTGCCTACA	222 222	Å, å
2220 2220	L GGACAACAGGCCGGTTCAGCTCTCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGAGCAG	216 216	P 04
2160 2160	TCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCC 	210 210	DP GA
2100 2100	L ATGCCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACTGAAGGACAG 	204	DЬ
2040 2040	GCAGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTGAAAGT 	9	Db Qy

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                                                                                                                                malaria; MSP-1; merozoite surface protein;
onal antibody; passive immunisation; parasit
                                                                                                                                                                                                                                                                                                                               standard;
                                                                                     falciparum
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Location/Qualifiers
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Matches 3626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 3c; 48pp; German.
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P-PSDB; AAW54145.
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                                                                                     GGCTCAGTGGCAAGCGGCGGTTCCGGGAACAGTCGAAGAACCAATCCATCTGACAACTCT
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                                         ACTATCAAGGAGCTGAAGTACCCACAGTTGTTCGACCTCACTAATCATATGCTGACACTG
                                                                                                                                  GGCTCAGTTGCTTCAGGTGGTTCAGGTAATTCAAGACGTACAAATCCTTCAGATAATTCA
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Pred. No. 0;
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1620 1620	1561 TCTTACAAAGTGGAGAAACTGACACACCATAATACCTTTGCATCCTATGAGAATTCTAAG	Qу
1560 1560	501 TCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGGAAAACGGTAC 	ОУ
1500 1500		ДУ
1440 1440	1381 GAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGC	DB Qy
1380 1380	1321 GAACCCTCTAAGAATATCTACACAGACAATGAGAAGAAAGA	Db Qy
1320 1320	261 AACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCTTCGATTATACGAAA	ОУ
1260 1260	1201 ACCGAACCTAATGAATATCCCAATGGTGTGACGGTACCCTCTGTCTTATAACGATATCAAC	р, _ў
1200 1200	1141 TACTTGAGAGAGAGAATAAGAATATAGACATCTCCGGCAAAGTCGAGACAAAGGAATCA. 	Оy
1140 1140	081 GCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGCTACGILIIII	D Qy
1080	21 AACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAGAGATCAAAGAGATC	Qу
1020 1020	961 CTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGCCA	ОУ
960	01 CTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATGAAAATATCAAAGAA	Фb
900	41 TTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAACA	Qу
840 840	781 GAATCCAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAG	Qу
780 780	21 ATGGAAGATTATATTAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAA 	Db
720 720	661 AAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGACAATGTGGGAAAG	Db Qy
660	601 AATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTG	Db Qy
600	541 CTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCC	Qу

ACC 2760	1 TCTCTCACACCTCAAGACAAGCCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGA	70	Qy
TA 2700	GAAGCGAAAAAGTATCCACATCTGTAAAAACTCTTTCAAGTTCATCAATGCAACCAT	264	Db
TG 2700	AACC	64	Qy
3AG 2640	1 GAAATGGTTTGTAATTTATATAAACTTAAGGATAATGACAAAATTAAAAATTTATTAG	258	В
3AG 2640	AGATGG	258	Qy
AAG 2580 AAA 2580	1 TCTATGTTCGATAGCCTCAACAATTCTCTCTCTCAACTGTTCATGGAGATATATGAGAAG	252 252	ОУ
25	AGTTCATGTGATCCATTAGACTTATTGTTTAATATACAAAATAACATACCTGTAATGTAT	46	Db
TAT 2520	1 TCCTCTTGTGATCCACTGGACCTGCTGCTTCAATATCCAGAACAACATTCCCGTTATG	246	Qy
TTA 2460	ACTATIGAACGAGAAGATTGTTAAACAGTACAGAGTAACCAGGAGGAAGGA	240	B 8
A 24	CICIAISMOIL CLOMAINCAICCINCAICISCOCACAAATATATTTTTGGTTTTCACACTC TTATATGAATTTTTAAATACTTCATATATATGTCACAAATATATTTTTGGTTTTCACACTC	344	Db 49
2 1		28) B
234	1 CCACCAGCTCCTGTGAATAACAAGACCGAGAATGTCAGCAAACTGGACTACCTTGAGAAA	28	Qy
22		22	Db
228	1 AAGCAGGCACAGCCTCCAGTGCCAGTGCCCGTTCCAGAGGCTAAAGCTCCAAGTGCCT	22	Qy
CAG 2220 	1 GEACAACAGGCCGGTTCAGCTCCGAAGGCGATAGCGTGCAAGCTCAAGCACAAGAGG. 	216 216	P Qy
CCC 2160	1 TCAGATAACTCCGAGCCTTCCACAGAAGGAGAGATAACCGGACAGGCTACCACCAAGCCC	210 210	Оy
CAA 2100	1 ATGCCCAAAGTCGAGAGCCTGATCAACGAAGAGAGAGAACATTAAAACTGAAGGCC	04	В Q
TC 20		98	Db
TTC 2040	CAGGAACCATACTACCTCATCGTACTC	9	Qy
AGAAT 1980 AAAAT 1980	CTGAAGAACGTGGAGTTAAĄACATAATATACATGTGCCGAATAGTTATAAGCAGG	1921 1921	Oy Db
TGATT 1920	1. CAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCL 	186	Db Qy
186	CTAAAGACGAAAATAAACCAGATGAAAAAATTTTAGAAGTATCTGACATTGTAA	ω.	В
GTC 1860	ACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTGTTAAAGTC	1801	Qy
ATT 1800	1 ATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATT	174 174	. pb 04
17	1. ATAGTAGTTGAAAAAGAATTAAAAATATTATAAAAATTTAATAA	89	Db
3AG 1740	1. ATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTCATAAGTAAG	83	Qy
AAC 1680 AAT 1680	1. CATAATCTTGAGAAGCTCACĆAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAAC 	162 162	Oy Db
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2761 ANTITIGAANTATRITTIAAAATTATTICAAAACCAARCTCGAGTCCTGGAAAAACCAAAAATT 2820 2821 ATCAACCAAGAACTTCTATAGGCCAGAACTGCGACAACTTCCTACGACAAAAACTACTACAAA 2880 2821 ATCAACCACGAACTTCTATAGGCCAAAAACTACTTCGAAAAACTATTATAAAA 2880 2821 ATCAACCACCACACTTCTATAGGCCAAAACTTCTAAACTTTATAAAAACTATTATAAAACTATTAT	 CAAATGA TCCTGTC
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                                                                                                                                                                                                                                          The sequence encoding the P195 protein of Plasmodium falciparum (AANSO530) and a peptide comprising at least one of its epitopes (see AAP50777) are claimed. Also claimed is a vaccine for inducir immunity to malaria comprising the novel peptide or P195 or a peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one epitope when derived from the new peptide comprising at least one of its epitopes.
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                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                               Cloned DNA useful for
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22-FEB-1984;
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DB; AAP50777.
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GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
                                                                     ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT
                           ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
                                       2; Fig 1; 51pp; English.
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ilarity 72.1%;
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84GB-0004692.
85GB-0004429.
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                                GAAAAAAATATATTGATATAAGTGCAAAGGTTGAAACAAAGGAATCAACTGAACCC
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3695	GAAGGAAAATTAAAGGATAATCTAAATTTAGAAAAGAAA	3636	Db
3447	CAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCT	3388	Qy
3635	GAAGAATCAATCAAACAGAAGATAATTATGCCAGTTTAGAAAACTTTAAAGTATTAAGT	3576	Db
3387	GAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGTCT	3328	Qy
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326/	AAGGAAGCCGAGATCGCCGAGACAGAGAACACTTCTGGACAACACACAGATTCTTCTCAAA 	3456	p Q
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3207 3455	AACTCACTGAACAATCCGAAACACGTACTACTACAAGAACTTCTCAGTGTTCTTCAACAAGAAG 	3148 3396	P 64
3395	AAATATAAAATGCAAATTAAAAAACTTACTTTATTAAAAGAACAATTAGAATCAAAATTG	3336	рь
3147	AAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAGGCAACTC	3088	Qy
3335	TTATATAATAAATATAAAATTAAAATTAGAAAGATTATTGATAAAAAGAAAACAGTTGGT	3276	Db
3087	CTGTACAACAAGTACAAACTGAAACTGGAGAGACACTCTTCGACAAGAAGAAGACAGTCGGC	3028	Qy
3275	AGGAAGAATTAGAAGAAGATATTAATAATTAAAAAAAAA	3216	Дb
3027	CGTAAGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGAACACTGCAACTGAGCTTCGAC	2968	Qy
3215	TTTACAAATTTTGTAAAATCTAAAGCTGATGATAATTCATTGAATGATGAATGA	3156	DЬ
2967	TCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTTAACGATGAATC	2908	Qy
3155	AGTAGTGAAAACTTTTATGAAAAGATATTAAAAGATAGTGATACATTTTATAATGAATCT	3096	Db
2907	AAGAT	2848	Оу
3095	GAAAACATATTGAGTCTTGGAAAAAAACAAAAATATATACCAAGAATTAATAGGTCAAAAA	3036	рь
2847	AGAACATCCTGTCTCTCGGCAAGAATAAGAACATCTACCAAGAACTTATTGGAC	2788	Qy
3035	GTAAGTGCAAATGATGATACATCACATTCTACAAATTTGAATAATAGTTTAAAATTATTT	2976	ф
2787	TG	2728	Qy
2975	AAAACTCTTTCAAGTTCAATGCAATGCAACCATTATCATTAACACCTCAGGATAAACCCGAA	2916	Db
2727	AAAACTCTCTCTTCCAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAAGCCCCGAA	2668	Qy
2915	AAGGATAATGACAAAATTAAAAATTTATTAGAGGAAGCGAAAAAAGTATCCACATCTGTA	2856	Ф
2667	NCAACGACAAGATTAAGAACCTTCTGGAGGAAGCTAAGAAGGTCTCCACCTCTG	2608	Qy
2855	GTATTTATATTACTTATGGAAATTTATGAAAAAGAAATGGTTTGTAATTTATATAAACTT	2796	Db
2607	CTCTCTCAACTGTTCATGGAGATATATGAGAAGGAGATGGTCTGCAACCTGTATAAACTC	2548	Qy
2795		2736	Дb
2547		2530	Qy
2735	GATCCATTAGACTTATTGTTTAATATACAAAATAACATACCTGTAATGTATTCTATGTTT	2676	ДЬ
2529	GATCCACTGGACCTGCTGTTCAATATCCAGAACAACATTCCCGTTATGTATTCTATGTTC	2470	Qy
2675	GAAAAGATATTAAAACAATATAAAATTACAAAGGAGGAAGAAAGCAAATTAAGTTCATGT	2616	рь
2469		2410	Qy

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                                                         ACCGATTATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAA
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                                      ACAGATTATAACCATAATAACTTATTGACAAAGTTCCTTAGTACAGGTATGGTTTTTGAA
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MSA-1 (N-terminal p83 or C-terminal gp42) genes, or a comb of these in non-essential regions of their genomes are cla These poxviruses (pref. with a virulence reducing genomic deletion or disruption) can be used as vaccines against ma and for the prodn. of Plasmodium immunogens. These viruses
                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum MSA-1 gene; recombinant multicomponent multistage malarial vaccines; malaria diagnosis; ss.
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                                                          AAQ80911 is the P. falciparum MSA-1 gene cDNA sequence. New recombinant poxviruses containing either the SERA, ABRA, Pfhsp70, AMA-1, Pfs25, Pfs16, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1.
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                                                                                                         Claim 3;
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09-JUN-1994;
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0 ~	2131 2216	GAGATAACCGGACAGGCTACCACCAAGCCCGGACAACAGGCCGGTTCAGCTCTCGAAGGC 2190 1 1 1 1 1 1 1 1 1	
0 ~	2191 2275	GATAGCGTGCAAGCTCAAGCACAAGAGCAGAGCAGGCACAGCCTCCAGTGCCAGTGCCC 2250	
0 ~	2251 2335	GTTCCAGAGGCTAAAGCTCAAGTGCCTACACCACCAGCTCCTGTGAATAACAAGACCGAG 2310	
0 ~	2311 2395	AATGTCAGCAAACTGGACTACCTTGAGAAGCTCTATGAGTTCCTGAATACATCCTACATC 2370	
0 ~	2371 2455	TGCCACAAATATATCCTCGTCTCTCACAGCACTATGAACGAGAAGATTCTTAAACAGTAC 2430	
0 ~	2431 2515	AAGATAACCAAGGAAGAAGAGAAGTAAACTGTCCTCTTGTGATCCACTGGACCTGCTGTTC 2490	
0 ~	2491 2575	AATATCCAGAACAACATTCCCGTTATGTATTCTATGTTCGATAGCCTCAACAATTCTCTC 2550	
0 ~	2551 2635	TCTCAACTGTTCATGGAGATATGAGAAGGAGAGGTGGTCTGCAACCTGTATAAACTCAAA 2610	
0 ~	2611 2695	GACAACGACAAGATTAAGAAACCTTCTGGAGGAAGCTAAGAAGGTCTC 2657 	
0 ~	2658 2755	ACATCCAGTCCTGGAAATACAACCGTAAATACTGCTCAATCCGCAACTCACAGTAATTCC 2814	
0 ~	2682 2815	CAGCTCCATGCAACCACTGTCTCTCACACCTCAAGACAA	
0 ~	2721 2875	GCCGAAGTGAGCGCTAACGACGACACCTCTCACTCGACCAACCTTAATAACTCA 2775	
0 ~	2776 2935	CTGAAACTGTTTGAGAACATCCTGTCTCTGGGCAAGAATAAGAACATCTACCAAGAA 2832 	
0 ~	2833 2995	CTTATTGGACAGAAATCGTCCGAGAAACTTCTACGAGAAGATACTGAAAGACAGCGACACA 2892	
0 ~	2893 3055	TTCTATAACGAGAGCTTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTT 2952	
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Best Local Similarity
Matches 1297; Conserv
                                                                                                                                                                                                                                 The present sequence encodes a chimeric protein that contains a mammalian signal and anchor sequence, and a merozoite surface antigen-1 (MSA-1) carboxy terminal peptide. The C-terminal fragment of MSA-1 provides a more specific response than the complete MSA-1, and attachment of anchor and signal sequences improve the immunogenicity of the protein better than the use of an adjuvant. The chimeric protein, and expression vectors (analogues that express MSA-1 without either signal or anchor peptides), particularly in the form of recombinant vaccinia virus, are used in vaccines to prevent or treat malaria caused by Plasmodium falciparum. The vaccinia vector expresses the antigen fragment for many days, or even years, generating a long-lasting immune response (humoral and/or cell-mediated) against the merozoite form of the paragite. in humans or other actuals
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Chimeric
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                                                                CAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCCAAGAT 3257
                                         TAACAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAAACACATTAGAAAAACACAAAAAT
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recombinant vaccinia virus; Plasmodium falciparum; anci
response; humoral; cell-mediated; merozoite; ss.
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response; humoral; cell-mediated; merozoite; ss.
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                      P-PSDB; AAY09372
                                             WPI; 1999-288313/24
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20-OCT-1997;
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97US-0062592
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CC This novel, modified nucleic acid encodes the 42 kDa C-terminal CC (MSP-1-42), an important target for the development of a vaccine CC (MSP-1-42), an important target for the development of a vaccine CC against Plasmodium falciparum. The nucleic acid sequence has been CC modified compared to the native sequence of MSP-1-42 (see AAX56009) CC such that 306 nucleotide positions have been replaced to lower the CC AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability CC motifs while maintaining the same protein amino acid sequence. CC These alterations allow MSP-1-42 to be expressed in mammalian cell CC culture and in transgenic mice. Native MSP-1-12 is known to be CC difficult to express in cell culture systems, mammalian cell CC culture systems or in transgenic animals. The invention allows CC expression of MSP-1-42 protein in the milk of transgenic animals, C and also provides a DNA vaccine comprising a vector containing the CC culture MSP-1-42 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use in anti-malarial vaccines
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Query Match

Sequence 1065 BP; 324 A; 254 C; 280 G; 207 T; 0 other;

Length

δÃ В Š 밁 Qy Ωy Qy οy ρ Qy Ъ 밁 В δÃ В В δÃ В δÃ 밁 В 멍 δÃ Matches 863; 4459 4279 4219 4159 4099 4039 3979 3919 3859 481 421 181 121 361 301 241 61 Local GACCTGTCTACCGATTATAACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATG AAAACAATCCAAGACAAGCTGGCAGATTTCAAGAAAAATAACAATTTCGTCGGAATTGCA CTCAACTATACTTACGAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTC CTGTACAAGACAGTGAACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCAAGGTC GGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACCTCTATTAAAAAGTAT AGTTACAACTATATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTG TACGTTGTCAAGGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCT 4098 AATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGGCCTCTAAC GTGATGACCTTCAACGTGAACGTGAAGGATATCCTGAACAGCCGGTTCAACAAGCGGGAG GTGATGACCTTCAATGTCAACGTGAAGGACATTCTGAACAGCCGCTTTAATAAGAGAGAAA CTGTACCTGAAGCCGCTGGCAGGGGTCTACCGGAGCCTGAAGAAGCAGCTGGAGAACAAC CTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAAC **AAGACCATCCAGGATAAGCTGGCCGATTTCAAGAAGAACAACAACTTCGTCGGGATCGCC** CTGAACTACACATATGAGAAGAGCAACGTGGAGGTCAAGATCAAGGAGCTGAATTACCTG TACGTGGTCAAGGATCCCTACAAGTTCCTGAACAAGGAGAAGAGAGATAAGTTCCTGAGC **AACTTCAAGAACGTGCTGGAGAGCGATCTGATCCCCTACAAGGATCTGACCAGCAGCAAC** AGTTACAACTACATCAAGGATAGCATTGATACCGATATCAACTTCGCCAACGATGTCCTG Similarity Conservative 15.1%; 81.3%; Mismatches Score 744.2; DB 20; Pred. No. 9.3e-171; Gaps 4518 4218 3918 4338 4278 4158 4038 660 600 540 480 420 360 30Ó 240 180 120 0,

GATCTGAGCACCGATTACAACCACAACAACCTGCTGACCAAGTTCCTGAGCACCGGTATG

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RESULT 9
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This novel, modified nucleic acid encodes a 42 kDa C-terminal part (see AXY05832) of malaria merozoite surface protein MSP-1 (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AXX25587) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell
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This novel, modified nucleic acid encodes a 42 kDa C-terminal part (see AAY09374) of malaria merozoite surface protein MSP-1 (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX56009) such that the AT content has been reduced and 10 mRNA instability motifs eliminated while maintaining the protein amino acid sequence. In addition, a sequence encoding a 15-amino acid beta-casein signal peptide has been added to the 5' end of the sequence, and N262Q
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DB; AAY09374.
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              GCGGCTGTTTCAGGCATCTGGACGAGCGCGAAGAGTGCAAGTGTCTCCTGAACTACAAAC
                                                              TGCAGGGCATGCTGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATA
                                                                                                                CTGGCATGGTGTTCGAAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACC
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                                                                                                   GAATCGCCGATCTGAGCACCGATTACAACCACAACAACCTGCTGACCAAGTTCCTGAGCA
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 GCGGATGCTTCAGACACCTGGATGAGAGGGAGGAGTGCAAGTGCCTGCTGAACTACAAGC
                                                   {\tt TGCAGGGAATGCTGCAGATCAGCCAGCACCAGTGTGTGAAGAAGCAGTGTCCCCAGAACA}
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               (MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The nucleic acid sequence has been modified compared to the native sequence of MSP-1-42 (see AAX25587) such that the AT content has been reduced and 10 mRNA instability motifs eliminated while maintaining the protein amino acid sequence. In addition, a sequence encoding a 15-amino acid beta-casein signal peptide has been added to the 5' end of the sequence, and N2620 and N1810 mutations have been introduced to eliminate N-glycosylation sites. These alterations allow MSP-1-42 to be expressed in the mammary gland (i.e. milk) of transgenic mice. The invention provides modified recombinant nucleic acid sequences and methods for increasing the methods are sequences and methods for increasing the methods and sequences and methods for increasing the methods and sequences and methods for increasing the methods are sequences and methods for increasing the methods for increasing the methods are sequences and methods for increasing the methods are sequences and methods for increasing the methods for increasing the methods for increasing the methods are sequences.
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preferred difficult protein candidates for expression are those derived from lower organisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered
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13-MAY-1999;
25-MAY-1999;
                                                   3799
                                                                                                                                                                                                                                          The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel variants of the C-terminal fragment of Plasmodium merozoite surface protein-1, useful as vaccines for treating or preventing
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GCGAGTGTACTAAGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGC
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llarity 79.3%;
Conservative
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99US-0311817.
99CA-2271451.
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                                                                                            GTGTTCGAAAACCTCGCCAAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGC
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RESULT 13 AAX56009 ID AAX56009 standard; cDNA XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nucleic acid encodes a 42 kDa C-terminal portion (see AAY09373) of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The 3' end of the sequence has been modified to include a 6xHis tag. The nucleic acid sequence has been modified (see AAX56008) according to a method of the invention in order to improve expression in mammalian host cells and in transgenic animals. In the modified coding sequence, 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs. The encoded amino acid sequence is unaltered. In another modified sequence (see AAX56021), a signal peptide sequence has been added and two N-glycosylation sites eliminated. The invention allows expression of MSP-1-42 protein in the milk of transgenic animals, and also
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20-OCT-1997;
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DB; AAY09373.
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                     AATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAAC
                                                               GTTATGACATTTAATGTTAATGTTAAGGATATTTTAAATTCACGATTTAATAAACGTGAA
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MSP-1; merozoite surface protein; malaria; protein engineering; protein expression; co
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                                                        Merozoite surface protein MSP-1-42 cDNA
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                                                                                                                                                                                                                                                                    This nucleic acid encodes a 42 kDa C-terminal portion (see AAY05833) CC of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an composition target for the development of a vaccine against important target for the development of a vaccine against composition of include a 6xHis tag. The nucleic acid sequence has been modified to include a 6xHis tag. The nucleic acid sequence has been modified to include a 6xHis tag. The nucleic acid sequence has been modified to improve expression in mammalian host cells and in the nucleic acid sequence. 306 nucleotide contains the form 76 to contain the form 76 to contain the form 76 to contain the form 76 to constitute and the eliminate 10 mRNA instability motifs. The encoded amino acid sequence is unaltered. In another modified sequence (see AAX25593), a signal peptide sequence has been added and two contain tucleic acid sequences and methods for increasing the mRNA levels and protein expression of proteins that are difficult to express in cell culture systems, mammalian cell culture systems candidates for expression are those derived from lower organisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content to which have mRNA instability motifs.
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                                                                                                                                                                                                                                                                                             vector containing the altered MSP-1-42 sequence.
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                                                                                                                                                                                                                                                                                                        rare codons relative to the recombinant expression system to be ed. The invention allows expression of MSP-1 protein in the milk transgenic animals, and also provides a DNA vaccine comprising a
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               AATTTCAAGAACGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAAC
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                                                                                                                        CTCTATCTGAAACCTCTGGCAGGCGTCTATAGGTCTCTCAAGAAACAGCTGGAGAATAAC
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Merozoite surface protein;
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                     surface
                                         (first entry)
                     protein-133
                                                                                 DNA;
                                                                                   786
protazoacide; vaccine;
                                                                                   ВP
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malaria;

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13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, an cash be used to treat malaria. The present sequence is the MSP-133
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                                                                                             GGGTATTACAAGATCCTGAGCGAAAAATACAAGTCTGACCTTGACCTCTATTAAAAAGTAT
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DB; AAB37610.
                                   ATCAACGATAAGCAAGGCGAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACC
                                                                                 GGTTACTACAAGATCTTGTCTGAGAAGTACAAGTCTGGACTTGGATTCCATCAAGAAGTAC
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01-DEC-1999;
22-AUG-2000;
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                                                                                                                                                                  producing malaria vaccine, useful for treatment or forms of malaria in humans, by expressing immunogen
                                                                                                          Example 3;
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UNIV CHINESE HONG
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                                                                                                          88-89;
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1..1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
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                                                                                                     95pp;
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                                                                                                                                                                                                                                                                                                 WKK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Qualifiers
                                                                                                                                              s, by expressing system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "major merozoite of 42kDa"
                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface protein-1 fragment of 42kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                  immunogenic merozoit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface
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                                                                                                                                                                    evention of all merozoite protein
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The present sequence encodes a major merozoite surface protein-1 C-terminal fragment of 42kba (MSB1-42). This fragment is linked melittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  malaria vaccine, which is used to treat or prevent malaria, caused any of the four species of Plasmodium that infect humans.
                                                                                                                                               4537
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                                                                                                                                                                                                                                                                                                                                                                   GACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCCAAGGTCCTCAACTATACTTACGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACAAGTTCCTCAATAAAGAGAGAGGGATAAATTTCTGTCTAGTTACAACTATATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGATAACATTCTGTCCAAAATCGAGAACGAATACGAAGTGCTCTATCTGAAACCTCTG
                CGCGAAGAGTGCAAGTGTCTCCTGAACTAACAAACAAGAAGGAGGATAAGTGCGTGGAGAAC
                                                      CACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGACGAG
                                                                                                                                                                                       AACCACAACAATCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAAACCTCGCC
                                                                                                                                                                                                                                                                                                        AAGAGCAATGTGGAAGTTAAAAATCAAGGAGCTGAACTACCTCAAAAACAATCCAAGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAATGAAAAATATCTGCCCTTCCTGAATAACATCGAAACCCTGTACAAGACAGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGAAAAATACAAGTCTGACCTTGACTCTATTAAAAAGTATATCAACGATAAG-----
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AGAGAAGAATGTAAATGTTTAATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAAT
                                                                                                               AATACAATAATATCAAAATTAATTGAAGGAAAATTCCAAGATATGTTAAACATTTCACAA
                                                                                                                                                                        ACGAAAAAGATATGCTTGGCAAATTACTTAGTACAGGATTAG---TTCAAAATTTTCCT
                                                                                                                                                                                                                                 ATAGATCTTTTTAAAAAACCCTTACGACTTCGAAGCAATTAAAAAATTGATAAATGATGAT
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                                                                                                                                            AAAACAGTGCTGAGCAATCTGCTCGACGGCAACCTGCAGGGCATGCTGAACATCTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%;
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Pred. No. 3.6
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RESULT 17
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ID AAN81
XX AAN81
AC AAN81
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C DNA S
C DNA S
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                                                                                                                                    Query Match
Best Local Similarity
Matches 391; Conserv
                                                                                                                                                                                                     The DNA encodes a region of a polypeptide. The region contains at one epitope of the 190kD precursor of the major merozoite surface of P.falciparum.
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                                                                                                                                                                                                                                                  Disclosure; ; pp; German
                                                                                                                                                                                                                                                                                                                                          Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAN81148;
                                                                                                                                                                                 Sequence 660 BP; 281
                                                                                                                                                                                                                                                                       New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor, useful in vaccines, and encoding DNA sequences
                                                                                                                                                                                                                                                                                                                      WPI; 1988-272339/39.
                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence
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                                           ACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAGATCAAT
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           TGCGCCAATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGAC
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 TGTGCTAATGATTATTGTCAAATACCTTTCAATCTTAAAATTCGTGCAAATGAATTAGAC
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                                                                                                                                                                                                                                                                                                                                                                 HOFFMANN-LA ROCHE &
                                                                                                                                                                                                                                                                                                                                          Gentz H,
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                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       87GB-0006599
                                                                                                                                                                                                                                                                                                                                                                                                             88EP-0103564
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                               6.3%;
                                                                                                                                                                                A; 84 C; 102 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Takacs
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                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                            В;
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                                                                                                                                               Score 308.8; DB 9
Pred. No. 7.1e-65;
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                                                                                                                                    Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 merozoite; vaccine
                                                                                                                                                          DB 9; Length
                                                                                                                                                            660;
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594 492

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714

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ARRESULT 18
AAN81151
ID AAN81
XX AAN81
AC AAN81
XX 11-NO
DE DNA S
XX POlyp
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                    Matches
                              Query Match
Best Local Similarity
                                                                                                                                  The DNA encodes a region of a polypeptide. The region contains at least one epitope of the 190kD precursor of the major merozoite surface antige
                                                                                                                                                                                                                 New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor, useful in vaccines, and encoding DNA sequences
                                                                                                                                                                                                                                                                     WPI; 1988-272339/39
P-PSDB; AAP80547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium
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                                                                                  Sequence 1068 BP;
                                                                                                                 of P.falciparum.
                                                                                                                                                                                  Disclosure; ; 5pp; German.
                                                                                                                                                                                                                                                                                                                   Ulrich C,
                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP283829-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide p190-3; P.falciparum; merozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence encoding polypeptide p190-3
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                  391;
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1..1068.
/*tag= a
                                                                                471 A; 129 C; 161 G; 307
                                6.3%;
74.1%;
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                  0,
                 Score 308.8; DB 9;
Pred. No. 9e-65;
0; Mismatches 137;
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 14-FEB-1996;
                                  14-FEB-1997;
                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT80403;
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                                                                   21-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                   falciparum.
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 96FR-0001821
                                  97WO-FR00291
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/note= *c
286..354
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                                                                                                                                  anchoring sequence"
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792

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sequence*

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ARPSULT 20
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ID AATT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INSP
         Plasmodium Synthetic.
                                                                                                                                                                                        4883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                      Plasmodium
                                                               PfMSP1(p19)A
                                                                                    25-MAR-1998
                                                                                                      AAT94550;
                                                                                                                       AAT94550 standard;
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                                                                                                                                                                                                                                                                                                                        Plasmodium species.
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                                                                                                                                                                                                                   AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCA 4882
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                                                                                                                                                                                                                                                                                                                                                                                                                                       354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nt protein containing Plasmodium merozoite surface p42 fragment - useful in antimalarial vaccines, a for diagnosis and protein purification
                                             Plasmodium vivax;
                   falciparum
                                    falciparum;
                                                                                                                                                                                                                                                                                                                                                                                                 .Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
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                                                               coding
                                                                                   (first
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                                                               sequence
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                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                        5.0%;
81.7%;
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                                      malaria;
                                                                                                                        354
                                              merozoite
                                                                                                                                                                                                                                                                                                                                                                                                Score 246.6;
Pred. No. 7.1e
0; Mismatches
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                                    vaccine; immunity; epit
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64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nato
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                     epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                       4931
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP)
                                                                          4763
                                                                                                             4703
                                                                                                                                                  4643
                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                vaccines, where
immunity since i
                                                                                                                                                                                                                                                                                                                                                                              purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9730158-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                            125
                  245
                                                       185
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                                                                                                                                                                                                                                               BP;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          from Plasmodium species.

The recombinant protein can be used for the production of vaccines, where the pl9 fragment provides a high level of
                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence encoding a recombinant protein comprising nucleotides encoding amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (p19), linked to a sequence encoding a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                   4583 TGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCA 4642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant protein containing the fragment - useful in anti-malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-425033/39
P-PSDB; AAW36103.
TCTCCTTCCTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATA 4931
                                                                                                                                                                       AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATTTCCTGGGCA 4882
                                                                                                                                                                                                                    TCAACATCTCGCAGCACCAATGCGTGAAAAAACAATGTCCCGAGAACTCTGGCTGTTTCA 64
                                                                        CCAAATGCACCGAGGAGGACTCGGGCAGCAACGGCAAGAAAATCACGTGTGAGTGTACCA
                                                                                               CTANATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTA 4822
                                                                                                                         AGTGCGTGGAGAACCCCAACCCGACCTGTAACGAGAACAACGGCGGCTGTGACGCAGACG
                                                                                                                                      AGTGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG
                                                                                                                                                                                                                                                                                                                                                since it includes epitopes not presented
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Longacre-Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-FR00290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96FR-0001822
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286..354
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "PfMSP1(p19)A with /note= "sequence contains 2 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..354
                                                                                                                                                                                                                                                                                                                        Α,
                                                                                                                                                                                                                                                                                   5.0%;
81.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE
                                                                                                                                                                                                                                                                                                                         92 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "glycosylphosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "sequence contains
the 3'-end"
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                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                         88 G;
                                                                                                                                                                                                                                                                                    Score 246.6; DB 1 Pred. No. 7.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ß
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendis
                                                                                                                                                                                                                                                                                                                         75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         merozoite surface protein-1 vaccines, diagnosis and pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠,
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                                                                                                                                                                                                                                                                                               DB 18;
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                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anchoring
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                                                                                                                                                                                                                                                                                                                                                 p42 fragment
                                                                                                                                                                                                                                                                                                                                                              protective
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TCTCGTTCTTGTTGATCCTCATGTTGATCTTGTACAGCTTCATTTAATA

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Best Local
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                                                                                                                                                                                                                           The DNA sequence encodes a Plasmodium falciparum, Plasmodium Plasmodium malariae and Plasmodium ovale antigen which may be in the diagnosis of malaria and as a vaccine against malaria. Nucleotides 293-422 and 429-530 are used in the preparation o
                                                                                                                                                                                                                                                                                             Prodn. of antigens of Plasmodium species, esp. recombinant DNA methods giving polypeptide(s) against malaria or for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Storage-specific, plasmid pFCC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN50355;
                                                                                                                                                                                                Sequence 737
                                                                                                                                                                                                                    monoclonal
                                                                                                                                                                                                                                                                           Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                  Mach B,
                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1991
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                                                                                                                             ATGAAAATCATTTTCTTCCTCTGTTCATTTCTGTTTTTTTATCATCAATACTCAGTGCGTG
                                                                                                                                                                                                                                                                                                                                    1985-223371/36.
DB; AAP50304.
          GCCGTTACAACCAGCACACCCGGTTCTAAAGGGTCTGTGGCTAGCGGTGGCTCCGGTGGG
GCTGTTACAACTAGTACACCTGGTTCAGGTGGTTCAGGTTACTTCAGGTGGTTCAGGTGGT
                                                 ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129
                                                                                                                    ACACATGAAAGTTATCAAGAACTTGTCAAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                      ACAGGTTATAGTTTATTTCAAAAGGAAAAAATGGTATTAAATGAAGGAACAAGTGGAACA
                                                                                                                                                                                                                                                                                                                                                                                    BIOGEN
                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                 Perrin L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggs
                                                                                                                                                                                                                  antibodies against the malaria antigen
                                                                                                                                                           Conservative
                                                                                                                                                                                                BP; 253 A; 90 C; 124 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                        84GB-0004378
                                                                                                                                                                                                                                                                                                                                                                                                                           85WO-GB00072
                                                                                                                                                                                                                                                                           6; 49pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 2..737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 late schizont merozoite malaria antigen insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                  4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                  McGarvey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria antigen
                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p31-1;
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                                                                                                                                                                  Score 243.4; DB 6; Pred. No. 6.2e-49;
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                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  Shaw
                                                                                                                                                                                                                                                                                                       . of
                                                                                                                                                                                                                                              Plasmodium vivax, which may be used
                                                                                                                                                                                                                                                                                                       falciparum protecting
                                                                                                                                                           Indels
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464
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Best Query Match Matches

Local Similarity nes 335; Conser

Conservative

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Score 240.2; Pred. No. 3.6e 0; Mismatches

.6e-48; DB 9;

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Indels

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RESULT 22
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                                    The sequence encodes a polypeptide which contains the unique sequence of the surface antigen of P. falciparum, but lacks the immunodominant repeat sequences which may allow the parasite to evade and decoy the immune system. The DNA for the stage-specific late schizoint merozoite antigen 31-1 in p31-1 (W08503725) was modified to delete the entire sequence coding for the repitope. The expression plasmid, 31-1 Repeated Delete, was introduced into E.coli K12 to produce the modified peptide. The transformant has been deposited in the Deutsche Sammlung von Microorganismen as E.coli K12 (9SG936cl) (p31-1 Repeat Delete). The peptide was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS;
Sequence
                                                                                                                                                                            Disclosure; ; p; English.
                                                                                                                                                                                                    surface antigen sequence
                                                                                                                                                                                                                Peptide(s) for prodn. of
                                                                                                                                                                                                                                                                             Shaw A,
                                                                                                                                                                                                                                                                                                      (BEHW ) BEHRINGWERKE
                                                                                                                                                                                                                                                                                                                               26-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                       20-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                03-FEB-1988
                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malaria; stage-specific late schizont-merozoite antigen 31-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-1 Repeated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTGGCCTCTGGGGGGTTCCGTCGCCTCCGGCGCGCAGCGTGGCATCAGGTGGCTCAGTG
                                                                                                                                                                                                                                                       1988-030152/05.
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  899
                                                                                                                                                                                                                                                                               Humbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                          to treat and
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protozoan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delete
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                                                                                                                                                                                                                                                                                                                                                       87EP-0108867.
  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                      AG
 A; | 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasite; repitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      899
                       31-1 Repeat Delete). The peptide was us prevent protozoan parasitic infections.
                                                                                                                                                                                                     antiprotozoal vaccines with deleted repitope
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 115 G;
  205 T;
 0 other;
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New immunogenic polypeptides - derived from Plasmodium falciparum 190 kD surface antigen precursor, useful in vaccines, and encoding DNA sequences
                                                  WPI; 1988-272339/39.
P-PSDB; AAP80546.
                                                                                                                               (HOFF ) F HOFFMANN-LA ROCHE & CO.
                                                                                                                                                               19-MAR-1987;
                                                                                                                                                                                             08-MAR-1988;
                                                                                                                                                                                                                             28-SEP-1988
                                                                                                                                                                                                                                                             EP283829-A
                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence
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                                                                                               Gentz H,
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 (HOFF ) F. HOFFMANN-LA ROCHE &
                                 19-MAR-1987;
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                           08-MAR-1988;
                                                        28-SEP-1988
                                                                                  EP283829-A
                                                                                                                                                                         Plasmodium
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                                                                                                                                                                                                                                                              11-NOV-1990
                                                                                                                                                                                                                                                                                                                      AAN81149 standard; DNA;
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20-APR-2000; 2000WO-GB01558
                                                                      Plasmodium
                                                                                                                                                                                         AAC68977 standard; DNA;
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                        26-OCT-2000
                                               WO200063245-A2
                                                                                             Merozoite surface protein; protazoacide; vaccine;
                                                                                                                 Merozoite surface protein-119 coding sequence
                                                                                                                                           27-FEB-2001
                                                                                                                                                                  AAC68977;
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hes 284;
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                                                                                                                                          (first entry)
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Pred. No. 6.6e-39;
0; Mismatches 137;
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RESULT 26
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Best Local
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13-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, compared to natural MSP-1_19. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is the MSP-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface
malaria
            Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; plasmodium falciparum; malaria; vaccine; immunity; epitope; s
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                                                    PfMSP1(p19)S coding sequence.
                                                                                25-MAR-1998
                                                                                                                                     AAT80404 standard;
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99US-0311817.
99CA-2271451.
                                                                                                                                       DNA;
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77.28;
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Pred. No. 3.7e-38;
""sematches 71;
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Plasmodium vivax.

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Best Local Similarity
Matches 226; Conserv
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence encoding a chimeric protein comprising nucleotides encoding amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to the nucleotide sequence encoding the 19 kD C-terminal fragment (p19) of MSP-1 from Plasmodium falciparum. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                            4643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant protein containing Plasmodium merozoite surface protein-l p42 fragment - useful in antimalarial vaccines, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnwell JW,
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(UYNY ) UNIV
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                                                                                                                                                      101
                                                                                                                                                                           TGAACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCA 4642
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DB; AAW22592.
AGTGCGTGGAGAACCCCAAACCCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATG
                                                                                       GACACTTGGACGAGAGAGGAGGGTGTAAATGTCTGCTGAACTACAAACAGGAGGGCGACA
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/product= PEMSP1(p19)S
/note= "sequence contains 2
/the 3' end"
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58..381
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1..387
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                                                                                                                                                                                                                                                                                                                             116 A; 94 C;
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                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                        52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frame stop codons
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                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                  387;
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RESULT 27
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                                                                                                                                                                                                                                                                                                                                      Key
                                   Recombinant protein of fragment - useful in
                                                           WPI; 1997-425033/39
P-PSDB; AAW36102.
                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                           Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                 Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       PfMSP1(p19)S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4823
              Disclosure; Fig 1C;
                             purification
                                                                                 Barnwell JW,
Roth C;
                                                                                                      (INSP ) INST
(UYNY ) UNIV
                                                                                                                              14-FEB-1996;
                                                                                                                                            14-FEB-1997;
                                                                                                                                                           21-AUG-1997
                                                                                                                                                                         W09730158-A2
                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGC 4860
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                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax
                                                                                                       NEW YORK STATE
                                                                                                               PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                       Longacre-Andre
                                                                                                                              96FR-0001822
                                                                                                                                             97WO-FR00290
                                                                                                                                                                                                                                             /note=
97..102
                                                                                                                                                                                                                                                                                                             /product= PfMSP1(p19)S
/note= "sequence"
                                                                                                                                                                                                                103..381
                                                                                                                                                                                                                                                                                  /*tag=
58..381
                                                                                                                                                                                                                                                                                                  1..57
                                                                                                                                                                                                                                                                   /*tag=
1..96
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                             /note= "sequence
                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                    containing the n anti-malarial
             85pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                    "sequence
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                                                                                         Mendis
                                     merozoite vaccines,
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                                     diagnosis
                                           surface
                                                                                                                                                                                                Ъ.
                                                                                                                                                                                                                             generated restriction
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                                                                                                                                                                                                                                                                                                                frame
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                                    protein-1 p19
is and protein
                                                                                                                                                                                                                                                                                                                stop codons
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This is the nucleotide sequence encoding a chimeric protein comprising

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RESULT 28
AAD22459
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Best Local :
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The invention relates to a variant DNA sequence useful in DNA vaccines The DNA sequence encodes a naturally occurring protein such as C3d white by virtue of third base redundancy and other variations permissible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotides encoding amino acids 1-32 of the plasmodium vivax merozoite surface protein 1 (MSP1) linked to the nucleotide sequence modding the 19 kD C-terminal fragment (p19) of MSP-1 from plasmodium falciparum. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                         Novel variant DNA sequence useful in DNA vaccine, encodes occurring protein and comprises a sequence non-identical toccurring DNA sequence encoding the protein -
                                                                                                                                                                                                                                                                               WO200177324-A1
                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                C3d;
                                                                                                                                                                                                                                                                                                                                                                   Plasmodium
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                                                                                                                             WPI; 2002-010909/01.
                                                                                                                                                     Steward
                                                                                                                                                                             (ADPR-)
                                                                                                                                                                                                     08-APR-2000;
                                                                                                                                                                                                                            09-APR-2001;
                                                                                                                                                                                                                                                      18-OCT-2001
                                                                                                                                                                                                                                                                                                                                          pUC105-01 vector; immunostimulant; vaccine; immunisation; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    AAD22459
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD22459 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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                                                                                                                                                                                                                                                                                                                               immune
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                                                                                                                                                     Cox VF;
                                                                                                                                                                                                                                                                                                                             response;
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                            2001WO-GB01599
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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81.3%;
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                                                  87pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                insert in pUC105-01 vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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to naturally
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RESULT 29
AAD22460
QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 230; Conserv
                                                                                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into a human or animal by administering the pharmaceutical composition in to the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is plasmodium falciparum prMSP1.19 insert in pUC105-01 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4705
                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4585 AACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGG
          WO200177324-A1
                                                         misc_feature
                                                                                               mat_peptide
                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                    Chimeric -
                                                                                                                                                                                                                                                                                                                 PfMSP1.19-human C3d3 DNA coding sequence from
                                                                                                                                                                                                                                                                                                                                          12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                           AAD22460
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                                                                                                                                                                                                                                                                              immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AACATTGCCCAACACCAATGCGTTAAGAAGCAATGTCCACAAAACTCCGGATGTTTCAGA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGTTGAGAACCCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGGACGAGAGAAGAATGTAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGCACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGTTACTTGCGAATGTACTAAG
                                                                                                                                                                                                                                                                              response;
                                                                                                                                                                                                                                                                                       immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 BP; 94 A;
                                                                                                                                                                                                                           Homo sapiens:
Plasmodium falciparum
Unidentified!
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                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                          /partial
                                                           /product=
                                  /*tag=
/note=
                                                                                                 /*tag=
73..3147
                                                                                                                                                /product= "Human C3d3-PfMSP1.19 protein"
/note= "CDS does not include stop codon"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                          nulant; vaccine; immunisation;
pVK104-01 vector; ds.
                                                                                    /*tag=
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                                                                                                                                                                                         ..3147
                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                  "Antigen
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                                                                      "Mature
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                                   sequence
                                                                        human C3d3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
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                                                                        protein"
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                                                                                                                                                                                                                                                                                                                 pVK104-01 vector.
                                                                                                                                                                                                                                                                                          therapeutic; C3d,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4873
                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULF 30
AAD22461
ID AAD22
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Best Local S
Matches 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into a human or animal by administration the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is plasmodium falciparum PfMSP1.19-human or animal. The present sequence is plasmodium falciparum PfMSP1.19-human or animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                              12-FEB-2002
                                                                                                     AAD22461;
                                                                                                                              AAD22461 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                        4585 AACATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGG 4644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3147 BP; 869 A; 754 C; 834 G; 690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a variant DNA sequence useful in DNA vaccines. The DNA sequence encodes a naturally occurring protein such as C3d which by virtue of third base redundancy and other variations permissible within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA requence according that protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 66-68; 87pp; English.
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                                                Human C3d3 DNA-PfMSP1.19 coding sequence from pVK104-02 vector.
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                            Human;
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                                                                                                                                                                                                        CCCGACTCCTATCCACTCTTCGACGGGATTTTTTGCTCCAGCTCTAATT
                                                                                                                                                                                                                                                                                                                                                       CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                                                                                                                                                                                         AAGTGCACCGAAGAGACTCTGGTTCTAACGGAAAGAATTACTTGCGAATGTACTAAG
                                                                                                                                                                                                                                                                                        TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                          AACATTGCCCAACACCAATGCGTTAAGAAGCAATGTCCACAAAACTCCGGATGTTTCAGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-010909/01.
                                                                                                                                                                                                                                                                  AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAG
                                                                                                                                                                                                                                                                                                                  TGCGTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT 4764
                                                                                                                                                                                                                                                                                                                                           CATCTGGACGAGAGAAGAATGTAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding sequence from vector pVK104-01.
             immunostimulant; vaccine; immunisation; therapeutic; C3d;
response; pVK104-02 vector; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                            (first
                                                                                                                              DNA;
                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 194.6; DB
Pred. No. 9.9e-37
0; Mismatches 5
                                                                                                                              ВP
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Chimeric - |
Chimeric - |
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                                                                                                                                                                                                                                                                         4585 AACATCTCCCCAGCACCAATGCGTGAAGAAAACAGTGCCCCCCAGAATAGCGGCTGTTTCAGG 4644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              within an amino acid codon, is non-identical to the naturally occurring DNA sequence encoding that protein. The DNA sequence is useful in a DNA immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA sequence encoding a naturally occurring protein into a human or animal by administering the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is Plasmodium falciparum PfMSP1.19-human
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4765 AAATGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAAATCACATGCGAGTGTACTAAG
                                                                                                                                                                                                                                                  2845
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3147 BP; 869 A; 754 C; 834 G; 690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a variant DNA sequence useful in DNA vaccines. The DNA sequence encodes a naturally occurring protein such as C3d which by virtue of third base redundancy and other variations permissible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to naturally occurring DNA sequence encoding the protein .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C3d3 DNA coding sequence from vector pVK104-02.
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                                                                                                                                                                     AACATTGCCCAACACCAATGCGTTAAGAAGCAATGTCCACAAAACTCCGGATGTTTCAGA
                                                                         TGCGTGGAGAACCCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-010909/01.
                                             TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
                                                                                                                                                 CATCTGGACGAGAGAAGAATGTAAGTGTCTGTTGAACTACAAGCAGGAAGGTGATAAG
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                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Unidentified
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                                                                                                                                                                                                                                                                                                                                                Conservative
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/product= "
2845..3142
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73..3147
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/note= "CDS does not include stop codon"
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Pred. No. 9.9
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RESULT 31
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                                                             sequence encoding a naturally occurring protein into a human or animal by administering the pharmaceutical composition into the human or animal, where the administration results in a therapeutic effect on the human or animal. The present sequence is Plasmodium falciparum PfMSP1.19 mutant DNA used in the exemplification of the invention.
                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                       Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to naturally occurring DNA sequence encoding the protein -
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                                                                                                                            immunisation vector to encode one or more naturally occurring human or non-human proteins with immunomodulatory properties. The DNA sequence is useful for inducing an immune response to an antigen in a human or animal. A pharmaceutical composition is useful for introducing a DNA
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by virtue of third base redundancy and other variations permissible
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                                       Sequence
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MSP1.19 gene; mutant; ds.
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 Local Similarity
                                                                                                                                                                                                                                       invention relates to a variant DNA sequence useful in DNA vaccines
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88..90
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/note= "Mutation
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78.9%;
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191.4; DB 2
No. 1.8e-36;
                                       74 T; 0 other;
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Chimeric
      Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to naturally occurring DNA sequence encoding the protein
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                                                  WPI; 2002-010909/01
                                                                                                                08-APR-2000; 2000GB-0008582
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                                                                   sig_peptide
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                                         mat_peptide
                                                                                                                                                                                                                                       immune
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                                                                                                                                                                                                                                    response;
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                                                                                                                                                                                Unidentified
                                                                                                                                                                                          Homo sapiens.
Plasmodium falciparum
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nilarity 78.9%;
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               C3d3-PfMSP1.19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel variant DNA sequence useful in DNA vaccine, encodes naturally occurring protein and comprises a sequence non-identical to natural occurring DNA sequence encoding the protein -
                                                                                                                                                                                                                                                                                                                                                             2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C3d3 DNA coding sequence from vector pVK104-04.
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                                                                                        CCCGACTCCTATCCACTCTTCGACGGGATTTTTTTGCTCCAGCTCTAATT 4873
                                                                      CCAGACTCTTACCCTTTGTTCGATGGAATCTTCTGTTCTTCCTCTAACT
                                                                                                                                            AAGTGCACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGATTACTTGCGAATGTACTAAG
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                                                                                                                                                                                                                 TGTGTTGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCT
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0; Mismatches
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Chicken
                        Chicken leucocytozoan; immunisation; vaccinat:
                                                           Chicken leucocytozoan DNA encoding immunogenic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of antigens of Plasmodium species, esp. recombinant DNA methods giving polypeptide(s) against malaria or for diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibodies against the malaria antigen
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leucocytozoan
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/label= malaria antigen
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                                     1mmunogen;
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Pred. No. 6.8e-19;
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                                    recombinant vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT05868 encodes a chicken leucocytozoan immunogenic proteir or a fragment of it can be used in a recombinant vaccine to against chicken leucocytozoan disease. The DNA is used in a and operatively linked to an expression regulatory sequence
                                                                                                                                                               2038
                                                                                                                                                                                                                1978
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                                                                                                                                                                                                                                                                                                                                                                1798 CATGAAGAAGAAAAAGAAGAAGTAACACATGAAGAAAAAAGAAAAAGAAGAAGAAGCATGAAGAA 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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(KITA ) KITASATO KENKYUSHO SH.
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nes 563; Conserv
                                    TCCCCTTGAGCTGGAGTACTACTTGAGAGAGAAGAATAAGAATATAGACATCTCCGCCAA 1181
                                                                            GAAAGAGATCAAAGAGATĆGCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGA 1121
                                                                                                                                      CAACTCTGGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGA 1061
                                                                                                                                                                                      GAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGC
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            ACACATGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAGAAGAAAAAGTAATACAT
                                                            ATAGAAAAAGAAGAAGCATGAAGAAGTAATACATGAAGAAGAAAAAAAGAAGAAGTAACACAT
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                                                                                                                                                                                                                                                                                      against chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 6-9;
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use as insert in a recombinant vaccine
against chicken leucocytozoan disease"
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              Plasmodium vivax
                                                 antigen-antibody
                                                           Merozoite surface
                                                                                    Plasmodium vivax merozoite surface
                                                                                                            07-SEP-2001
                                                                                                                                    AAS00655;
                                                                                                                                                          AAS00655 standard; DNA; 618
                                                                                                                                                                                                                       AAAGTAACACATGAAGAAGAAGAA
                                                                                                                                                                                                                                                                      GAAGAAGAAGAAAAAGTAACACATGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAGAA
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                                                 composite;
                                                           protein;
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                                                           ,malaria; blood;
                                                Enzyme Linked
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                                               Immunosorbent Assay;
                                                           serum; diagnosis; vaccine;
                                                                                  C-terminal region
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Best Local Similarity
Matches 234; Conserva

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4488 TCTCCTGACCAAGTTTCTGTCCACTGGCATGGTGTTCGAAAACCTCGCCAAAACAGTGCT 4547

TCTTCTGGAAAAATTGATGAAATCAAAATTGATTAAAGAAAAACGAGTCCAAGGAAATATT

248

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ATCCCAGCTGCTAAATGTGCAAACTCAGTTATTAACTATGAGCTCCGAGCACACATGTAT

4848

4907

536

CTCTAACGGAAAGAAATCACATGCGAGTGTAATTAAGCCCGACTCCTATCCACTCTTCGA 4847

-AATAAAATCGTCTGTAAATGTACAAAAGAAGGTTCTGAGCCACTCTTTGA

369

CTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGGAAGACAGCGG GAGATGCTTGTTAAACCTTTAAAGAAGAAGGCGGCAAGTGTGTGCCCAGGATCGAATGTGAC

TTGTAAGGATAACAATGGTGGTTGTGCCCCCTGAAGCTGAATGTAAAATGACGGACAGC--

486

309

GAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCATCTGGACGAGCGCGAAGAGTG 4667

CAAGTGTCTCCTGAACTACAAACAAGAAGGAGATAAGTGCGTGGAGAACCCAAACCCTAC AGACACCAATGTGCCTGATAATGCAGCCTGCTATAGGTACTTGGACGGAATGGAAGAATG

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249

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Query Match
Best Local :
                                                                             The sequence represents a DNA encoding the Plasmodium vivax merozoite surface protein (MSP) C-terminal region. The C-terminal region of the merozoite surface protein has a strong antigenicity in malarial diseases. For diagnosis of malaria, recombinant proteins with enhanced antigenicity, obtained by addition of fusion proteins to surface protein C-terminal regions, can be reacted with serum or blood of a Plasmodium infected patient. Antigen-antibody composites will be formed, and these recombinant antigens provide a guick and reliable diagnosis of malaria, with good sensitivity and selectivity.
                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-1999;
25-APR-2000;
20-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                      Sequence
                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                      WPI; 2001-343809/36
P-PSDB; AAU00669.
                                                                                                                                                                                                                                                                                                                                                Park H;
                                                                                                                                                                                                                                                                                                                                                                          ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200136587-A2
                                                                                                                                                                                                                                                           gene encoding merozoite surface protein of Plasmodium vivax, \boldsymbol{u}_{\boldsymbol{i}} producing protein for diagnosis of malaria and for vaccination
                                                                                                                                                                                                                                   <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                          HUMANBIO CO LTD
                                                      618 BP; 207 A; 114 C; 147 G; 150 T; 0 other;
                                                                                                                                                                                                                                   Page 23; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   99KR-0050616.
2000KR-0022041.
2000KR-0027305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-KR01302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partial
/product= "P. vivax merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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            2.1%;
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"No start or stop codon"
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Score 104; DB 22;
Pred. No. 4.9e-15;
D; Mismatches 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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RESULT 37
AAT93729
ID AAT9:
                                                                                                                                                                                          CC immunogenic merozoite surface antigen-1 peptide that is used in a malaria CC immunogenic merozoite surface antigen-1 peptide (MSA-1), and a CC mammalian signal (AAW34595-96) and/or anchoring sequence encoding an CC The signal peptide contains 3 regions, a first or c region at the CC carboxy end of the peptide which serves as the cleavage site for a CC signal peptidase enzyme, a second or h region which is N-terminal to the c region (and highly hydrophobic), and a third region or n region. CC the c region (and highly hydrophobic), and a third region or n region. CC anchor peptides), particularly in the form of recombinant vaccinia crirus, are used in vaccines to prevent or treat malaria caused by Plasmodium falciparum. The chimeric proteins can also be used in vaccines con generating a long-lasting immune response (humoral and/or cell-mediated) against the merozoite form of the parasite, in tumans or other animals.
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Matches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT93729 standard;
                                                                                                                                                                        Sequence 165
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 19; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davidson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding signal peptide 2 which is used in a malaria vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT93729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria vaccine - comprises expression vector expressing fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEOU ) UNIV GEORGETOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lmmune response; humoral; cell-mediated; merozoite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 TTTCCT 602
                                                                                                                             Local Similarity
61
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             ACCCACGAATCCTATCAGGAGCTGGTTAAGAAACTGGAAGCTTTGGAAGATGCCGTCCTT 129
                                                                       ATGAAAATCATTTTCCTCCTCTGTTCATTTCTGTTTTTTATCATCAATACTCAGTGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-393372/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCCT 4913
                                                        ATGAAGATCATATTCTTTTATGTTCATTTCTTTTTTTTATTATAAAATACACAATGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGTTTTCTGTAGCTCCTCCAGCTTCCTAAGCTTGTCCTTCTTGTTGCTCATGTTGCT
ACACATGAAAGTTATCAAGAACTTGTCAAAAAACTAGAAGCTTTAGAAGATGCAGTATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant vaccinia virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EA,
                                                                                                                Conservative
                                                                                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US01395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malaria; vaccine;
                                                                                                                                                                        65
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                                                                                                                                                                       A; 16 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                            2.0%;
75.2%;
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                                                                                                               0;
                                                                                                                            Score 99.4
Pred. No.
                                                                                                                                                                       24 G; 60 T; 0 other
                                                                                                                Mismatches
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Plasmodium falciparum:
                                                                                                                                           99.4;
                                                                                                                               3.3e-14;
                                                                                                                                           DB 18;
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                                                                                                                Indels
                                                                                                                                        Length
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                                                                                      stage major merozoite surface antigen (MSP-1) immunogenic peptide, cpl15MSP-1 (see AMS0527). The invention relates to a malaria vaccine comprising an expression vector, preferably a defective venezuela equine encephalitis (DVEE) viral vector system, which expresses pl15MSP-1 or its immunogenic fragment raises a humoral and/or cell-mediated response to the erythrocytic merozoite malaria antigen, protecting the patient from a subsequent malaria infection. The DVEE viral vector system continues to express antigen in the patient for a pariod of days, months or even years. Inclusion of a signal peptide and/or an anchor peptide sequence in the p115MSP-1 antigen produces an immunogenic response which is significantly (i.e. at least about 2 times and as much as 100 times or more) greater than the immunogenic response produced by p115MSP-1 which does not contain the signal or anchor peptide sequence.
   Matches 124;
                                                               Sequence 165 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel vaccine for immunizing mammals against plasmodium falciparum infection, comprises a viral vector system expressing protein corresponding to specific domain of major merozoite surface protein of plasmodium falciparum,
                                                                                                                                                                                                                                                                                                                           The present sequence is that of DNA encoding a typical mammalian signal peptide sequence (see AAM50529). Such a signal peptide sequence may be incorporated into chimeric proteins of the invention that also include the plasmodium falciparum erythrocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merozoite surface antigen; 1; MSP-1; pl15MSP-1; antigen; immu malaria; vaccine; Venezuela equine encephalitis virus; DVEB; vector; immunisation; Plasmodium falciparum; signal peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 20; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAM50529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) UNIV GEORGETOWN.
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No. 3.
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RESULT 39
ABL26543
ID ABL266
XX ABL266
XX ABL26
XX Drosc
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XX Ph W0200
XX Ph W0200
XX Ph W0210
XX PR 11-U
XX PR 11-U
XX PT Vente
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                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016176-ABL30511).
                                          4730
                                                                               1307
                                                                                                                        4670
                                                                                                                                                                                                                                                                        Sequence 5688 BP; 1925 A; 1719 C; 1147 G; 897 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 31102; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
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                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                          ATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACTTGATTAACCCCT 1306
                                                             TCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAATTGAGAGTGACAAGAAAA 1426
                                      AAAATAACATCCAAAGCCAGAATGAGAACAACAACCAAAATAACATCCAAAGCAAGAATC
                                                                                                                    ATGAGAACAGCAACCACAATAACAACGAGAACAACCATCCAAAGCAAGAATGAGAACAACC 4729
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2000US-0614150
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Pred. No. 6.4e-10;
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11-JUL-2000;
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               ACAACCAGAACACCATCCAAAGCAGAAATCAGAACATGCAAAGCAGAAATCAAAACAACA
                                      TTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCG
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                                                                  ACATCCAAAGCAAGAATCAGAACAACACCCAGAACAGCATCCAAAGCAAAAATCAGAACA
                                                                                          AGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGT
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                                                                                                                                                                                                                  AAQ87587-89 encode polypeptides having a whole or partial epitope of a structural protein of Leucocytozoan protozoa (see AAR70491-93). The polypeptides and DNA encoding them are useful in the production of vaccines for the treatment of leucocytozoanosis of fowl.
                                                                                                                                                                                                                                                                                                            Claim 1; Page 12-14; 20pp; Japanese
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AGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTAT
                                    ATATTGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGA
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                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
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                                                                                                                                                                                                                                               neurofibromatosis;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
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for diagnosis and treatment
cytosine methylation •
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01-SEP-2000;
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                                       CTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGAC
                                                                                                                                            CCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCC
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                                                               GTACCCTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGA
                                                                                          CTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGAGAAGAATAAGAATATAGACAT
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RESULT 43
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New recombinant multivalent protein deriyed from more than one stage in
                              WPI; 2001-514557/56
P-PSDB; AAB85697.
                                                                                                  31-JAN-2000; 2000US-0179213
                                                                                                                                          02-AUG-2001.
                                                                                                                                                             WO200155181-A2
                                                                                                                                                                                                                                  Plasmodium vivax.
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                          Synthetic gene ViVac
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                                                                                                                                                                                                                                                                                                                                   AAH47054;
                                                                                                                                                                                                                                                                                                                                                                                                     Lai AA,
                                                                                                                      29-JAN-2001; 2001WO-US02937
                                                                                                                                                                                                                                                                                                                                                     AAH47054 standard; DNA;
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                                                           Xiao L,
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/product= "ViVac1p"
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comprising antigenic determandity a life cycle of Plasmodium
          determinants
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by plasmodium parasites, such as P. vivax. (I) is especially useful in the treatment, prevention and reduction of malarial infection, as research or diagnostic reagents for the detection of Plasmodium species in a biological sample, and for conferring immunity against multiple stages of the malarial parasite. The antibodies produced are useful for the detection or measurement of antigenic epitopes derived from one or more stages in a life cycle of a parasite, particularly P. vivax. The vaccine comprising the recombinant proteins, is cost-effective, health-promoting intervention for controlling, preventing or treating the incidence of malaria. The present sequence represents a synthetic gene vivacle encoding the recombinant protein vivacle, a multivalent and
                                                                                                                                                                                                                                                                                                                                                                               5404
                                                                                                                                                                                                                                                                                                                                                                                                                                            5344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             than one stage in a life cycle of a Plasmodium vivax parasite. (I) is useful as a vaccine for stimulating an immune response, specifically a protective immune response that confers increased resistance to infection
                                                           CDS
                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5164 AGCTCCGAGCACACGTATAGACACCAATGTGCCTGATAATGCAGCCTGCTATAGGTAC
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                                                                                                                                                     protozoacide;
                                                                                                                                                                                                   Synthetic gene ViVac2
                                                                                                                                                                                                                                   29-OCT-2001
                                                                                                                                                                                                                                                                   AAH47055;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multistage vaccine against P. vivax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to recombinant multivalent proteins (I) that stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
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                                                                                                        Plasmodium
                                                                                                                                                                       Multivalent
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                                                                                                                                                                                                                                                                                                                                                                                                         GACTCCTATCCACTCTTC
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                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                        vivax.
                                                                                                                                                                    protein; immune response; Plasmodium vivax; parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                        vaccine;
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                          /rtag= a
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                                                                        Location/Qualifiers
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                                                                                                                                                                                                   encoding recombinant protein ViVac2p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038 C; 1389 G; 1150 T;
                           "ViVac2p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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Pred. No. 7
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                                                                                                                                                        recombinant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                 AAA70099
                                                 AAA70099 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to recombinant multivalent proteins (I) that mulate an immune response to Plasmodium vivax. (I) comprises an
                                                                                                                                                                                                                                                                                                                                           TTGGACGGAACGGAAGATGGAGATGCTTGTTAACCTTTAAAGAAGAAGGAGCGCAAGTGT
                                                                                                                                                                                                                                                                                              GTGGAGAACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAA
                                                                                                                                                                                                                                                                                                                                                                              ATCTCCCAGCACCAATGCGTGAAGAAACAGTGCCCCCAGAATAGCGGCTGTTTCAGGCAT 4647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-514557/56
                                                                                                                                         CCCTTTGAGGGAGTTTTC
                                                                                                                                                                         GACTCCTATCCACTCTTC
                                                                                                                                                                                                                                         TGCACCGAGGAAGACAGCGGCTCTAACGGAAAGAAATCACATGCGAGTGTACTAAGCCC
                                                                                                                                                                                                                                                                           GTGCCAGCATCGAATGTGACTTGTAAGGATAACAATGGTGGTTGTGCCCCTGAAGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTCCGAGCACACGTATAGACACCAATGTGCCTGATAATGCAGCCTGCTATAGGTAC
                                                                                                                                                                                                       TGTAAAATGACGGACAGCAATAAAATCGTCTGTAAATGTACTAAAGAAGGTTCTGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 45-48; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xiao L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2077 A; 1168 C; 1534 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        against P. vivax.
                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%;
                                                                                                                                                                       4845
                                                                                                                                       6084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72.4; DB 22; Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1322 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                           Also described are: (1) numbertide sequences (11) encoding (1); and (2) (2) vaccines against P. falciparum infection comprising (1) or (11). (2) (1) and (11) are useful for the development of vaccines against CC (1) and (11) are useful for the development of vaccines against CC P. falciparum infection. (1) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1), are useful in the detection of infection with P. falciparum. Furthermore, (1) (especially when they are rifins or secreted or membrane proteins) CC (1) (especially when they are rifins or secreted or membrane proteins) CC (1) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC infection, or they can be used to identify drug resistance in the p. falciparum CC infection, or they can be used to identify drug resistance in the composition of proteins encoded by it will help to expand CC understanding of parasite biology, a process hampered by the CC complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many C parts of the world, and there is a pressing need for vaccines and new AMATORR to AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMATORR and AMAT
                                                                                                     Query Match
                                                        Matches
  1610 AGAATTCTAAGCATAATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATT 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in th diagnosis of P.falciparum infection - \frac{1}{2}
                                                                                                                                                           Sequence 3579 BP; 1904 A; 398 C; 552 G; 725 T; 0 other;
                                                                                                                                                                                                        and protein sequences given in the present invention, specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 457-458; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum; antimalaria; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum chromosome 2 related DNA sequence
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                                                                                                                                                                                                                                                           drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VENT/) VENTER J
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carucci D,
                                                        Conservative
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                                                                                1.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 2; human malaria parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardner M,
                                                     0;
                                                                                                        Score 70.6;
                                                                                Pred. No.
                                                        Mismatches
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                                                                                  1.6e-06
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XX O1-S
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The meth is used: (1), for diagnosis and/or prognosis of side effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphi SNP; cell differentiation; ds.
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therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABG13410-ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                              Sequence
                                                                                                       disclosure of the invention.
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Score 70.2;
Pred. No. 8
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Query Match Best Local : Matches

Local Similarity

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AACAATACGAATAACGATAACAATCAAAATAACGATAAC
                                     AAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATC
                                                                               AACGATAACAATCAAAATAACGATAACAATCAAAATAACGATAACAATACGAATAAAAAT
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RRESULT 47
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XX BAQ4
XX BAQ4
XX BQ7
DT 12-J
DT 0119
XX O119
XX Huma
KW drug
KW gast
KW gast
KW SNP;
XX Homc

Oligonucleotide

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cytosine

methylation

SEQ IJ

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(first

entry)

standard;

DNA;

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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism snp; cell differentiation; ds.

polymorphism;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of CC is used: (1) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC systems etc., particularly by detecting mutations or single nucleotide cystems etc., particularly by detecting mutations or single nucleotide cytoes and for investigating call differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously.

CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the control of the invention.
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Best Local S
Matches 268
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                     CGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTAT
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                                 TACTCTTACAAAGTGGAGAAACTGACACCACATAATACCTTTGCA---TCCTATGAGAAT 1614
                                                                                                            GATTCCAAATTCAACAATAACATCGACCTGACCAACTTCGAGAAAATGATGGGAAAACGG
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Mismatches 308;
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ARESULT 48
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                       cc methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CDNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one come commence common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common 
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
.6e-06;
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91

Query Match
Best Local Similarity
Matches 412; Conserv

Conservative

0;

Score 68.6; DB 24; Pred. No. 2.6e-06; 0; Mismatches 524;

DB 24;

Length Indels

969;

9:

Gaps

2

1.48;

690 TCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAAGAATAAGAA 749

31 TCTTACTAAAATTACTAATAAAAACGAATACGAATATAAAATACGAATAAAAATACTAATAA

90

750 GACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATAA 809

AACGAATAAAAATACGAATAAAAATACTAATAAAACGAATAAAAATACGAATAAAAATAC

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RESULT 49
AB039491
ID AB0399
XX AB039
XX AB039
XX Oligo
XX Human
KW Grug;
XX Grad
OS Homo
XX WO200
XX O7-M2
XX O7-M2
XX O7-M2
XX O7-M2
XX O7-M2
XX O1-SI
PF 01-SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method
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gastrointestinal; respiratory system;
SNP; cell differentiation; ds.
                                                    ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate t method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                            systems etc., particularly by detecting mutations or single nucleotide polymorphisms (\mathsf{SNP'S}); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
                                                                                                                                                                                                                                                                                                                           is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
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05-SEP-2000; 2000DE-1044543
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   969 BP; 645 A; 93 C; 54 G; 177 T; 0 other;
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RESULT 50
AAH47056
ID AAH47
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AC AAH47
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DT 29-OC
XX
Synth
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KW proto
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OS Synth
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             Synthetic
                                       Multivalent protein; immune response; Plasmodium vivax; parasite; protozoacide; vaccine; malaria; recombinant; ViVaclp; ds.
                                                                                 Synthetic gene
                                                                                                            29-OCT-2001
                                                                                                                                        AAH47056
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RESULT 51
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ID AAA65
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AAA65171 standard;

DNA;

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AAA65171;

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stimulate an immune response to Plasmodium vivax. [1] comprises antigenic conterminants, fragments or conservative substitutions, derived from more than one stage in a life cycle of a Plasmodium vivax parasite. [1] is cuseful as a vaccine for stimulating an immune response, specifically a protective immune response that confers increased resistance to infection by Plasmodium parasites, such as parasite. It is especially useful in the treatment, prevention and reduction of malarial infection, as cresearch or diagnostic reagents for the detection of Plasmodium species in a biological sample, and for conferring immunity against multiple stages of the malarial parasite. The antibodies produced are useful for the detection or measurement of antigenic epitopes derived from one or correction for controlling, preventing or treating the recombinant proteins, is cost-effective, health-correction intervention for controlling, preventing or treating the controlling, preventing or treating the controlling, preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating the controlling preventing or treating 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5643 BP; 1584 A; 1197 C; 1503 G; 1359 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant multivalent protein comprising antigenic determinants derived from more than one stage in a life cycle of Plasmodium vivax, useful as a vaccine for treating, preventing and reducing malarial
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TTCTGAGCCACCCTTCGAGGGAGTTTTCTGTTCC
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Query Match
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            7690
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             AGACAACAACAAGACAAC
                                          AGAAAATGATGGGAAAAC
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                                                                                                                                                            ACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAAA
                                                                                                                                                                                         AGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory, ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fractor diagnosis and treatment
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01-SEP-2000;
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Best Local Similarity
Matches 249; Conserv
                                                        GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite; merozoite; diarrhoea; protozoacide; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that encoding the GP900 antigen which may be used in the production of anti-Cryptosporidium antibodies. These can be used for the prophylaxis, treatment, inhibition or retardation of a Cryptosporidium infection in humans or in animals such as calves. They can also be used for the detection and diagnosis of related
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Key
                           Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5163 BP;
                                                                                                                       ORF encoding a portion of Cryptosporidium parvum NINC isolate GP900
                                                                                                                                                       28-OCT-2000
                                                                                                                                                                                      AAA61849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 32; Pages 60-62; 89pp; English
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                                                                                                                                                                                                                                                                                                                                                            CAACAACAACAACAACAACAACAACAACAACTACCACGAAAACCAACAACAACAACAACAA 1154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                           parvum
Location/Qualifiers
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Pred. No. 0.00053;
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Best Local (
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29-MAY-1992;
03-APR-1995;
14-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the GP900 glycoprotein of the protozoan cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 or fragments thereof to a host to elicit anti-GP900 antibody production, and to a method of cryptosporidiosis treatment or prophylaxis comprising administration of anti-GP900 antibodies to an individual. Cryptosporidium parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and
                                                                                                                                                                                                                                                                                                   agriculture. GP900 fragments, fusion proteins and antibodies may also used for the diagnosis of Cryptosporidium parvum infections, and for t detection of the parasite in the environment. The present sequence represents the open reading frame (ORF) encoding a portion of the GP90 protein of the NINC isolate of Cryptosporidium parvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       competitively inhibit sporozoite or merozoite attachment or invasion, and are also useful for the generation of anti-GP900 antibodies. The antibodies also inhibit sporozoite or merozoite attachment/invasion and additionally inhibit the binding of GP900 ligands to GP900. GP900 proteins, fragments and antibodies may therefore be used to treat or
                                   4050
                                                                                                    3990
                                                                                                                                                                                                                                                                                                                                                                                      prevent cryptosporidiosis. Infection with Cryptosporidium is a common cause of diarrhoea in humans and causes life-threatening diarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in a cause of disease in animals, resulting in financial losses in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
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CGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACCTACGTTGTCAA 4049
                                 GGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTA 4109
                                                                                                                                     2000-422065/36.
)B; AAB11727.
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92US-0891301.
95US-0415751.
96US-0700651.
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Pred. No. 0.00053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                   The present invention relates to a method of detecting Cryptosporidium biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNA, or its variant, mutant or fragment. The method is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4470
                                                                                                                                      Detecting Cryptosporidium in biological and environmental samples and diagnosis of cryptosporidiosis involves, contacting the sample with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or RNJ
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                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                    Cryptosporidium
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Best Local
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                                                                                                                                 GP900; NINC isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; sporozoite;
                                                                                                                                                                      DNA encoding
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   3'UTR
                                                                                                Cryptosporidium
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                                                                                                                                                                                                                        AAA61848;
                                                                                                                                                                                                                                               AAA61848 standard; DNA; 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4050 GGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTA 4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5163 BP;
                                                                                                                       diarrhoea; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                      a portion of Cryptosporidium parvum NINC isolate GP900
                                                                                                                                                                                               (first entry)
                                                                                                parvum
/product= "Cryptosporidium parvum NINC isolate GP900"/note= "No start codon given in the specification" 5167..5318
                                                             1669..7182
                                                                         Location/Qualifiers
                                      /partial
                                                  /*tag=
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Pred. No. 0.
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                                                                                                                                                                                                                            Cryptosporidium parvum, DNA encoding it, G9900 fragments, and fusion CC proteins comprising GP900 fragments. The invention also relates to the CRYptosporidium parvum, DNA encoding it, G9900 fragments, and fusion CC groteins comprising GP900 or fragments thereof to a host to elicit anti-
CC GP900 antibody production, and to a method of cryptosporidiosis treatment CC individual. Cryptosporidium parvum GP900 and GP900 fragments are able to CC competitively inhibit sporozoite or merozoite attachment or invasion, and CC are also useful for the generation of anti-GP900 antibodies. The CC antibodies also inhibit sporozoite or merozoite attachment /invasion and CC antibodies also inhibit sporozoite or merozoite attachment/invasion and CC additionally inhibit the binding of GP900 ligands to GP900. GP900 CC proteins, fragments and antibodies may therefore be used to treat or CC cause of diarrhoea in humans and causes life-threatening diarrhoea in CC immunocompromised persons. Cryptosporidiosis can be contracted from CC contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in CC agriculture. GP900 fragments, fusion proteins and antibodies may also be
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01-JUN-1993;
29-MAY-1992;
03-APR-1995;
                                                                       detection of the parasite in the environment. The represents genomic DNA encoding a portion of the NINC isolate of Cryptosporidium parvum.
                                                                                                                                                                                              agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-422065/36
P-PSDB; AAB11727.
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93US-0071880.
92US-0891301.
95US-0415751.
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                                                                                                                      The present sequence the GP900 protein of
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Sequence 5318 BP; 1939 A; 1158 C; 890 G; 1331 T; 0 other;

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                     3990
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mes 249; Conserv
 CGTCTTGGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTCTAACTACGTTGTCAA 4049
                                          Conservative
                                                                                          1.2%;
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Q DЬ Qy

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TATCAAGGACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAA 4169

GGACCCATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTA 4109

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853

В

Query Match

Local Similarity

1:28;

Score 60.6; Pred. No. 0.

DB 24

Length

5318;

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RESULT 57
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XX ABT04
XX CTypi
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                                detecting and identifying individual Cryptosporidium isolates based on
the genetic characteristics, and for diagnosis of prior or concurrent
Cryptosporidium infection. The present sequence is a C. parvum coding
sequence used in the exemplification of the invention.
                                                                                                                                      The present invention relates to a method of detecting Cryptosporidium biological and environmental samples, and of diagnosing cryptosporidiosis. This involves obtaining a sample and contacting it
                                                                                                                                                                                                                                                                Detecting Cryptosporidium in biological and environmental samples diagnosis of cryptosporidiosis involves, contacting the sample wit Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DNA or
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Sequence
                                                                                                      with Cryptosporidium GP900, P68 or cryptopain antigen, antibody, DRNA, or its variant, mutant or fragment. The method is also useful
                                                                                                                                                                                                             Disclosure; Page 101-103; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000; 2000US-0588995
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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Local Similarity 42.28;
GAAGAATAAGAATATAGACATCTCCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAA 1211
                                                                                                                                                                                                TAAGTTCAACATAGATTCTCTCTTTACTGATCCCCTTGAGCTGGAGTACTACTTGAGAGA 1151
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RESULT 59
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                                           The sequence represents a DNA encoding a Plasmodium vivax merozoite surface protein (MSP). The C-terminal region of the merozoite surface protein has a strong antigenicity in malarial diseases. For diagnosis malaria, recombinant proteins with enhanced antigenicity, obtained by addition of fusion proteins to surface protein C-terminal regions, can reacted with serum or blood of a Plasmodium infected patient. Antigen-antibody composites will be formed, and these are detected by Enzyme Linked Immunosorbent Assay (ELISA). The recombinant antigens
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                      provide a quick and reliable diagnosis
and selectivity.
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25-APR-2000;
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                                                                                                                                                                                                                                                                             (HUMA-)
                                                                                                                                                                              gene encoding merozoite surface protein of Plasmodium vivax, \boldsymbol{u}_{\boldsymbol{\tau}} producing protein for diagnosis of malaria and for vaccination
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DB; AAU00668.
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Query Match Best Local Similarity

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; Patent No. 5766597
; GENERAL INFORMATION:
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                                                                                                                                             LENGTH: 5181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-257-073-10
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Best Local S
Matches 2912
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TELEFAX: (212) 840-0712
TELEX: 425066 CURTWS|
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                      FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07,
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,5(
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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COUNTRY:
ZIP: 100
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ATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTCTTTTACTGATCCCCTT 	GGGAACACCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAGGAGCACGAGAAAG 	AATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCAGGCAAGCTCT 	AAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAGAAGAATG 	GAAAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAACAGCTTGAA 	GAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAATAAGAATGCAACCAAGGAGG 	AATGTGGGAAAGATGGAAGATTATATTAAAAAGAATAAGAAG	TTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCTCTCGACAACATCAAGGAC 	GACGTTTGCGGCAATGACTATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAG 	ATCAATGAACTCCTGTACAAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTG 	ATGCTGACACTGTGTGATAACATTCATGGCTTCAAATATCTGATTGACGGTTACGAAGAG 	AACTATCTCCTCACTATCAAGGAGCTGAAGTÂCCCACAGTTGTTCGACCTCACTAATC	FAGCGATTCCG	CGAAGAACCAATCCATCTGACA	GCCTCCGGCGGCAGCGTGGCATCAGGTGGCTCAGTGGCAAGCGGCGGTTCCGGGAACAGT	TCTAAAGGGTCTGTGGCTAGCGGTGGCTCCCGGTGGGTCTGTGGCCTCTGGGGGTTCCGTC	GGGACGACTGGCACGGCCGTTACAACCAGCACACCCGGT	CGGATACAGCCTGTTCCAGAAGGAGAAGATGGTGCTGAATGAA	acacatgaaagttatcaagaacttgtcaaaaaactagaagctttagaagatgcagtattg
TTAAGTTCAA TTAAATTTAA	TGGACAAGAA TTGATAAGAA	AGATTAATGA AGATAAATGA	TACTGGAGAA TTTTAGAAAA	CCCAGTACGA	AGACCATAGA AAACAATTGA	ATATTAAAAA ACATTAAAAA	TCTTCGGATA	GTCAAATTCC GTCAAATACC	TGAATTTCTA	ATTCATGGCTT	AGCTGAAGTÁ AACTCAAATA	ACGCCAAGTC ATGCTAAÁTC	CTTTACCTCG	CAGGTGGCTC	GTGGCTCCGG	GGACGAGTGG	NAGGAGAAGAT NAGGAAAAAAT	TTGTCAAAAA
CATAGATTCT CATTGATAGT	CAAGAAGATA CAAAAAAATC	AATTAAGAAT AATTAAAAAT	GCGCATAGAC	CCTGTCCATC	CAAAAATAAG TCAAAATAAG	GAATAAGAAG AAATAAAACA	TCGCAAGCCT 	ATTCAATTTG	CTTCGACTTG	CAAATATCTG	CCCACAGTIG	CTACGCCGAC	TTCAAATACT	AGTGGCAAGC	TGGGTCTGTG	CACGGCCGTT	GGTGCTGAAT	ACTAGAAGCT
CTCTTTACTG TTATTTACTG	GAGGAGCACG GAGGAACACG	CCCCCACCGG	ACCCTCAAGA	TATAACAAAC TACAATAAAC	AATGCAACCA	ACCATCGAGA	CTCGACAACA TTAGACAATA	AAGATCAGAG	CTAAGGGCCA TTAAGAGCAA	ATTGACGGTT ATTGATGGAT	TTCGACCTCA	CTCAAGCACC	TCATCTGGTG	GGCGGTTCCG	GCCTCTGGGG	ACAACCAGCA	GAA GAAGAAGAAATT	TTAGAAGATG
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GAGAAGAAGAACATTAAAACTGAAGGACAGTCAGATAACTCCGACCCTTCCACAGAAGGA 2130	GAGAAGAAGAACA	2071	y Oy
	AAAAAAGAAGTAG	2098	D D
AAGAAAGAGATAGACAAACTGAAAGTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAA 2070	AAGAAAGAGATAG	2011	Qy
GTACCAAATATTTATAAACCACAAAATAAACCAGAACCATATTATTTAATTGTATTA 2097	CATGTACCAAATA	2038	Db
CATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGAACCATACTACCTCCTCATCGTACTC 2010	CATGTGCCGAATA	1951	Оу
	 ATAGAAGACTTA!	1978	Db
GATGAACTCAAGAAGACTCAACTCATTCTGAAGAACGTGGAGTTAAAACATAATATA 1950	ATTGATGAACTC	1891	Qy
TCCTTAGAAGTATATGATATTGTAAAATTACAAGTACAAAAAGTTTTATTAAATAAA	TCCTTAGAAGTAI	1918	Db
CTGGAGGTCTCCGATATTGTTAAAGTCCAAGTGCAGAAGGTGCTCCTCATGAACAAG 1890	ATCCTGGAGGTCT	1831	Оу
AGTGAAAACAAAATTCTAGAAAAAAATTTTAAAGGACTAACACATTCAGCAAATGCT 1917	AGTGAAAACAAA	1861	Db
GAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAG 1830	GATGAAGAACAGI	1771	Qy
TATACTTTGAAAACTGGCCTCGAAGCTGATATAAAAAAATTAACAGAAGAAATAAAGAGT 1860	TATACTTTGAAA	1801	Db
RATCTCATAAGTAAGATCGAAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAG 1770	AAGAATCTCATA	1711	Qy
TCATATCTTGAAGATTATTCTTTAAGAAAAGGAATTTCTGAAAAAGATTTTAATCATTAT 1800	TCATATCTTGAAC	1741	DЪ
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AATAAATTTTCATCCTCTAATAATTCTGTATATAATGTTCAAAAATTAAAAAAGGCTCTT 1740	AATAAATTTTCA	1681	Db
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AATCACACAAAAGAACAAAATAAAAAATTACTTGAAGATTATGAAAAAGTCAAAAAAAGGAT 1560	AATCACACAAAA	1501	рb
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4369 GTTTTAGCGAAATATAAGGATGATTTAGAATCAATTAAAAAAGTTATCAAAGAAGAAGAAAG 4428	Db
AATACAAGTCTGACCTTGACTCTATTAAAAAGTATATC	Qy
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ACTCCATCGACACCGATATCAATTTCGCTAATGATGTGCTGGGGTATTACAAG	Qy
4054 CCATACAAGTTCCTCAATAAAGAGAAGAGAGGGATAAATTTCTGTCTAGTTACAACTATATC 4113	Qу
TAGAATCTGATTTAATGCAATTTAAACATATATCCTCAAATGAATACATTATTGAAGAT 42	В
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ATCTTACAAGAAGTTCCTGCCTGAAGGAACAGATGTCGC3	Qy
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GAACAAGAACTACACGGCAATAGCCCAAGCGAGAATAATACAGACGTGAATAACG	Qy
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                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08195705 Patent No. 6420523
COUNTRI: ___
ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                    APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACCLOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
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                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: Davis Hoxie Faithfull Hapgood STREET: 45 Rockefeller Pl.
CITY: New York
STATE: N.Y.
COUNTRY: USA
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Hui, George
Barr, Philip
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APPLICATION NUMBER: US/08,
FILING DATE: 14-FEB-194
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
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4245
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEPHAX: 212-586-1461
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CLONE: flq5LFU
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LENGTH: 1219 base pairs
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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Pred. No. 7.3e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application Patent No. 5670367 GENERAL INFORMATION:
                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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CORRESPONDENCE ADDRESS:
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                                PRIOR APPLICATION DATA:
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CITY: Alexandria
                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: FILING DATE:
                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: MESSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCIDES, ANTIBODIES, PROTITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILLE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                            1045 CAGCCAAGCTCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 26-AU
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ER: 30472/114 IMMU
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EARLIER FILING DATE: 1995-04-03 NUMBER OF SEQ ID NOS: 15

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; ORGANISM: Cryptosporidium
US-08-700-651-1
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SEQ ID NO 1
LENGTH: 5163
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Best Local Similarity
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                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                            APPLICANT: Petersen, C
TITLE OF INVENTION: PE
TITLE OF INVENTION: FC
TITLE OF INVENTION: SI
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                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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                                                                                                                    NUMBER OF SEQUENCES:
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COMPUTER READABLE FORM:
                          STREET: 385 Sher
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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                                                                                                                             n, Carolyn

PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
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REGISTAN NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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Local Similarity 44.2%;
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                                                                                                                   TTACGAGAAGAGCAATGTGGAAGTTAAAATCAAGGAGCTGAACTACCTCAAAACAATCCA 4409
                                                                                                                                                                               CCACAACAACAACAACAACAACAACTACAACTACCAAGAAACCAACAACTACTACTA 1033
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CAACTACTACTACTACAACC
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                                                          CAACAACAACAACAACAACAACAACAACAACTACCACGAAAACCAACAACAACAACAA 1153
                                                                                     AGACAAGCTGGCAGATTTCAAGAAAATAACAATTTCGTCGGAATTGCAGACCTGTCTAC
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Pred. No. 1e-05;
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Sequence 3, Application Patent No. 6071518
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Best Local Similarity
Matches 249; Conserv
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LENGTH: 5318
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CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
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APPLICANT: NELSON, RICHARD,
APPLICANT: GUT, JIRI
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Pred. No. 1.1e-05;
0; Mismatches 314
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US-08-928-361B-3
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Best Local Similarity
Matches 249; Conserv
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INFORMATION FOR SEQ ID NO
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TOPOLOGY: li
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 30,518
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                               AGTGAACGACAAAATCGACCTCTTCGTAATTCACCTGGAGGCCCAAGGTCCTCAACTATAC 4349
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
ADDRESSEE: PETERS AVEnue, Suite 6
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
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TYPE: nucleic acid
STRANDEDNESS: double
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CLASSIFICATION:
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REGISTRATION NUMBER: 30,518
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                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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ATACAAGTTCCTCAATAAAGAGAAGAGGGATAAATTTCTGTCTAGTTACAACTATATCAA 4115
                                                                  GGAGAGCGACTTGATTCCCTATAAAGACCTGACCTCCTAACTACGTTGTCAAGGACCC 4055
                                                                                                     CCACGACAACTACAACCACAACCACCAACTACCAAGAAAACCAACAACAACAACAACAACAA 1153
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45.2%;
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THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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                                                                                                                                                                                            Score 58.8; DB 3; Pred. No. 3.2e-05;
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                                                                             US-08-928-361B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
Query Match
Best Local Similarity
Matches 216; Conserv
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                                                                                                                                                                                                         TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
ADDRESSEE: PATERS AVENUE, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1454
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                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4296
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1514 CTACTACTACAACCAAGAAACCAACAACAACTACCACTGCCACAACAACAACTACTAC 1571
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                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1274 CAACAACAACAACAACAACAACAACAACTACTACTACAACCACGACAACAACAACCACGA 1333
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                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                       TELEPHONE: 650-72-
TELEPHONE: 650-324-1678
                                                                                                                                 STRANDEDNESS:
                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                  LENGTH:
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                                                                                                                                                   nucleic acid
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                                                                                                                                                                  7334 base pairs
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                                                                                                                  linear
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12-SEP-1997
                                                                                            DNA (genomic)
                                                                                                                                 double
                   1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carolyn
                                                                                                                                                                                                         <u>..</u>
 Score 58.8; DE Pred. No. 3.8e-0; Mismatches
                                                                                                                                                                                                                                                                                  480.76-1(HV)
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                 DB 3;
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                                    Length 7334;
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US-08-938-105-2
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                                                                                                                  TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMÁTION:
NAME: CLOOK, WANNELM M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 35
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Leinwand, APPLICANT: Vikstrom,
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                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3182 CTACTACTACAACCAAGAAACCAACAACAACTACCACTGCCACAACAACAACTACTAC 3239
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CLASSIFICATION:
TOPOLOGY: 1
                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                              LENGTH:
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                                                        5661 base pairs ucleic acid
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                                                                                                                                      : (303) 863-9700
(303) 863-0223
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                      Linear
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TRANSGENIC MODEL FOR HEART FAILURE
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                                                                                                                                                                                                       3595-4
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                                                                                                                                                                                                                                                                                                                                                              Version
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                      INFORMATION FOR SEQ ID NO
                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,452A
FILING DATE: 18-JUL-1994
CLASSIFICATION: 455
CLASSIFICATION: 455
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Clarke, Adrienne E
TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2556
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SEQUENCE
                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                          TELEFAX:
                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                              NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                              TELEPHONE:
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  CHARACTERISTICS
                                           49617824
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5370 Manhattan Circle, Suite
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Du, He
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                          Sequence 25, Application Patent No. 5830747 GENERAL INFORMATION: APPLICANT: Chen, Chac
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LOCATION: misc_feature
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US-08-798-744-25
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TELEX: 49617824
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/2
FILING DATE: 18-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Plant Arabinogalactan Protein (AGP) Genes
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CITY: B
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REGISTRATION NUMBER: 34,40
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GENERAL INFORMATION:
                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/276,452A FILING DATE: 18-UUL-1994 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner,
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                                                                                                                                                                                                                       NAME: Caruthers, Jennie M. REGISTRATION NUMBER: 34,464 REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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NAME/KEY: CDS
LOCATION: '60..1442
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                                                                            STRANDEDNESS:
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VENTION: Plant Arabinogalactan
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LOCATION: 135..179
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                                                                                          TACACAGACAATGAGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAA 1391
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TION: 135..179
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Ala; 37 and 39 can also be undetermined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acids 27 to 36, 38, and 40 are identical to that in the obtained by direct microsequencing"
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corresponding to the peptide sequence by protein
microsequencing"
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (303)499-8080
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                                                NAME/KEY: misc_feature LOCATION: 135..179
OTHER INFORMATION: /not OTHER INFORMATION: and
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NAME/KEY:
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REFERENCE/DOCKET NUMBER: 27-91A
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                                                                                                                                                                                                                               segment"
                             /note= "Amino acids 27 to 36, 38,
and 40 are identical to that in the peptide
obtained by direct microsequencing"
                                                                                                                               /note= "Derived amino acid sequence
corresponding to the peptide sequence by protein
microsequencing"
                                                                                                                                                                                                                                                                                                                 obtained by PCR which does not overlap with the cDNA clone"
                                                                                                                                                                                                                                                                                                                                                  /note= "Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/276,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version
                                                                                                                                                                                                                                                  /note= "Predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of America
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; LOCATION: 135..179
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-798-744-24
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9510668 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                   APPLICATION NUMBER: FILING DATE: Herew
                                 CLASSIFICATION:
                                                                                                     SOFTWARE:
                                                                                                                                         COMPUTER:
                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                         COUNTRY:
                                                                                                                     OPERATING SYSTEM: WINDOWS
                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                           210 Lake Drive
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                                                                                                     WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                 James Eberwine
                                                                                                                                       IBM 486
                                                                                                                                                                                                                                                         Jane Massey Licata, Esq.
0 Lake Drive East, Suite
                                                                                                                                                                                                                                           Hill
                                                                                                                                                       DISKETTE,
                                                   Herewith
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Epitope Ordering and Protein
Restriction Mapping
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Ala; 37 and 39 can also be undetermined residues"
 08/294,133
                                                                   PCT/US95/10668
                                                                                                                                                       3.5 INCH, 1.44 Mb STORAGE
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Pred. No. 0.
                                                                                                                     FOR WORKGROUPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application PC/TUS9510668 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: PENN-0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-8488
                                                                                                                                                                                                     OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1417 GACAAGAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTATGAA 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1357 AAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGT 1416
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: August 22, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                           APPLICATION NUMBER: 08/294,133 FILING DATE: August 22, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: Single
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                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Herewi
                                                                                                                                                                                                                                                            COMPUTER:
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Local Similarity 52.6%;
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                                                                                                                                                                                                                                                                                                                                                       Cherry Hill
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                                                                               Jane Massey Licata
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                                                                                                                                                                                                                                                                                                                                                                       3: Jane Massey Licata, Esq.
210 Lake Drive East, Suite 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James Eberwine
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                                                                                                                                                                                              PCT/US95/10668
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Pred. No. 0.0085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6270771
GENERAL INFORMATION:
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Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DRUILHE, Pierre TITLE OF INVENTION: DESTINE SEQUENCES SPECIFIC FOR THE TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1417 GACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAAACGATATCACTAAAGAGTATGAA 1476
                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-FEB-1
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                                               SEQUENCE CHARACTERISTICS
                                                                                                               TELECOMMUNICATION INFORMATION:
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 STRANDEDNESS:
                                                                                                 TELEPHONE:
                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                 NAME: McGowan, Malcolm K.
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-NO
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States
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EDNESS: Single
             nucleic acid
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O. Box 1404
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Pred. No. 0
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RESULT 18
US-08-462-625-37
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Best Local Similarity
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                              APPLICATION NUMBER: US 00 FILING DATE: 24-NOV-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 9:
                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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DOCUMENT NUMBER: WO 9
FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                    STREET: P.O. BOX CITY: Alexandria
                                                                                                                CLASSIFICATION:
                                                                                                                                              APPLICATION NUMBER: US/08/462,625
                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                          Virginia
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                                                                                                                                                                                                                                                                          United States
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..954
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
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              ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGA 980
                                                        ACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAG
                                                                                      TCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAG
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ACTTGCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA
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RESULT 19
US-08-098-327E-34
; Sequence 34, Application US/08098327E
hatent No. 6270771
hatent No. This colour GENERAL INFORMATION:
APPLICANT: GUERIN
APPLICANT: DRUILH COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Do TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: STATE: CITY: Alexandria STREET: E: Virginia TRY: United 22313-1404 P.O. Box 1404 DRUILHE, Pierre GUERIN-MARCHAND, Claudine States PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEJOF STIMULATING THE T LYMPHOCYTES Doane, Swecker & Version Mathis #1. BEARING EPITOPES

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                                                                                                                                                                                                                                                                                                     US-08-462-625-34
                                                                                                                                                                                                                                                                                                                      RESULT 20
                                                                                                                                                                                                                                                                    Sequence 34, Application US/08462625 Patent No. 6319502
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                         APPLICANT: DRUILHE, Pierre
TITLE OF INVENTION: HEPATIC STACES OF P. FALCIPARUM BEARING
TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
                                                                                                                                                                                                              APPLICANT:
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PUBLICATION INFORMATION:
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 COMPUTER
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                                                                    STREET:
CITY: A
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                                 COUNTRY:
                                                   STATE:
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                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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22313-1404
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 READABLE
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                                                                                    P.O. Box 1404
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Pred. No. 0.022;
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                                                                                                 Patent No. 5559223
GENERAL INFORMATION:
                                                                                                                        Sequence 104, Application Patent No. 5559223
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
            APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
NUMBER OF SEQUENCES: 113
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PUBLICATION INFORMATION:
 CORRESPONDENCE
                                                                                    APPLICANT: Saverio Carl Falco
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FILING DATE: 24-NO
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CURRENT APPLICATION DATA:
APPLICATION MINISTER
                               3213
                                                                                                                                                     3093 TAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTCAACTC
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APPLICATION NUMBER: 07/7
FILING DATE: 9 August 19
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy Disk
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302
                                                                                                                        182 GATGAAGAAGCTCGAAGAGAAGATGAAGGTCATGGAGGAGAAGATGAAAAAGCTCGAAGA 241
                                                                                                                                                                                    122 GAAAAAGCTGGAAGAAAAGATGAAGGCTATGGAGGACAAGATGAAATGGCTTGAGGAAAA 181
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OTHER INFORMATION:
                                                                                                                                                                                                                                                   62 GAAACTGAAAGAGGAAATGAAGAAGCTCGAAGAGAAGATGAAGGTCATGGAGGAGAAGAT 121
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CELL TYPE: DH5 alpha
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les 122; Conserv
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LOCATION: 3..326
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                             AGCCGAGAT 3221
                                                                                        ACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAGAAGGA 3212
AGAGAAGAT 310
                                                            AAAGATGAAGGCAATGGAAGACAAAATGAAGTGGCTTGAGGAGAAAATGAAGAAGCTCGA
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1007 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (302) 892-7949
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                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                              0.9%;
                                                                                                                                                                                                                                                                                                                                                                                           /function= "synthetic seed
/product= "protein"
/gene= "ssp"
/standard_name= "SSP-534"
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Pred. No. 0.
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Best Local Similarity
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                                                                                                                                                                                                                            Matches
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                                                              3093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
3153 ACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGAAGAAGGA 3212
                                                                                                                            3033 CAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGAAGACAGTCGGCAAGTA 3092
                                                                                                                                                                                          2973 GAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGTA 3032
                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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APPLICATION NUMBER: 07/743,006
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                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 3..326
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                               182
                                                                                                                                                            62
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OPERATING SYSTEM: M
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TELEX: 835420
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                                                            TAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGAAAGCAAACTCAACTC
                                                                                                                                                            GAAACTGAAAGAGGAAATGAAGAAGCTCGAAGAGAAGATGAAGGTCATGGAGGAGAAGAT 121
                              GATGAAGAAGCTCGAAGAAGATGAAGGTCATGGAGGAGAAGATGAAAAAGCTCGAAGA
                                                                                              GAAAAAGCTGGAAGAAAAGATGAAGGCTATGGAGGACAAGATGAAATGGCTTGAGGAAAA
                                                                                                                                                                                                                            122;
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                                                                                                                                                                                                                            Conservative
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Pred. No. 0.01
0; Mismatches
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RESULT 24
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                                                                                                                                                                                                                    ;Patent No. 5171843
; APPLICANT: NUSSENZWEIG, VICTOR
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
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5171843-10
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; APPLICANT: NUSSENZWE
; TITLE OF INVENTION:
; PURIFYING IT
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Best Local Similarity
Matches 141; Conserv
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 754,645
FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1749
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                ID NO.:8:
                                                                                                                                                                       NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/
FILING DATE: 30-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                1929 CGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGCAGGA 1988
                                                                                                                                                                                                                                                                                                                                                                                                                   1869 GAAGGTGCTCCTCATGAACAAGATTGATGAACTCAAGAAGACTCAACTCATTCTGAAGAA 1928
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FILING DATE: 9-JUL-1985
APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
                                                                                                                                         APPLICATION NUMBER: US/07/175,112 FILING DATE: 30-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 697
 LENGTH: 1137
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                                                                                                                                                                                                                                                                                                                                  GCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGA 1808
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Pred. No. 0.03;
0; Mismatches 159;
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                                            ; ANTI-SENSE: PCT-US95-10668-1
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PCT-US95-10668-1
Query Match
Best Local Similarity
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CLASSIFICATION:
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Best Local Similarity 47.u
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                                                                                                                                                                  TELEFAX: (609) 779-84 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     FILING DATE: August 22, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Jane Massey Licata, Esq. STREET: 210 Lake Drive East, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1749 GCTTGTTGAGAACATTAAGAAGGATGAAGAACAGTTGTTTGAGAAGAAGATTACAAAAGA 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 210 Lanc -
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                         Nucleic Acid
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Epitope Ordering and Pr
Restriction Mapping
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22, 1994
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INFORMATION FOR SEQ ID NO:
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                                                                   1366 ATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAGAGTGACAAGAAA 1425
1426 AGTTACGAAGACCGCAGCAAAAGTCTAAAACGATATCACTAAAGAGTATGAAAAGCTGCTG 1485
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                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PENN-0137 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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STRANDEDNESS: Sing
                                                                                                             Local
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                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                              NAME: Jane Massey Licata REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: August 22,
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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Epitope Ordering and Protein
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RESULT 28 US-08-098-327E-32

Sequence 3 Patent No.

32, Application US/08098327E o. 6270771

GENERAL INFORMATION:

APPLICANT: GUERIN-MARCHAND, Claudine APPLICANT: DRUILHE, Pierre TITLE OF INVENTION: PEPTIDE SEQUENCES TITLE OF INVENTION: HERATIC STAGES OF TITLE OF INVENTION: OF STIMULATING TH NUMBER OF SEQUENCES: 46

PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEARING OF STIMULATING THE T LYMPHOCYTES

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US-09-412-554A-3
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Best Local
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CURRENT FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Ellsworth, Jeff L.
TITLE OF INVENTION: FOLLISTATIN RELATED PROTEIN ZFSTA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: variation LOCATION: (1)...(2949) OTHER INFORMATION: Each N is independently any nucleotide
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                                                                  595 GARYTNACNCARGTNATHAARCARGARGARYTNGGNAARGAYYTNTTYGAYTGYACNYTN 654
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                              TATAACAAACAGCTTGAAGAAGCCCATAAC
TAYGTNYTNYTNAARTAYGAYGAYTTYAAY 684
                                                                                                AATGCAACCAAGGAGGAAGAAAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATC
                                                                                                                                    YTNGTNGAYCARATGTTYAARTAYTTYGAYGCNGAYWSNAAYGGNYTNGTNGAYATHAAY 594
                                                                                                                                                                    ACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATAAG
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             Sequence 32, Application US/08462625
Patent No. 6319502
GENERAL INFORMATION:
APPLICANT: GURRIN-MARCHAND, Clau
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LENGTH: 950 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR 91 01286 FILING DATE: 05-FEB-1991
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                                                                                                                                                                                                                          ACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAG
                                                                                                                                                                                                                                                       TCTATAACAACAGCTTGAAGAAGCCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAG
                                                                                                                                                                                                                                                                                          CGATTTAGAACAAGAGAGAGCTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGA
                                                                                                                                                                                                                                                                                                                          AGAATGCAACCAAGGAAGAAAAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCA
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                                                                                                                                                       ACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA 380
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GUERIN-MARCHAND,
DRUILHE, Pierre
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: 20-AUG-1992
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Pred. No. 0
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US-08-462-625-32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: 05-JUN-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
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329
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TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 24-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                CTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGAATTATATTAAAAAAGAATAAGA 748
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ACGTGCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA
                                  ACACCCTCAAGAAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGA 980
                                                                        ACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAG
                                                                                                          TCTATAACAAACAGCTTGAAGAAGCCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAG
                                                                                                                                                                               AGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCA 868
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Alexandria
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20-AUG-1992
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US-08-098-327E-41
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-- rocal Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 92/13884
PUBLICATION DATE: 20-AUG-1992
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REFERENCE/DOCKET NUMBER: 010830-045
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: FR 91
FILING DATE: 05-FEB-1991
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CURRENT APPLICATION DATA:
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                                                                                                                                                                     CTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAAGAATAAGA 748
                                                                                                                                                                                                       TAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAA 98
CGATTTAGAACAAGAGAGACGTGCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGA
                                AGAATGCAACCAAGGAGGAAGAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCA 868
                                                                  ACAACAAAGCGATCTAGAACAAGAGAGAGGCTGCTAAAGAAAAGTTGCAAGAACAACAAAG
                                                                                                  AGACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATA 808
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nucleic acid
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P.O. Box 1404
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
OF STIMULATING THE T LYMPHOCYTES
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                                                                                                                                                                                                                                                        Matches 160; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1.1482
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 92/13884
PUBLICATION DATE: 20-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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CURRENT APPLICATION DATA:
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                                                      689 CTCTCGACAACATCAAGGACAATGTGGGAAAGATGGAAGATTATATTAAAAAAGAATAAGA 748
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-NOV-1993 CLASSIFICATION: 424
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o. 6270771
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P.O. Box 1404
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Pred. No. 0.
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Best Local Similarity

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US-08-462-625-41
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                                   US-08-462-625-41
 Query Match
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Patent No. 631950
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MEDIUM TYPE: Floppy disk
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                                                                                 LOCATION: 1.1482
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                    FEATURE:
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COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 39,300 REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FR 9 FILING DATE: 05-FEB-1991
                                                 PUBLICATION DATE:
                                                                   DOCUMENT NUMBER:
                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                nucleic acid
EDNESS: single
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P.O. Box 1404
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DRUILHE, Pierre
                                                                                                                                                                    linear
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05-JUN-1995
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                                                 WO 92/13884
: 20-AUG-1992
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   0.9%;
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Patent No. 6319502
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                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                  APPLICATION NUMBER: FR 91 01286 FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            FILING DATE: 24-NOV-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Painner
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                                                                                                                                                REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
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STRANDEDNESS
                                                                                                           TELEPHONE:
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                                1482 base pairs
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05-JUN-1995
                                                                                          3) 836-6620
836-2021
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0; Mismatches 192;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 9
PUBLICATION DATE: 20-
                                                                                                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/075,783
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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APPLICANT: de Taisne, Ch
APPLICANT: Tine, John A.
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                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 11-JUN-1993
                                                                                                                                              APPLICATION NUMBER: US/08/257,073 FILING DATE: 09-JUN-1994 CLASSIFICATION: 424
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                                     FILING DATE:
                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Taisne, Charles
                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
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SYSTEM: PC-DOS/MS-DOS
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: 20-AUG-1992
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                                                                                                                                                                                                               Release #1.0,
US 07/672,183
                                                    US 07/852,305
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                                                                                                                                                                                                                   Version #1.30
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Query Match
Best Local Similarity
Watches 97; Conserve
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PCT-US93-07261-10
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TITLE OF INVENTION:
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TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927
APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
                              TELEFAX: 201-822-7039 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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             SEQUENCE CHARACTERISTICS
                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 201-822-7398
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                                                                                                                                                                                                                                                                     COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          APPLICATION NUMBER: POFILING DATE: 19930805
                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Word 5.la
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ZIP: 07940-1000
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LENGTH:
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(212) 840-0712
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Best Local Similarity 41.8%;
Matches 332; Conservative
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MOLECULE TYPE: cl
ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
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LOCATION: 3..4766
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GATTTATCTAATAA 3580
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                                 GGACAGTCAGATAA 2108
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                                                                                                            GTGTTCATGCCCAAAGTCGAGAGCCTGATCAACGAAGAAGAAGAAGAACATTAAAACTGAA 2094
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                                                                      GGATTAAAAGAAAATGTATATACAAATAATGATTTAAAGAATAACGATATTCAAAAATAAA
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Pred. No. 0.19;
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Best Local Similarity
Matches 185; Conserv
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APPLICANT: COLLINS,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard
REGISTRATION NUMBER: 36,62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                               1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                         410
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                  AGGAACCATACTACCTCA---TCGTACTCAAGAAAGAGATAGACAAACTGAAAGTGTTCA 2041
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ARGARATHAARGGNMGNACNGTNGCNGTNGAYTGGGCNGTNGCNAARGAYAARTAYAARG 589
                                                                                    GNTTYGTNCARTTYAARAAYYTNYTNGARGCNGGNAARGCNYTNAARGGNATGAAYATGA
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RESULT 37
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                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                       TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                             1685
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                       MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                           Local
                                                                                                                                                                                                             LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                            NAME: Osman Ph.D., Richard A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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RESULT 38
US-09-098-487-2
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TELEFAX: (415)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                            ZIP: Y4.V7
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                              TELEPHONE: (415)343-4341
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                                                                                                        REFERENCE/DOCKET NUMBER:
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268 Bush Street, Suite 3200
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RESULT 39
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Best Local Similarity
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                                                                                          GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
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LENGTH: 2277 base pairs
                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                              TITLE OF INVENTION: SEQUESTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1625 ATCTTGAGAAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTG 1684
                                                                                                                                                                                                                                                                                                                          2282 CACCAGCTCCTGTGAATAACAAGACCGAGAAT 2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                     ADDRESSEE:
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USA MRMC -
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                   John Moran
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MCMR-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                     1600
                                                                                                                                                                                                                                                                                                                                                                          1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1360 AAGTTTATCAACGAAATCAAGGAGAAGAAGATCAAAATTGAGAAGAAGAAATTGAGAGTGAC 1419
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LENGTH: 1956 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 619-2065
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft WO CURRENT APPLICATION DATA
 1612
                                                                                                                                                                                                                                                          1660 GAGGACTATTCTCTGCGGAACATTGTTGTGGAGAAAGAACTAAAGTATTACAAGAATCTC
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TYPE: Nucleic acid
STRANDEDNESS: Double
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STATE: MARYLAND
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REGISTRATION NUMBER: 26
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 217; Conserv
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TOPOLOGY: Li
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                                GTCTCCGATATTGTTAAAGTCCAAGT 1865
                                                                                                                                                                                 ATAAGTAAGATCGAAAACGAGATCGAGACGCTTGTTGAGAACATTAAGAAGGATGAAGAA
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ATAACAAATATTGATATAAAAAATGT 1637
                                                                                                         CAGTTGTTTGAGAAGAAGATTACAAAAGACGAAAATAAACCAGATGAGAAGATCCTGGAG
                                                                                                                                                CAACATAAGAAGGAAAATCAAGTAGATGTTGTCAGGAAAAATATTCAGATTATTCAAGAG
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                                                                       GATAATATAAAAAATAAAGGCCAAAAGGATAACACTGAAATGTTAGATAATAATAAGGAA
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Best Local S
Matches 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 08/218,018

APPLICATION DATA:

APPLICATION NUMBER: US 08/017 ^-

FILING DATE: 25-MAP
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INFORMATION FOR SEQ
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 3032
                                                             2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: P-40,403
REFERNCE/DOCKET NUMBER: CGC:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 919-541-8582
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APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
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APPLICANT:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                               LOCATION: 9..1238
OTHER INFORMATION:
OTHER INFORMATION:
                                  88
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                               Local Similarity
                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pace, Gary M. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 1241 base pairs
ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                              AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCCAAGATGAACAACTTCCTGG
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7 Skyline Drive
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Koziel, Michael G
Mullins, Martha A
                                                                                                  Conservative
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ZENTION: No. 5770696el Pesticidal Proteins and Strains
EQUENCES: 50
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Kostichka, N. Kristy
Duck, Nicholas B
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                                                                                                                                                                             /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed as contained in pCIB5527"
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                                                                                                Score 43; DB Pred. No. 0.2; 0; Mismatches
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                                                                                                              DB 1; Length 1241; 0.2;
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                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
                                                                                 FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                     CLASSIFICATION: 530
                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Duck, Nicholas B
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Michael G
, Martha A
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No. 5770696el Pesticidal Proteins and
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                                                                                                                    US 08/314,594
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RESULT 42
US-08-471-044-39
; Sequence 39, Applicatic
; Patent No. 5840868
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
SEQUENCE C1241 base pairs
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LOCATION: 9..1238
OTHER INFORMATION:
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Local Similarity 44.7%;
Les 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                9, Application US/08471044 
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Warren,
Kóziel,
Gregory
Michael
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-471-044-39
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: |
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
                               3032 ACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                      2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3033
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = | Synthetic DNA"
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                                                                                                                                      Local Similarity
nes 215; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 -
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ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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Patent No. 5
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APPLICANT:
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                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
PTITING DATE: 09-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: NO. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                  FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
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Kostichka, N. Kristy
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Koziel, Michael
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JMBER: US 08/037,057
25-MAR-1993
                                                      23-MAR-1994
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-6582
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LOCATION: 9..1238
OTHER INFORMATION:
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Sequence 39, Application US/08463483A Patent No. 5849870 GENERAL INFORMATION: APPLICANT: Warren, Gregory W APPLICANT: Koziel, Michael G

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Best Local :
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
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ADDRESSEE: CIBA-GEIGY CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTR
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TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
                                                               3092 ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
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OTHER INFORMATION:
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LOCATION: 9...
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TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
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Kostichka, N. Kristy
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/desc = "Synthetic DNA"
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25-MAR-1993
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Pred. No. 0.2;
0; Mismatches
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REFERENCE/DOCKET NUMBER: (32,943 REFERENCE/DOCKET NUMBER: CGC TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8615
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                                                                                                                                                     FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
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                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
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                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                     APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                            APPLICATION NUMBER: CFILING DATE: 09-SEP-1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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STREET: 7 Skyline
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Koziel, Michael
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Patent No. 5
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Best Local Similarity
Matches 215; Conserv
                                                                                                                              GENERAL INFORMATION:
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APPLICANT:
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LOCATION: 9..1238
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Mullins, Martha
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Best Local Similarity
Matches 215; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 05-JUN-1995
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                                                               ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
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                                 TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA
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"Synthetic
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                                                                                                                                                                                                                                  Score 43; DB 2
Pred. No. 0.2;
0; Mismatches
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RESULT 47
US-08-471-046A-42
; Sequence 42, Applic
; Patent No. 5866326
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                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 06-UUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT:
                                                                                      FILING DATE: 23-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Protein Genes NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
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                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                              APPLICATION NUMBER: US 08/314,594 FILING DATE: 09-SEP-1994
                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                       APPLICATION NUMBER:
                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               SOFTWARE:
 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA 567
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Kostichka, N. Kristy
Duck, Nicholas B
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Koziel, Michael G
Mullins, Martha A
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                                                                                                                                                                                                                                                   06-JUN-1995
                                                                                                                                                                                          05-JUN-1995
                                                            25-MAR-1993
                                                                                                                   US 08/218,018
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               38,241
 CGC1695/CIP3/DIV8 -
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LOCATION: 9..1238
OTHER INFORMATION:
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US-08-470-566B-39
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                                                                                      Patent No. 5872212
GENERAL INFORMATION:
                                                                                                                   Sequence 39,
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                           APPLICANT:
                                                         APPLICANT: APPLICANT:
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APPLICANT:
                APPLICANT:
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                           Warren, Gregory I
Koziel, Michael (
Mullins, Martha
Nye, Gordon J
                Carr, Brian
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/note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion removed and the eukaryotic secretion signal inserted as contained in pCIB5528"
              Score 43; DB
Pred. No. 0.2;
Mismatches
                              2;
260;
                                Length 1241;
Indels
6,
Gaps
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3146 TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205 2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3386 CTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACC 3266 AACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAGACTCTCT 3206 AGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCAAGATTCTTCTCA 3265 3092 ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145 148 ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT 88 AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147 CCAAGGCCGGCGTGATCCTGAACAACAGCGGTACAAGATGCTGATCGACAACGGCTACA GCAAGGAGCGCGTGATCCTGAAGGTGACCGTCCCCAGCGGCAAGGGCAGCACCACCCCCA 507 CCGAGGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGT GCAACAGCATCACCTACAAGAACGTGGAGCCCACCATCGGCTTCAACAAGAGCC ACCGCGACATCAAGTTCGACAGCTACCTGGACACCCACCTGACCGCCCAGCAGGTGAGCA 447 TGACCGAGGGCAACACCATCAACAGCGACGCCATGGCCCAGTTCAAGGAGCAGTTCCTGG TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA ACAACAAGTACAAACTGAAACTGGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091 387 327 267 207

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Best Local Similarity
Matches 215; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                    3032
                                   3092
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TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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                                                                   148
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 23-MAR-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                            ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                                                ACAACAAGTACAAACTGAAACTGGAGAGAGTCTTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                                                                  AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCCAAGATGAACAACTTCCTGG 147
TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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F: 3054 Cornwallis Road
Research Triangle Park
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/desc = "Synthetic
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                                                                                                                                                                                                                                                                                       /note= "Maize optimized DNA
sequence encoding VIP2A(a) with the Bacillus secretion signal
removed as contained in pCIB5527"
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                                                                                                                                                                                                                    Score 43; DB Pred. No. 0.2;
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                     2; Length 1241;
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US-08-470-566B-42
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                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
                                                                                                                                                           FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5872212el Pesticidal Proteins
NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                            FILING DATE: 05-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         FILING DATE:
                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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                                   NAME:
                                                                                                                                                                                             APPLICATION NUMBER:
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 REFERENCE/DOCKET NUMBER:
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Kostichka, N. Kristy
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Koziel, Michael
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                                 J. Timothy
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CGC1695/CIP3/DIV4 - SQLv4
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                                                                                          Sequence 39, Applicat Patent No. 5990383 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                            Application US/08469334
                                          Warren, Gregory
Koziel, Michael
Mullins, Martha
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/desc = "Synthetic DNA"
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APPLICANT:
                                                                                                                                           3032
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
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CURRENT APPLICATION DATA
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TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
                                                                     3092
                                                                                                                                                                                                               2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 303:
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                                  208
                                                                                                        148
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OPERATING SYSTEM:
                                                                                                                                                                              88
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                                                                                                                                                                                                                                                  Local Similarity
les 215; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                   ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC
                                                                                                                                                                              AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147
                                  TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAAGCCTGA 267
                                                                                                          ACAACAAGAACGACCATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
                                                                                                                                         ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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25-MAR-1993
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Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Desal, Nallni M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5990383el Pesticidal Proteins
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                                                                                        APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY, AGENT INFORMATION:
NAME: SPINITIN MUTTAY
DESCRIPTION NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUMBER: SPINITIN NUM
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FILING DATE: 06-JUN-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                         ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER:
FILING DATE: 09-SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 23-MAR-1994
                                             REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Koziel, Michael (
Mullins, Martha /
Nye, Gordon J
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Best Local Similarity
Watches 215; Conserve
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                                                                                                                                                                                                                   Sequence 39, Application US/09300529 Patent No. 6066783
                                                                                                                                                                                               GENERAL INFORMATION:
                                                              APPLICANT:
APPLICANT:
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                         APPLICANT:
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  APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                     568
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                                                                                                                 Warren, Gregory
Koziel, Michael
Mullins, Martha
                                                                                             Nye, Gordon J
Duck,
                      Desai, Nalini M
Kostichka, N. Kristy
                                                                    Carr, Brian
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  Nicholas B
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
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LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3032 ACAACAAGTACAAACTGAAACTGGAGAGAGCTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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LOCATION: 9..1238
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                         CCGAGGAGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTCCTGT 3385
CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA 567
                                                CTAAGCTCGAAGGCAAGCTGAAGCAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACC 3445
                                                                                                          GCAAGGAGCGCGTGATCCTGAAGGTGACCGTCCCCAGCGGCAAGGGCAGCACCACCCCCA
                                                                                                                                                                                                                                                                     AACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAGACTCTCT 3325
                                                                                                                                                                                                                                                                                                                                                                                  AGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCCAAGATTCTTCTCA 3265
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAACAGCATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC
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                                                                                                                                                                                                                 ACCGCGACATCAAGTTCGACAGCTACCTGGACACCCACCTGACCGCCCAGCAGGTGAGCA
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Pred. No. 0.
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                                                                                                                                                                                 Matches
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                                                                                       3032
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                            3092 ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC 3145
                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/218,018 FILING DATE: 23-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUN-
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APPLICATION NUMBER:
FILING DATE: 06-JUN-
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Genes Encoding Insecticidal Proteins
                                                                                                                                                  2972 AGAAGCTGGAAGAGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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                                                           148
                                                                                                                                                                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                             Local Similarity
                                                                                      ACAACAAGTACAAACTGAAACTGGAGAGAGACTCTTCGACAAGAAGAAGACAGTCGGCAAGT 3091
TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 267
                                                                                                                     AGAAGGAGAAGGAGTGGAAGCTTACCGCCACCGAGAAGGGCAAGATGAACAACTTCCTGG 147
                                                          ACAACAAGAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCT
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1: 3054 Cornwallis Road
Research Triangle Park
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/desc = "Synthetic DNA"
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06-JUN-1995
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44.78;
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                                                                                                                                                                                                                                                        /note= "Maize optimized DNA
sequence encoding VIP2A(a) with the Bacillus secretion
removed as contained in pCIB5527"
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Pred. No.
                                                                                                                                                                               ed. No. 0.2;
Mismatches
                                                                                                                                                                                                            DB 3; Length 1241;
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RESULT 53
US-09-300-529-42
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Patent No. 6(
GENERAL INFO
                                                                                                                                                                    PRIOR APPLICATION UMBER: US 08/4
PRIOR APPLICATION DATA: | 08/4
PRIOR DATE: 05-JUN-100"
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                         PRIOR APPLICATION DATA:
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CITY: R
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APPLICATION NUMBER: FILING DATE: 25-MA
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                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAAGCTCGAAGGCAAGCTGAAGGACAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACC 3445
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Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
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ENTION: Genes Encoding
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Kostichka, N. Kristy
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05-JUN-1995
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MBER: US 08/037,057
25-MAR-1993
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                                                  Sequence 45, Application US/08471033 Patent No. 5770696
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                                   GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
 APPLICANT:
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LOCATION: 9..1238
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Warren,
Koziel,
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US-08-471-033-45
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                                2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
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APPLICATION NUMBER:
FILING DATE: 25-MAR-
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APPLICATION NUMBER: US 0
FILING DATE: 09-SEP-1994
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TITLE OF INVENTION: NO. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 9..1355
COTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              DESCRIPTION:
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Kostichka, N. Kristy
Duck, Nicholas B
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Nye, Gordon J
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44.78;
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US-08-471-044-45
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GENERAL INFORMATION:
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TITLE OF II
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                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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NAME: Pace, REGISTRATION
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                                                                                                                                                                                                                                                                                                             FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Kostichka, N. Kristy
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                                      Gary M
                                                                                                           JMBER: US 08/037,057
25-MAR-1993
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                                                                                                            Sequence 45, Application Patent No. 5849870
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                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO
                                             APPLICANT: APPLICANT:
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LOCATION: 9..1355
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OTHER INFORMATION:
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les 215; Conserv
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                                                                                                                                                                                                                                                                                CCAAGGCCGGCGTGATCCTGAACAACAGCGAGTACAAGATGCTGATCGACAACGGCTACA
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           Warren, Gregory
Koziel, Michael
Mullins, Martha
Nye, Gordon J
Carr, Brian
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Pred. No.
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0.21;
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Best Local :
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1358 base pairs
TYPE: nucleic acid
                              3146 TCAACTCACTGAACAATCCGAAACACGTACTGCAGAACTTCTCAGTGTTCTTCAACAAGA 3205
                                                                                                                                                                                                                                    2972 AGAAGCTGGAAGAGGACATCAATAAGCTGAAGAAGACACTGCAACTGAGCTTCGACCTGT 3031
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DESCRIPTION:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 1
FILING DATE: 23-MAR-
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TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 01 FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                              TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 384
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                                                                                             ATAAGATGCAGATCAAGAAGTTGACTCTGCTCAAGGAGCAGCTTGA-----AAGCAAAC
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.21
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                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/463,483 FILING DATE: 05-JUN-1995 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT:
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 -
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                            FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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Koziel, Michael
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Kostichka, N. Kristy
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23-MAR-1994
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US-08-470-566B-45
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                                                                                                                                                                             Sequence 45, Application US/08470566B Patent No. 5872212
                                                                                                                                                                         Patent No.
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Best Local Similarity 44.7%;
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INFORMATION FOR SEQ ID NO:
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LOCATION: 9..1355
COTHER INFORMATION:
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Desai, Nalini M
Kostichka, N. Kristy
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                                                                                    Nye, Gordon J
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                                                                                                                        Koziel, Michael
Estruch, Juan J
                Duck, Nicholas B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meigs, J. Timothy
REGISTRATION NUMBER: | 38,241
REFERENCE/DOCKET NUMBER: CGG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5872212el Pesticion MUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5872212artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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APPLICATION NUMBER: US 01
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
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MOLECULE TYPE:
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LOCATION: 9..1355
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                                                                                                                                                                                                                                                                                                                                  Local Similarity
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GCAACAGCATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCC 444
                                                                          TCGAGGACGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGA 384
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with the Bacillus secretion signal removed
targetting signal inserted as contained in
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Pred. No.
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TELEFAX: 91
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APPLICANT:
                                                       REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                                                                                   APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY_AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
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FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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TELEPHONE: 919-541-8689
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INVENTION: NO. 5990383el Pesticidal Proteins and Strains
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Kostichka, N. Kristy
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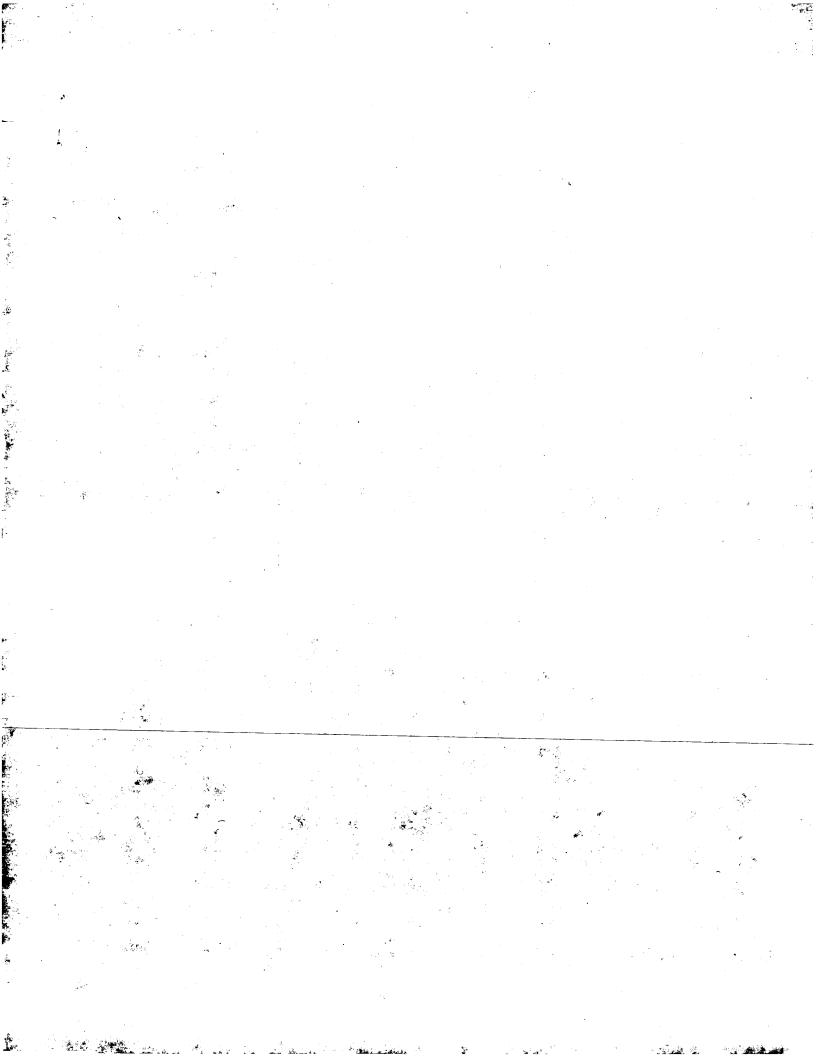
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                                                                                      CTAAGCTCGAAGGCAAGCTGAAGCAACCTGAACCTGGAGAAGAAGAAGCTCAGCTACC
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Fax: 314 286 Email: est@wa Library was c Washington Un obtaining a c (sibley@borci Seq primer: - High quality High quality cory /org //clo //lab	Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I. Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I. Taggareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Materston, R., Wilson, R. and Sibley, D. Waterston, R., Wilson, R. and Sibley, D. TITLE WashU Plasmodium EST Project Unpublished (2001) COMMENT Contact: L. David Sibley WashU Plasmodium EST Project WashU Plasmodium EST Project WashIngton University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800	124	BI815756 PfESToda32c09.y1 falciparum cDNA	155 57.8 1.2 876 157 57.8 1.2 878 158 57.8 1.2 931 159 57.8 1.2 1042 160 57.8 1.2 1059 161 57.8 1.2 1079 163 57.8 1.2 1079 164 57.6 1.2 297 165 57.6 1.2 617 167 57.6 1.2 829 168 57.6 1.2 829 170 57.6 1.2 964 170 57.6 1.2 964 170 57.6 1.2 1215 170 57.6 1.2 964 171 57.2 1.2 571 172 57.4 1.2 829 173 57.2 1.2 571 174 57.2 1.2 1215 175 57.2 1.2 1215 176 57.2 1.2 1215 177 57.2 1.2 124 178 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382 179 57.2 1.2 1382	3 57.8 1.2 539 9 4 4 57.8 1.2 542 13

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                                      malaria parasite P. falciparum Plasmodium falciparum
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               Eukaryota; Alveolata; Apicomplexa;
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(bases 1 to 600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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                                                                                                        GI:21255427
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Pred. No. 9.3e-43;
0; Mismatches 180;
                  Haemosporida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           3124 AAGGAGCAGCTTGAAAGCAAACTCAACTCACTGAACAATCCGAAAACACGTACTGCAGAAAC 3183
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                                                                                                                                                                                                                                                                3244 GAGAACACCAAGATTCTTCTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAG 3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3064 TTCGACAAGAAGAAGACAGTCGGCAAGTATAAGATGCAGATCAAGAAGTTGACTCTGCTC 3123
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                                                                                                       TCATCTCCATTAAAAACTTTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAAT 300
                                                                                                                                                      TCTTCTCCTCTGAAGACTCTCTCCGAGGAGGAGCATCCAGACCGAGGATAACTACGCCAGC 3363
                                                                                                                                                                                                              GAAAACACAAAAATATTATTGAAACATTATAAAGGACTTGTTAAATATTATAATGGTGAA 240
                                                                                                                                                                                                                                                                                                                        TTTTCTGTTTTCTTTAACAAAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAACACATTA 180
                                                                                                                                                                                                                                                                                                                                                                       TTCTCAGTGTTCTTCAACAAGAAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTG 3243
                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGAACAATTAGAATCAAAATTGAATTCACTTAATAACCCACATAATGTATTACAAAAC
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Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
obtaining a clone please contact: David Sibley
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WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
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Marra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Thelsing,B.
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I
Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
Waterston,R., Wilson,R. and Sibley,D.
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/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-1ysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
clones were mass excised using the Exassist helper phage
(Stratagene), the phagemids were precitptated with PEG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DHIOB cells."
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/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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                                       CTCTCCGAGGAGCATCCAGACCGAGGATAACTACGCCAGCCTCGAGAACTTCAAGGTC 3381
                                                                                                        CTCAAACACTACAAAGGCCTCGTCAAGTATTATAATGGCGAGTCTTCTCCTCTGAAGACT 3321
                                                                                                                                                                                                            AAGAAGGAAGCCGAGATCGCCGAGACAGAGAACACTCTGGAGAACACCAAGATTCTT 3261
                                                                                                                                                                                                                                                     AAATTGAATTCACTTAATAACCCACATAATGTATTACAAAACTTTTCTGTTTTCTTTAAC 64
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                                                                                                                                                                    AAAAAAAAAGAAGCTGAAATAGCAGAAACTGAAAACACATTAGAAAACACAAAAATATTA 124
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TTAAGTGAAGTATCAATTCAAACAGAAGATAATTATGCCAATTTAGAAAAATTTAGAGTA 244
                                                                                  TTGAAACATTATAAAGGACTTGTTAAATATTATAATGGTGAATCATCTCCATTAAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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...r precursor of major
AU088128
AU09911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. FULL-malaria: a database for a full-length enriched from human malaria parastte, Plasmodium falciparum Nucleic Acids Res. 29~(1), 70-71 (2001)
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Plasmodium falciparum 3D7

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases_1 to 500)
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The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-3-5449-5378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                         Conservative
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/db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="XPPn6559"
/clone="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
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                                                                                                                                                                                                                                                                                                                                                           3.9%;
                                                                                                                                                                                                                                                                                                                                                           Score 194; DB 9;
Pred. No. 2.1e-33;
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Contact: L. David Sibley
WashU Plasmodium EST Project
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Library was constructed by Debopam Chakrabarti DNA sequencing l
Washington University Genome Sequencing Center For information
obtaining a clone please contact: L. David Sibley
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                                         Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected erythrocytes by the accidic guanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap cDNA synthesis kit (Stragene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb cDNA inserts in the library was between 1.0 and 1.5kb clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were preciptated with PEG (Stratagene), the phagemids were preciptated with PEG
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                                                                                                                    WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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                                                                                                                                                                                                                     Contact: L. David Sibley
                                                                                                                                                                                                                                                     Unpublished (2001)
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   Library was
                                   Email: est@watson.wustl
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KEYWORDS SOURCE

EST. AU086832 AU086832.1

GI:12388973

ORGANISM

Plasmodium falciparum Plasmodium falciparum

3D7 3D7

Eukaryota;

karyota; Alveolata; Apicomplexa; Haemosporida; (bases 1 to 500)

Plasmodium.

VERSION ACCESSION

REFERENCE

TITLE AUTHORS

Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. FULL-malaria: a database for a full-length enriched cDNA library

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RESULT 6
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AU086832 Sugano Malaria cDNA library Plasmodium falciparum clone XPFn3463 similar to Plasmodium falciparum train HNS merozoite surface protein 1 precursor (msp1) gene, mRNA seg
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Seq primer: ~40UP from Gibco.
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//Clones were mass excised using the Exassist helper phage (Stratagene, Inc.)*
//Iab_host**DH10B (GeneHog, Invitrogen, Inc.)*
//Incle**Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhOI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage saponin(0.1%)*-lysed P. falciparum 3D7 infected erythrocytes by the acidic guanidinium phenol chloroform method. The poly A+ RNA was isolated by the polyAT*Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhOI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells.*
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,BI814631.1
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Nucleic P
20574754
                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The University of Tokyo, Department of Parasitology 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Tel: 81-3-5449-5378
 Plasmodium
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki,ř., Yoshitomo Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                  malaria parasite P. falciparum.
                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-3-5449-5410
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eic Acids Res. 29 (1), 70-71 (2001)
                                                                                                       sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jwatanab@manage.ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:36329"
/clone="xPFn3463"
/clone_lib="Sugano Malaria cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="erythrocytic stage"
51 c 52 g 146 t
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falciparum
Alveolata;
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                                                                                                     Plasmodium falciparum 3D7 asexual CDMA Plasmodium falciparum 3D7 asexual CDMA Plasmodium 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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Pred. No. 1.2e
0; Mismatches
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 Apicomplexa; Haemosporida;
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Plasmodium
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Best Local Similarity
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                                            4894
                                                                                                                                      4834
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                                                                                                                                                                                                                                                                                  441
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                                                                                                                                                                                                                                                                               CTGATCCTCATGCTGATCCTGTACAGCTTCATCTAATAGATCGATG
                                                                                                                   AACCCAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACC 4773
  TTAATACTCATGTTAATATTATACAGTTTCATTTAAAAAATGTAGG
                                                                                          TATCCACTTTTCGATGGTATTTTCTGCAGTTCCTCTAACTTCTTAGGAATATCATTCTTA
                                                                                                                                                                                     GAAGAAGATTCAGGTAGCAGCAGAAAGAAAATCACATGTGAATGTACTAAACCTGATTCT 322
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Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D
Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I
Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
Watterston,R., Wilson,R. and Sibley,D.
Washu,Plasmodium_EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 261.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001) Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb.
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Total RNA samples were isolated from mixed stage
saponin(0.18)-lysed P falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
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/note="Vector: pBluescript SK plus; Site_1:
XhoI; Library was constructed by Debopam Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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/db_xref-"taxon:5833"
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72.78;
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                             4778 AAGACAGCGGCTCTAACGGAAAAGAAATCACATGCGAGTGTACTAAGCCCGACTCCTATC 4837
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                                                                                                                                                                                                                           4 GAGAAGAATGTAAATGTTTATTAAATTACAAACAAGAAGGTGATAAATGTGTTGAAAATC 63
                                                                                                                                               CAAACCCTACCTGCAATGAAAACAATGGCGGGTGTGACGCCGATGCTAAATGCACCGAGG 4777
                                                                                                            CAAATCCTACTTGTAACGAAAATAATGGTGGATGTGATGCAGATGCCACATGTACCGAAG 123
AAGATTCAGGTAGCAGCAGAAAGAAAATCACATGTGAATGTACTAAAACCTGATTCTTATC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: L. David Sibley
WashU Plasmodium EST Project
WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -400p from Gibco.
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WashU Plasmodium EST Project
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Marra,M., Hillier,L., Martin,J., Wylle,T., Dante,M., Theising,B.,
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314 286 1810
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/lab_host="DHIOB (GeneHog, Invitrogen, Inc.]
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.18)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyA7-Tract
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/db_xref="taxon:5833"
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                                                                                                                                                                                                                                                                                                                                                               3.2%;
                                                                                                                                                                                                                                                                                                                                                               Score 160.4;
Pred. No. 9.5
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BASE COUNT
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Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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1 (bases 1 to 522)
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BQ452445.1 GI:21255557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sibley@borcim.wustl.edu),
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                                 204
                                 ۵
                                                        mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional CDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precititated with PBG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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KhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
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Query Match
Best Local Similarity 73.3
Matches 205; Conservative

3.2%; 73.2%;

Score 160; DB 14, Pred. No. 1.2e-25, 0; Mismatches 7

DB 14;

Length 522; Indels

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Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B. Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I Tsagareishvili,R., Belaygorod,L., Fankklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
WashU Plasmodium EST Project
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Plasmodium falciparum
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/note, "Vector: pBluescript SK plus; Site_1: ECORI |
/note, "Vector: pBluescript Sk plus; Site_2: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Site_3: Plus; Plus; Site_3: Plus; Plus; Site_3: Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Plus; Pl
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                                                                                                                                                                                                                                                                                           Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction land characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Junichi Watanabe
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The University of Tokyo, Department of Parasitology
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                                                                                      /clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
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                                                                                                                                                                        Institute of Medical Science
The University of Tokyo, Department of Tokyo, Department of Tokyo, Tokyo
Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
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                                                                               Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuk1,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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                                                                 WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
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Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I.,
Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,
Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
Waterston,R., Wilson,R. and Sibley,D.
WashU Plasmodium EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library was constructed by Debopam Chakrabarti DN/
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco.
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Washington University School of Medicine
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Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precitytated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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/db_xref="taxon:5833"
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                                                                    AAGATTCAGGTAGCAGCAGAAAGAAAATCACATGTGAATGTACTAAACCTGATTCTTATC
                                                                                                                                                                                                                                                                                                                                                                       161;
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Contact: L. David Sibley
WashU Plasmodium EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
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Putative full length read
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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Contact: L. David Sibley
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418 bp mRNA linear EST 29-MAY-2002 PfESTOab06b11.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab_host="Plasmodium falciparum 3D7 inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
xhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from that d stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
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Washu Plasmodium EST project

Unpublished (2001)

Contact: L. David Sibley
Washu Plasmodium EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810

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Final: est@watson.wustl.edu
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                                                                       mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EccRI and XhoI sites of 1 ZapII vector using the Zap CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the Exassist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/clone_lib-"Plasmodium falciparum 3D7 asexual cDNA"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
xhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-1ysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Bio: 97001675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z. Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the Plasmodium falciparum genome project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 365)
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1183C3 czapPFDd2.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: dchak@pegasus.cc.ucf.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: T3
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                                                            Conservative
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                                                                                                                                                    /note="Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho /II; Propage in the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dr Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II vector. "
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5833"
/clone="PF1183C"
                                                                                                                                                                                                                                                                                                                                   /clone_lib="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Dd2
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Debopam Chakrabarti Plasmodium
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0; Mismatches 61;
                                                                            Score 119.8; DI
Pred. No. 1.7e-
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                                                            Mismatches
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
Plasmodium yoeli EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 301-838-0208
Email: carltonetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
Fax: 301-838-0208
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Seg primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    for clone info, please contact the
/dev_stage="Asexual blood stages"
//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                    /organism="Plasmodium yoelii
/strain="17XL"
                                                                                                                                                                                                                                                                                        /clone="PYCJG14"
                                                                                                                                                                                                                                                                     /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:73239"
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                                                                                                                                 AAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCA
                                                                                                                                                                              CAATTAGCTGAAATACAAAAGGTTGTCGAAGTCTTAGAAAAACGAGTTTCTACATTAAAG
                                                                                                                                                                                                                     CAGCTTGAAGAAGCCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAATTTTAGGTTATAGAAAACCAATAGAAAATATTCAAGACGATATTGAAAAGTTAGAA
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                                                                                        AAAAATGATGCCATCAAACCATTATGGCAACAAATTGAAGTTCTCAATGCTGCCCCCGTC
                                                                                                                                                                                                                                                                                                                                                     ACAAAAAAAATACAACCTGAAGGTAACGAAGATTGCAATGACGCTAGTTGTGATAGCGAT
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S246
AU086246
AU086246 Sugano Malaria cDNA library Plasmodium falciparum 3D7 cDNA clone xprn2175 similar to p.falciparum gp190 (MSA1, MSP1, PMMSA) for precursor of major merozoite surface antigens, mRNA sequence.
ION AU086246
AU086246.1 GI:12388387
ORDS EST.
ORDS EST.
CE Plasmodium falciparum 3D7.
GANISM Elasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RENCE I (bases 1 to 500)
Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
FULL-malaria: a database for a full-length enriched cDNA library from human malaria parasite, plasmodium falciparum URNAL Nucleic Acids Res. 29 (1), 70-71 (2001)
DLINE Contact: Junichi Watanabe
Contact: Junichi Watanabe
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

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RESULT 21
BM159731
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ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGACGAAAATAAACCAGATGAGAAGATCCTGGAGGTCTCCGATATTTGTTAAAGTCCAAG 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATACAATAATTAACAGAAGAAATAAAGAGTAGTGAAAAACAAAATTCTAGAAAAAATTTA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAAGTCGAGAGCCTGATCAACGAAGA 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAACGTGGAGTTAAAACATAATATACATGTGCCGAATAGTTATAAGCAGGAGAATAAGC 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGACTAACACATTCAGCAAATGGTTCCTTAGAAGTATCTGATATTGTAAAATTACAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAAGTAAAAGACATGTTAAAGAAAGA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzukl,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 755)
                                         Email: carlton@tlgr.org
For clome info, please contact the Malaria Research and
Reagent Resource Center, ATCC
                                                                                                                        Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301-530-9319
                                                                                                                                                                                                                                   Plasmodium yoelii EST project at Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BM159731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM159731 FST562254 PyBS Plasmodium
                                                                                                                                                                                                               Contact: Jane Carlton
                                                                                                                                                                                                                                                                             Fraser, C.M. and Carucci, D.J.
                                                                                                                                                                                                                                                                                              Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W.,
                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii.
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                   http://www.malaria.mr4.org/mr4pages/index.htm
primer:
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81-3-5449-5410
                                                                                                        301-838-0208
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/clone=lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
/dev_stage="erythrocytic stage"
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/strain="3D7"
/db_xref="taxon:36329"
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Pred. No. 6e-14;
0; Mismatches 137;
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m yoelii
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yoelii cDNA clone
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PYCJH95 5' end,
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                                             519
                                                                                         940 AAGAATGAAAATATCAAAGAACTGCTCGACAAGATTAATGAAATTAAGAATCCTCCGCCA 999
                                                                                                                                                                                  880 CAGCTTGAAGAAGCCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCTCAAG
                                                                                                                                                                                                                                   399 AAATATAATAAAAAAAAAACCAATATACCAAGCTATGTACAATGTTATATTTTACAAAAAA
                                                                                                                                                                                                                                                                                                                                                                            787
                                                                                                                                                                                                                                                                                                                                                                                                                        279 ATTTACATAGAAAGAAATAAAGAAACTGTTGCAGCTTTAAACGCTCTTATTGCTGAAGAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727
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                                                                                                                                         CAATTAGCTGAAATACAAAAGGTTGTCGAAGTCTTAGAAAAACGAGTTTCTACATTAAAG
                                                                                                                                                                                                                                                                                AAGGAGGAAGAAAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATCTATAACAAA 879
                                                                                                                                                                                                                                                                                                                                                                            AAAAAGACCATA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTTGAATTTCTACTTCGACTTGCTAAGGGCCAAACTGAATGACGTTTGCGCCAATGAC 606
                                             AAAAATGATGCCATCAAACCATTATGGCAACAAATTGAAGTTCTCAATGCTGCCCCCGTC
                                                                                                                                                                                                                                                                                                                              ACAAAAAAATACAACCTGAAGGTAACGAAGATTGCAATGACGCTAGTTGTGATAGCGAT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTATATAAAAAAGAATAAGAAGACCATCGAGAACATTAACGAGCTGATCGAAGAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-tractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated.
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pADD-GAL4, At 20-25% parasitemia, blc
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:73239"
/clone="pYCJH95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="17XL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Plasmodium yoelii yoelii"
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                                          607 TATTGTCAAATTCCATTCAATTTGAAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAG
                                                                                                                                                   547
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                                                                                              232 GCAATAAATTTTTATTATGATGTACTTAGAGATAAATTAAATGATATGTGTGCAAATAAT 291
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Plasmodium yoelii yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: carlton@tigr.org
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                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhOI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybrizAP arms directionally using EcoRI-XhOI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated.
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/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blocollected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over parasites, and leukocytes collumns. Total RNA was
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/clone="PYCJR11"
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Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD .20850, USA
Tel: 301-530-9319
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For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
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/lab_host="D. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was
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                                                                                                                                                                                          Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                      Marra,M., Hiller,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I., Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
WashU Plasmodium EST Project
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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402 bp mRNA linear EST 12-SEP-2001 PfEST0aa02e11.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5', similar to TR:043995 043995 MEROZOITE SURFACE
                                                                             Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley
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                              High quality sequence stop: 352
                                                                                                                             Email: est@watson.wustl.edu
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                                                            (sibley@borcim.wustl.edu),
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               Location/Qualifiers
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                                                                                                                                                                              Box 8501,
                                                            Washington University
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                                                      Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S., X.-Z., Thompson, J.K., Vital, F., Wellems, T. E. and Werner, E. Current status of the Plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                                            Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                clone PF1114C, mRNA sequence N97689
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Hinterberg,K., Holder,A.A., Holt,D., Kemp,D., Lanzer,M.,
                                                                                                                                                                                                                              Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, 2.,
Contact: Debopam | Chakrabarti
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Total RNA samples were isolated from mixed stage
saponin(0.1%)-1/sed P. falciparum 3D7 infected
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/note="Vector: pBluescript SK plus; Site_1:
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mes 167; Conserv
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                                                                                                                                                                                                             malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 354)
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Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
                                                             Dame, J.B., Arnot, D.E., Bourke, P., Chakrabarti, D., Christodoulou, Z., Coppel, R., Cowman, A., Craig, A., Fischer, K., Foster, J., Goodman, N., Hinterberg, K., Holder, A.A., Holt, D., Kemp, D., Lanzer, M., Lim, A., Newbold, C., Ravetch, J.V., Reddy, G.R., Rubio, J., Schuster, S.M., Su, X.-Z., Thompson, J.K., Vital, F., Wellems, T.E. and Werner, E. Current status of the plasmodium falciparum genome project Mol. Biochem. Parasitol. 79, 1-12 (1996)
                                                                                                                                                                                                                                                                                                                                                                1039C3 czapPFDd2.1, clone PF1039C, mRNA
Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
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N97605.1 GI:1674623
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primer: T3.
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/lab_host="E. coli XL-1 blue"
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/clone="PF1114C"
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Pred. No. 2.5
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Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
Email: dchakpegasus.cc.ucf.edu
Seq primer: T3
                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 647)

Carlton,J.M.-R. and Dame,J.B.

The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)

Contact: Dame JB

Dept. of Pathobiology, College of Veterinary Medicine University of Florida

2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA Tel: 352 392 4700

Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                    AZ526918
261PbC05 Pb
AZ526918
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                                                                                                                                                                                                                                                                                                     AZ526918.1
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
                                                                                                                                                                                                                                                              Plasmodium berghei.
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//Lab_host="E. coli XL-1 blue"
//Lab_host="E. coli XL-1 blue"
// note="vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho I; PolyA+ RNA, from asynchronous blood stage parasites of the Dd2 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I + Xho I digested lambda ZAP II vector. "
a 50 c 49 g 103 t 1 others
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/db_xref="taxon:5833"
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Matches 177; Conserv
                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                              AACAAAAAAT 626
              1 (bases 1 to 660)
Carlton,J.M., Daly.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelli EST project at TIGR
Unpublished (2001)
                                                                                                       Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alvoolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                    mRNA sequence.
BM159472
                                                                                                                                                                                                                                                      BM159472 660 bp mRNA linear EST 04-DEC-200 EST561995 PyBS Plasmodium yoelii yoelii cDNA clone PYCJE56 5' end,
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/db_xref="taxon:5821"
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Query Match
Best Local Similarity
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                                        BM170928 7777 bp EST573451 PyBS Plasmodium yoelii mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
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The Institute for Genomic Research
BM170928.1 GI:17304160
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//dev_stage="Asexual blood stages"
//dev_stage="Asexual blood stages"
//lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybrlZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybrlZAP vector and plasmid DNA
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/strain="17xL"
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Seq primer: ADF.
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For clone info, please contact the Malaria Research
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The Institute for Genomic 1
9712 Medical Center Drive,
Tel: 301-530-9319
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Fraser,C.M. and Carucci,D.J.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Pyl7XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was microcrystalline cellulose collumns.
Size-fractionated cDNA was precipitated and ligated HybriZAP arms directionally using EcoRI-XhoI cleaved
                                              with XhoI and separated on a Sephacryl S-500 column.
                                                                   5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was clearly below the sample was clearly below the sample was clearly below the sample was clearly below to the blunt ends.
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N yoelii yoelii cDNA clone PYCJN11 5' end,
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                                                                                                                                                                                                           Contact: Debopam Chakrabarti
Department of Molecular Biology
University of Central Florida
Orlando, FL 32816-2360
Tel: 407 384 2061
Fax: 407 384 3095
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T18122 T18122
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                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malaria parasite P. falciparum
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/clone_lib="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
/note="Vector: Lambda ZAP II; Site_1: EcoR I;
                                                         /clone="0676c"
                                                                          /strain="Dd2"
/db_xref="taxon:5833"
                                                                                                                                                   Location/Qualifiers
                                                                                                                   ∕organism="Plasmodium
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No. 1.6e-09;
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RESULT 32
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                                                                                                                                                                                                   Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of
4444 Forest Park Parkway, Box
                                                                                                                                                                                                                                                                                                                                            Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marram, Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D.
                                                              Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
obtaining a clone please contact: L. David Sibley
                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                (sibley@borcim.wustl.edu), Washington University Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malaria parasite P. fa
Plasmodium falciparum
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BQ451205.1 GI:21254317
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35 c 35 g 98 t l others
Location/Qualifiers
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RESULT 33
BQ577302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACTTTTCGATGGTATTTTCTGCAGTTCCTCTAACTTCTTAGGAATATCATTCTTATTA 121
                                                                                                                                                                                                                                                                                      Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marran, M., Hiller, L., Martin, J., Wylle, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D. Washu Plasmodium EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   805//302 352 bp mRNA linear EST 19-JUN-2002 PfEST0abl7c05.yl plasmodium talciparum 3D7 asexual cDNA plasmodium
                    Library was constructed by Debopam Chakrabarti DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley
                                                                                                                                                                Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                               Unpublished (2001)
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(sibley@borcim.wustl.edu), Washington University
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314 286 1810
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/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
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/db_xref="taxon:5833"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' similar to TR:Q9UAI8 Q9UAI8 SURFACE PROTEIN-1;
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                                                                                                                                                                St. Louis, MO 63108, USA
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Matches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 bp mRNA linear EST 30-AL 0325c3 cbsPfHB3.1, Debopam Chakrabarti Plasmodium falciparum clone 0325c 5', mRNA sequence.
                                                                                                                                                                                                               Department of Molecular Biology University of Central Florida Orlando, FL 32816-2360
                                                                                                                                                                                                                                                                                                                                                Chakrabarti,D., Reddy,G.R., Dame,J.B., Almira,E.C., Laipis,P.J., Ferl,R.J., Yang,T.P., Rowe,T.C. and Schuster,S.M. Ferl,R.J., Yang,T.P., Rowe,T.C. and Schuster,S.M. Analysis of Expressed Sequence Tags from Plasmodium Falciparum Mol. Biochem. Parasitol. 66, 97-104 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                Contact: Debopam Chakrabarti
                                                                                                                                                                                                                                                                                                                               95075403
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                                                                                                                                                               Fax: 407 384 3095
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                                                                                                    il: dchak@pegasus.cc.ucf.edu
primer: T3.
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/note="vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
XhoI; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum 3D7 infected
erythrocytes by the acidic guanidinium-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT Tract
mRNA isolation system (Promega, WI) using streptavidin
Magnesphere particles. Directional CDNA libraries were
constructed by oligo d(T) priming of poly(A)+ RNA (5mg)
into EcoRI and XhoI sites of 1 ZapII vector using the Zap
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the ExAssist helper phage
(Stratagene), the phagemids were precitptated with PEG
8000 and extracted with phenol/chloroform. Phagemid DNA
was electroporated into DH10B cells."
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
                                                                              Location/Qualifiers
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/db_xref="taxon:5833"
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70.4%;
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                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entamoeba histolytica.
Entamoeba histolytica
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                                                                                                                                                 Class: shotgun
                                                                                                                                                                                                          Email: bjloftus@tigr.org Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 878)
Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
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BH153470
                                                                                                                                                                     primer: M13-Forward
                                                                                                     quality sequence start: 16 quality sequence stop: 840
                                                                                                                                                                                                                                                      301 838 0208
301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBlueScript SK(+); PolyA+ RNA, from asynchronous blood stage parasites of the cloned Honduran HB3 isolate cultured in vitro, was reverse transcribed using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ligated to the cDNA ,and it was cleaved with Xho I. Prepared fragments were ligated into EcoR I + Xho I double-digested pBlueScript SK(+), and transformed I \times III + IIII = III
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XL1-Blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="cbsPfHB3.1, Debopam Chakrabarti"
/lab_host="E. coli XL1-Blue"
/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7%;
62.0%;
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Pred. No. 4.5e-08;
0; Mismatches 75
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                                                                                                                                                                                                               Entamoeba
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Parasite Genomics The Institute for

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JOURNAL
                                                                                             AUTHORS
                                                                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3385 TCTAAGCTCGAAGGCAAGCTGAAGGACAACCTGGAGCAAGAAGAAGA 3433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 AAGAACAACCAAAACAAGAAGAAGAAACTCCTCTCGTTGAAGAAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AATCAAAACAAGAAGAACAACCACAACAAGAAGAAGTACAAGAATCAAAACAAGAAGAAC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234;
                                                                                                          Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 483)
                                                                                                                                                                                                                                                                                     BM165179 EST567702 PyBS Plasmodium mRNA sequence.
                 Plasmodium yoelii EST project at Unpublished (2001)
                                                                 Carlton, J.M., Dally, T.M., Long, C.A., Bergman, L.W., Fraser, C.M. and Carucci, D.J.
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EST.
Contact:
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/note="Vector: pHOS1; Site_1: BSt I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Jane Carlton
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Pred. No. 1.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                              483 bp mRNA linear EST 04-DEC-2001 yoelii yoelii cDNA clone PYCM147 5' end,
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1.9e-07;
nes 229;
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139;
                                                                                                                                                      EST.
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
                                                                                 Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                        BM167609 FST570132 PyBS Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone info, please contact the Malaria Research Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                            BM167609
BM167609.1 GI:17300841
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Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                  Plasmodium yoelii yoelii.
                                                                                                                                                                                                                  mRNA sequence.
                                                                (bases 1 to 703)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated CDNA was precipitated and ligated to Size-fractionated CDNA was precipitated and ligated to MybriZAP arms directionally using EcoRI-XhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RMA was isolated using the guandinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blc
collected from BALB/cByJ mice infected with Py17XL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated."
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Pred. No. 3.8e-07;
0; Mismatches 100; Indels
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                                            Vaidya, A.B
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Best Local Similarity
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361 TACAAAAGGTTGTCGAAGTCTTAGAAAAACGAGTTTCTACATTAAAGAAAAATGATGCCA
                                                  893 CCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACCCCTCAAGAAGAATGAAAATA 952
                                                                                                         301
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                                                                                                                                                            AACCTGAAGGTAACGAAGATTGCAATGACGCTAGTTGTGATAGCGATAAATATAATAAAA 300
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA isolated using oligo(dT)-cellulose chromatography.

First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
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/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and isolated using the guanidinium isothiocyanate method, and
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                                                                                           TTCACTAACTTCGTGAAATCTAAAGCCGATGATATCAACTCTCTTAACGATGAATCTAAA 2967
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Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 769)
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The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
Tel: 301-530-9319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii EST project at TIGR Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser, C.M. and Carucci, D.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: carlton@tigr.org
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/lab_host="E. coli XL-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood
collected from BALB/CByJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose collumns. Total RNA was
isolated using the guanidinium isothlocyanate method,
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1 (bases 1 to 1147)
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Class: BAC ends
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Fax: 215-898-8780
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University of Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feng, J., Dewar, K.,
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/organism="Arabidopsis thaliana"
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CAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAA
                                                                                    CATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAAATAAGAA 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 w. Gude Dr.,
Tel: 2404533151
Fax: 2404534580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM656118
17000687387385 A.Gam.ad.
19600449658190 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Celera Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African malaria mosquito
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                                                                                                                                                                                                                                                300
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HoltRA@celera.com
                                                                                                                                                                                                                                                 D
                                                                                                                                                                                                                                             /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)." 7 t
                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome)
                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="A.Gam.ad.cDNA1"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                              /clone="19600449658190"
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                                                                                                                                                                       Score 77.2; DB 13;
Pred. No. 9.9e-07;
0; Mismatches 198;
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.cDNA1 Anopheles
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGCACGAGAAAGAGATCAAAGAGATCGCCAAAAACCATTAAGTTCAACA 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
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Contact: Jane Carlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Âlveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 344) Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,Ā.B., Fraser,C.M. and Carucci,D.J.
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BM159366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
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                                                                                                                           /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Pyl7xL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRT. XhoI cleaved arms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carlton@tigr.org
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                                                                           After packaging, the phagemid vector (pAD-GAL4) excised from the HybriZAP vector and plasmid DNA
                                                     isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="17XL"
/db_xref="taxon:73239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Plasmodium yoelii yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                         59 g
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m yoelii
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                                                                                                       (pAD-GAL4) was
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RESULT 42
AZ813205
LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                    seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0080 row: C column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reil
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 540)
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.
                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic musculus C57BL/6J (male) was obtained fr
                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                         Laboratory Mouse DNA Resource
                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                   /clone="UUGC2M0080C24"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    .540
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57.9%;
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10kb plasmid UUGClM library Mus musculus genomic
C24 F, DNA sequence.
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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3.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 20-FEB-2001
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                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAAGTTCAACAT 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM415494 948 bp mRNA linear ES OP20570 Mixed Stage EST's from Globodera pallida, the
                                                    Email: warthog@unity.ncsu.edu
GT11-4PCN_F_H07_PCN_4_F_060.ab1
Location/Qualifiers
                                                                                                                                                Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7616; Raleigh, NC 27695, USA
                                                                                                                                                                                                                              Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. Mixed Stage EST's from Globodera pallida, the Unpublished (2001)
                                                                                                                                                                                                                                                                                                         Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                                                                                            Contact: Opperman, C
                                                                                                                                                                                                                                                                                                                                                                   Globodera pallida.
                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                       BM415494
BM415494.1 GI:18382210
                                                                                                                                                                                                                                                                                                                                                                                                                                             nematode Globodera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil47321.41 gbj.AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicallin resistance."
/organism="Globodera pallida"
/db_xref="taxon:36090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%;
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No. 6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 28-JAN-2002
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                               GAAAAAGCTGCTGAACGAGATCTATGATTCCAAATTCAACAATAACATCGACCTGACCAAC 1533
                                                                                                                               AGTGACAAGAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCACTAAAGAGTAT 1473
                                                                                                                                                                                 AGAAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGAAGAAAATTGAG 1413
                                                                                                                                                                                                                                                                TTGATTAACCCCTTCGATTATACGAAAGAACCCTCTAAGAATATCTACACAGACAATGAG 1353
                                                                                                                                                                                                                                                                                                                                TACCCTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGAC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGACACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAGACCATAGACAAAAATAAGAAT 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCCAGCCAACTCTGGGAACACCCCCTAACACGCTGCTGGACAAGAACAAGAAGATAGAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode" /note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted." a 89 c 20 g 744 t 79 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%;
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                                                                                                                                                                                                                                                                                  631 AAGATCAGAGCCAACGAGTTGGACGTATTGAAGAAGTTGGTCTTCGGATATCGCAAGCCT
                                                                                                                                                                                                                                                                                                                                   Local
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                             TATTANCAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCATAGAC
                                                                                        AATGCAACCAAGGAGGAAGAAAGAAGAAGTTGTACCAGGCCCAGTACGACCTGTCCATC
                                                                                                                                          ACCATCGAGAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACCATAGACAAAAATAAG
                                                                                                                                                                                                                    362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 BE420745 18 HWM002.B02 ITEC HWM Barley HWM002.B02, mRNA sequence.
BE420745 BE420745 GI:9418588
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Menzinger Str. 67
Fax: 49 30 171683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="HWM002.B02"
/clone_lib="ITEC HWM Barley Leaf Library"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare"
/cultivar="Barke"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescriptSK(~); 850 bp average insert
size."
                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="14 day old"
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                        Contact: Shaying | Zhao Department of Eukaryotic Genomics
                                                                                                                                                                                         GSS.
                                                                                                                                                                                                                  DNA sequence.
BH040136
                                                 Unpublished (1999)
Other_GSSs: RPCI-24-255A23.TJ
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                Mus musculus
                                                                                                                                                                             house mouse.
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           Institute for Genomic
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c Research
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            Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                               mRNA sequence.
BM170771
BM170771.1 GI:17304003
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                                                                                                                               EST573294 PyBS Plasmodium
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
(bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
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/clone="RPCI-24-255A23"
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/strain="C57BL/6J"
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Fraser,C.M. and Carucci,D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: ADF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: carlton@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/lab_host=E. coli XL-1 Blue*
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the guanidinium isothicyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dcTp. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with NhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to Hybrilap arms directionally using EcoRI NhoI cleaved arms.
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                                                    GATGATGATGAAGAAGAAGAAGATGATGAAGATGATGAAGACGATGAAGACGAC 246
                                                                               CATCGACCTGACCTTCGAGAAAATGATGGGAAAACGGT---ACTCTTACAAAGTGGA 1574
                                                                                                                                 GAAGAAGATGAAGATGAAGATGAAGACGATGAAGACGACGAATATGAATTAGAA
                                                                                                                                                                        TATCACTAAAGAGTATGAAAAGCTGCTGAACGAGATCTATGATTCCAAAATTCAACAATAA 1517
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High quality sequence stop: E
Location/Qualifiers
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ENTEK30TR Entamoeba histolytica
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The Institute for Genomic Research
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from
HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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/note="Vector: pHOS1; Site_1: Bat I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole general recommendation projects.
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/db_xref="taxon:5759"
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
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BJ420171 Dictyostelium discoideum cDNA library,
discoideum cDNA clone ddv38p08 5', mRNA sequence
BJ420171
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EST.
                                                                                                                                                                                                                                                             Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                             National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                         stage
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1 (bases 1 to 544)
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                                                                                                                                                                                                                                                 81-559-81-6855
                                                                                                                                                                                                                 tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                     /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddv38p08"
                                                                          /dev_stage="Growth
39 c 94 g
                                                                                                        /clone_lib="Dictyostelium
/sex="mat A"
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              Score 68.4; DB 13; Pred. No. 0.0001;
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                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0265 row: I column: 2
                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                               University of Utah Genome Center 
University of Utah
                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C:, Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0265124"
                                                                                Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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purified. The sheared, auaptored into adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. Tage 145 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                       was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarnse gel
                                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114)gblaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from the musculus C57BL/6J (male) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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736 AAAAAGAATAAGAAGACCATCGAGAAACATTAACGAGCTGATCGAAGAATCCAAAAAAGACC
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AAGAACAAGAAGATAGAGGAGCACGAGAAAGAGA 1069
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                           TACGACCTGTCCATCTATAACAAACAGCTTGAAGAAGCCCATAACCTCATCAGCGTACTG
                                                                                                                                                                                               ATAGACAAAAATAAGAATGCAACCAAGGAGGAAGAAAAGAAGAAGTTGTACCAGGCCCAG
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Roest-Crollius,H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                           Dasilva, C., Bouneau, L., Fisher, C.
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                                                                                                                                                                                               MSMACYAASAAWASCAAAAABACATAAAAAAAAAAAAAAAWBKAAAAAAAAAAATHTYA 449
                                                                                                                                                                                                                            AGCACGAGAAAGAGATCAAAGAGATCGCCAAAACCATTAAGTTCAACATAGATTCTCTCT 1114
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ACCCTCTGTCTTATAACGATATCAACAACGCTCTCAACGAGCTCAATAGCTTCGGTGACT 1294
                                                              AAARAGAAAGGGAGNADDAGAAAAAAAAAATACTAYTAYGABAHCAATDAAAAAAAAAAAA
                                                                                             CCGCCAAAGTCGAGACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGT 1234
                                                                                                                              337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Tetraodon nigroviridis DNA sequence
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/db_xref="taxon:99883"
/clone="225N09"
/clone_lib="G"
/note="Genoscope sequence ID : COAGZ
PUC-Ori"
a 30 c 22 g 759 t 69 c
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Pred. No. 0.00014;
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AGAAAATTGAGAGTGACAAGAAAAGTTACGAAGACCGCAGCAAAAGTCTAAACGATATCA 1462
                                                           CAGACAATGAGAAGAAGAAGTTTATCAACGAAATCAAGGAGAAGATCAAAATTGAGAAGA 1402
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                                                                                                                                                                                                                   162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyostelium.

1 (bases 1 to 494)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the
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BJ360881 Dictyostelium discoideum
discoideum cDNA clone ddc8k12 5',
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Dictyostelium discoideum
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Location/Qualifiers
                                                                                                                                                                                                                                                                                           /dev_stage="Culmination stage"
129 c 34 g 48 t
                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:44689"
/clone="ddc8k12"
/clone_lib="Dictyostel
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Dictyostelium
/strain="AX4"
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                                                                                                     ACAAGATCCTACGAAATCTGTTCAAATACCAAAAGTTCCTTATCCAAATGGTATTGTATA
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                                                                                                                                                                                                                                                                             238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Junichi Watanabe
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.
FULL-malaria: a database for a full-length enriched cDNA library
from human malaria parasite, plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
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                                                                                                                                                                                                                                                                                                                                              /clone="xPPn5428"
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/dev_stage="erythrocytic stage"
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/dev_stage="erythrocytic stage"
                                                                                                                                                                                                                                                                                                                                                                                                        /strain="3D7"
/db_xref="taxon:36329"
                                                                                                                   -GACAAAGGAATCAACCGAACCTAATGAATATCCCAATGGTGTGACGTA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Plasmodium falciparum
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AATAACAACAATAACAACAACAACAACAATRACAACAACAATRACAGCRATAACAACAAT 268
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                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS02156 827 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 224F10 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Bernot, A., Fizames, C., Wincker, P., Brottier Saurin, W. and Weissenbach, J. Human gene number estimate provided by gend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; genome survey sequence. Tetraodon nigroviridis.
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Direct Submission
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Bouneau, L., Billault, A.,
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                                                                                       Conservative
                                                                                                                                                                                                                                            /clone="224F10"
/clone_lib="G"
/note="Genoscope sequence
                                                                                                                                                                                                                                                                                                                /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Pred. No. 0
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Brottier,P., Quetie
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Quetier,F.,
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AGENCOURT_8929072 NIH_MGC_40
5', mRNA sequence.
BQ931326
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information ca found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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                                                                                                                                                                                                                                                                late: LLCM2670 row: i column:
igh quality sequence stop: 297.
Location/Qualifiers
/tissue_type="carcinoma, cell line"
/lab_host="DHIOB (phage=resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="Organ: prostate; Vector: pOTB7; Sites using the birectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1020 Col=16 Row=G, DNA sequence. AZ191902 AZ191902.1 GI:8375081 GSS.
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Class: BAC ends
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Tel: (626) 395-8421
Fax: (626) 793-3047
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California Institute of Technology
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AAGCCCATAACCTCATCAGCGTACTGGAGAAGCGCCCATAGACACCCTCAAGAAGAATGAAA
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Determination of this BAC-end sequence was
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                                                                                                                                                                                                              Dictyostelium discoideum Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. 1 (bases 1 to 626) Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                       BJ426817 bictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv60i07 5', mRNA sequence.
                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                      stage
                                                                                                                                                                                                                                                                                                                                         вJ426817
                                                                                                                                                                    Unpublished (2002)
                                                                                                                                                                                                                                                                                         Dictyostelium
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                                                                                                                                                                                                    length cDNA of Dictyostelium discoideum at the vegetative
                                                                                 Yata, Mishima,
81-559-81-6856
                                                                 81-559-81-6855
                             tshini@genes.nig.ac.jp.
Location/Qualifiers
/organism="Dictyostelium
                                                                                                                                                                                                                                                                                                                          GI:19344253
                                                                                                                                                                                                                                                                                         discoideum.
                                                                                                    Shizuoka
                                                                                                  411-8540,
discoideum"
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RESULT 58
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Best Local Similarity
Matches 242; Conserv
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 783)
                                                                                                                                                                                                                                 CNSO11L2 . 783 bp
Drosophila melanogaster genome sur
BACN06P17 of DrosBAC library from
£ly), genomic survey sequence.
AL100400
AL100400.1 GI:5612011
Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Seq Submitted (23-JUL-1999) Genoscope - Centre National de Seq 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the European Drosophila Genome Project http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster
                                                                                                                                                                                                                      GSS
                                                                                                            Genoscope
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/db_xref="taxon:44689"
/clone="ddv60107"
/clone_lib="Dictyostelium"
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38 c 104 g 42
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Pred. No. 0.00051;
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survey sequence SP6 end
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                                                                                                                                                                          CNS07ABZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
                                                                                      Debaryomyces hansenii.
Debaryomyces hansenii
                                                                                                                    GSS.
                                                                                                                                              Debaryomyces hansenii, genomic survey sequence. AL436389
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
                              Souciet, J.L., Aigle, M., Artiguenave, F.,
                                                                                                                               AL436389.1 GI:12219802
                                                          Saccharomycetales; Saccharomycetaceae;
                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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/plasmid="pBeloBAC11"
/note="end : SP6"
a 58 c 155 g
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BACN06P17"
                                            1 to 897)
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41.7%; Pred. No. 0
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                                                         AAGCTCACCAAAGCTCTTAAGTATATGGAGGACTATTCTCTGCGGAACATTGTTGTGGAG 1692
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/db_xref="taxon:4959"
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Mismatches

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others

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Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                        2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lepingle, A., Casaregola, S., Neuveglise, C., Bon, E., N
Artiquenave, F., Wincker, P. and Gaillardin, C.
Genomic exploration of the hemiascomycetous yeasts:
Debaryomyces hansenii var. hansenii
FEBS Lett. 487 (1), 82-86 (2000)
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Genomic exploration of the hemiascomycetous yeasts: 1. A set o yeast species for molecular evolution studies
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submission
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